

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 18, 2003, 20:56:26 ; Search time 86 Seconds
(without alignments)
5091.303 Million cell updates/sec

Title: US-09-383-579C-9

Perfect score: 992
Sequence: 1 gaataacttaacaacattgc.....aacacaaacgcgaacgac 992

Scoring table: IDENTITY NUC
Gapop 10-0, Gapext 1.0

Searched: 569978 seqs, 220691566 residues

Total number of hits satisfying chosen parameters: 1139956

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

*look for patents
w/ good bases that
supply a suggestion &
using seeds to
improve word
quality*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	681	68.6	681	2	US-08-440-517A-1
2	681	68.6	681	3	US-09-092-160-1
3	276.4	27.9	537	2	US-08-845-539-5
4	276.4	27.9	537	4	US-09-362-642-5
5	262.6	26.5	727	1	US-07-885-970A-6
6	262.6	26.5	727	1	US-08-298-687A-6
7	262.6	26.5	727	1	US-08-530-797-5
8	262.6	26.5	727	1	US-08-298-829-6
9	262.6	26.5	727	2	US-08-787-335-5
10	256.6	25.9	2415	1	US-07-885-970A-26
11	256.6	25.9	2415	1	US-08-298-687A-26
12	256.6	25.9	2415	1	US-08-298-829-26
13	251.6	25.4	702	2	US-08-845-539-1
14	251.6	25.4	702	4	US-09-362-642-1
15	242.8	24.5	501	2	US-08-845-539-3
16	242.8	24.5	501	4	US-09-362-642-3
17	92	9.3	279	4	US-09-313-294A-1276
18	68	6.9	7218	1	US-08-232-463-14
19	46.6	4.7	2614	4	US-09-004-056-1
20	46.6	4.7	4177	3	US-09-023-082A-23
21	40.2	4.1	289	3	US-09-007-005-17
22	40.2	4.1	289	3	US-09-244-796-17
23	38.6	3.9	53526	3	US-08-658-136-2
24	38.6	3.9	53526	3	US-08-658-136-1
25	38	3.8	20966	4	US-09-984-880-3
26	37.6	3.8	1664976	4	US-08-916-421B-1
27	37.4	3.8	248	3	US-09-007-005-32

C 28	37.4	3.8	248	3	US-09-244-796-32	Sequence 32, Appl
C 29	37.4	3.8	277	3	US-09-007-005-3	Sequence 3, Appl
C 30	37.4	3.8	277	3	US-09-244-796-3	Sequence 3, Appl
C 31	37.4	3.8	99500	4	US-09-798-096-10	Sequence 10, Appl
C 32	37	3.7	580073	4	US-08-545-528D-1	Sequence 1, Appl
C 33	36.8	3.7	1305	4	US-09-516-143A-1	Sequence 1, Appl
C 34	36.8	3.7	246240	2	US-08-724-394A-20	Sequence 20, Appl
C 35	36.8	3.7	246240	2	US-08-724-394A-21	Sequence 21, Appl
C 36	36.8	3.7	246240	2	US-08-724-394A-22	Sequence 22, Appl
C 37	36.6	3.7	5852	1	US-07-867-106-2	Sequence 2, Appl
C 38	36.2	3.6	1762	3	US-08-851-843A-3	Sequence 3, Appl
C 39	36.2	3.6	1762	3	US-08-974-549A-115	Sequence 15, App
C 40	36.2	3.6	1762	3	US-08-854-050-3	Sequence 3, Appl
C 41	36.2	3.6	1762	4	US-09-430-323-3	Sequence 3, Appl
C 42	36.2	3.6	72604	4	US-09-268-992-7	Sequence 7, Appl
C 43	36.2	3.6	72604	4	US-09-657-474-7	Sequence 7, Appl
C 44	36	3.6	152331	3	US-09-128-155-16	Sequence 16, Appl
C 45	36	3.6	176373	3	US-09-128-155-17	Sequence 17, Appl

ALIGNMENTS

RESULT 1
US-08-440-517A-1
Sequence 1, Application US/08440517A
Patent No. 5959082
GENERAL INFORMATION:
APPLICANT: COSGROVE, DANIEL J.;
APPLICANT: GUILTINAN, MARK;
APPLICANT: SCHERBAN, TATYANA;
APPLICANT: SHI, JUN
TITLE OF INVENTION: PURIFIED EXPANSIN PROTEINS
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: INTELLECTUAL PROPERTY OFFICE, THE
ADDRESS: PENNSYLVANIA STATE UNIVERSITY
STREET: 113 TECHNOLOGY CENTER
CITY: UNIVERSITY PARK
STATE: PENNSYLVANIA
COUNTRY: UNITED STATES OF AMERICA
ZIP: 16802-7000
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: NEC 286
OPERATING SYSTEM: DOS
SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/440,517A
FILING DATE:
CLASSIFICATION: 530
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 681
TYPE: NUCLEIC ACID
STRANDEDNESS: SINGLE
TOPOLOGY: UNKNOWN
US-08-440-517A-1
Query Match 68.6%; Score 681; DB 2; Length 681;
Best Local Similarity 100.0%; Pred. No. 2e-197;
Matches 681; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

*all looked at
marked up
9(✓)*

QY 223 GACTACGGTGGCTGGGACGCGGCGCCACCTTTATGCTGGTGCACGATCTGGC 282
DB 1 GACTACGGTGGCTGGGACGCGGCGCCACCTTTATGCTGGTGCACGATCTGGC 60
QY 283 ACCATGGGTGGACCTTGGGTATGGAAATTATACAGCCAGGGTATGCGACGAACAGC 342
DB 61 ACCATGGGTGGACCTTGGGTATGGAAATTATACAGCCAGGGTATGCGACGAACAGC 120
QY 343 GTGGCGGTGACGACCTGGGCTATTTAACAATGATGAATTAGTGTGCTCTTCAATG 402

APPLICATION NUMBER: US/08/845,539
FILING DATE: 25-Apr-1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Baerlan, Kevin L.
REGISTRATION NUMBER: 34,774
REFERENCE/DOCKET NUMBER: 023070-078200US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 537 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 1..537
OTHER INFORMATION: /product= "melon CmEx1"
US-08-845-539-5

Query Match 27.9%; Score 276.4; DB 2; Length 537;
Best Local Similarity 71.4%; Pred. No. 2.4e-74;
Matches 380; Conservative 0; Mismatches 146; Indels 6; Gaps 1;

QY 248 ACCGACCTTTTATGAGTGTGATGACCATCTGCGACCATGGGTGGAGCTTTGGGTATG 307
DB 5 ACGCACGTTTATGAGGAGGAGCGATCTTCCGAAACATGGGTGGGTGGGTATG 64
QY 308 GGAATTTATACAGCCAGGATATGACAGAACAGGTGGCGCTGAGCACTGGCTATTTTA 367
DB 65 GCAATCTCTACAGCCAGGCTATGCGCTCAACACAGCTGCTTTAGTACTCTTTCTTCA 124
QY 368 ACAATGATTAAGTTGTGTGCTTCTTCAAAATGACTTGTACAAACGACCTTAATGT 427
DB 125 ACAATGCTCAGCTGTGTGCTTCTTCAAAATGACTTGTACAAACGACCTTAATGT 184
QY 428 GCGTCCGGGAA-----CTATTAGGTCATCGCACCAACTTTGGCCCTCTTAACCTTG 481
DB 185 GCAATCTCTGAGCCCTTGTATCTTCAATACCGCTACCAATTTTGTCCCTTAACCTTG 244
QY 482 CTCCTCTTAACAACATGATGATGATGACCACTCTCTCAACACCTTGAACATGAGCTG 541
DB 245 CTCCTCTTAACAACATGATGATGATGACCACTCTCTCAACACCTTGAACATGAGCTG 304
QY 542 AGCTGCTCTTCTTCAAAATGCTCAATACCGAGCTGTATGTCCTCCGTCTCTTGTGA 601
DB 305 TGCTTATGTTCTCAAGATGCTGATACCGCGCTGGAATCGAATCGTCTTACCGCC 364
QY 602 GGGTACCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 661
DB 365 GGGTTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 424
QY 662 ACCCTGTTTGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 721
DB 425 ATTGGTGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 484
QY 722 GGTCTGCAACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 773
DB 485 GATCAACAACCGGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 536

RESULT 4
US-09-362-642-5
Sequence 5, Application US/09362642
Patent No. 6350935
GENERAL INFORMATION:
APPLICANT: Bennett, Alan B.
APPLICANT: Rose, Jocelyn K.C.
APPLICANT: The Regents of the University of California
TITLE OF INVENTION: Fruit-Specific and Ripening Regulation Expansin Genes

TITLE OF INVENTION: to Control Fruit Texture and Softening
FILE REFERENCE: 023070-078210US
CURRENT APPLICATION NUMBER: US/09/362,642
CURRENT FILING DATE: 1999-07-27
NUMBER OF SEQ ID NOS: 8
SOFTWARE: Patentln Ver. 2.1
SEQ ID NO 5
LENGTH: 537
TYPE: DNA
ORGANISM: Cucumis melo
FEATURE:
NAME/KEY: CDS
LOCATION: (1)..(537)
OTHER INFORMATION: melon expansin (CmEx1) partial cDNA clone
US-09-362-642-5

Query Match 27.9%; Score 276.4; DB 4; Length 537;
Best Local Similarity 71.4%; Pred. No. 2.4e-74;
Matches 380; Conservative 0; Mismatches 146; Indels 6; Gaps 1;

QY 248 ACCGACCTTTTATGAGTGTGATGACCATCTGCGACCATGGGTGGAGCTTTGGGTATG 307
DB 5 ACGCACGTTTATGAGGAGGAGCGATCTTCCGAAACATGGGTGGGTGGGTATG 64
QY 308 GGAATTTATACAGCCAGGATATGACAGAACAGGTGGCGCTGAGCACTGGCTATTTTA 367
DB 65 GCAATCTCTACAGCCAGGCTATGCGCTCAACACAGCTGCTTTAGTACTCTTTCTTCA 124
QY 368 ACAATGATTAAGTTGTGTGCTTCTTCAAAATGACTTGTACAAACGACCTTAATGT 427
DB 125 ACAATGCTCAGCTGTGTGCTTCTTCAAAATGACTTGTACAAACGACCTTAATGT 184
QY 428 GCGTCCGGGAA-----CTATTAGGTCATCGCACCAACTTTGGCCCTCTTAACCTTG 481
DB 185 GCAATCTCTGAGCCCTTGTATCTTCAATACCGCTACCAATTTTGTCCCTTAACCTTG 244
QY 482 CTCCTCTTAACAACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 541
DB 245 CTCCTCTTAACAACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 304
QY 542 AGCTGCTCTTCTTCAAAATGCTCAATACCGAGCTGTATGTCCTCCGTCTCTTGTGA 601
DB 305 TGCTTATGTTCTCAAGATGCTGATACCGCGCTGGAATCGAATCGTCTTACCGCC 364
QY 602 GGGTACCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 661
DB 365 GGGTTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 424
QY 662 ACCCTGTTTGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 721
DB 425 ATTGGTGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 484
QY 722 GGTCTGCAACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 773
DB 485 GATCAACAACCGGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 536

RESULT 5
US-07-885-970A-6
Sequence 6, Application US/07885970A
Patent No. 5495070
GENERAL INFORMATION:
APPLICANT: John, Maliyakal E.
TITLE OF INVENTION: GENETICALLY ENGINEERING COTTON
NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS:
ADDRESSER: Nicholas J. Seay, Quarles & Brady
STREET: P.O. Box 2113, First Wisconsin Plaza
CITY: Madison
STATE: Wisconsin
COUNTRY: USA
ZIP: 53701
COMPUTER READABLE FORM:

```

1      MEDIUM TYPE: Floppy disk
2      COMPUTER: IBM PC compatible
3      OPERATING SYSTEM: PC-DOS/MS-DOS
4      SOFTWARE: Microsoft Word
5      CURRENT APPLICATION DATA:
6      APPLICATION NUMBER: US/07/885,970A
7      FILING DATE: 19920518
8      CLASSIFICATION: 435
9      PRIOR APPLICATION DATA:
10     APPLICATION NUMBER: US 07/617,239
11     FILING DATE: 21-NOV-1990
12     PRIOR APPLICATION DATA:
13     APPLICATION NUMBER: US 07/253,243
14     FILING DATE: 04-OCT-1988
15     ATTORNEY/AGENT INFORMATION:
16     NAME: Seay, Nicholas J.
17     REGISTRATION NUMBER: 27,386
18     TELECOMMUNICATION INFORMATION:
19     TELEPHONE: (608) 283-2478
20     TELEFAX: (608) 251-5139
21     INFORMATION FOR SEQ ID NO: 6:
22     SEQUENCE CHARACTERISTICS:
23     LENGTH: 727 base pairs
24     TYPE: NUCLEIC ACID
25     STRANDEDNESS: double
26     TOPOLOGY: linear
27     MOLECULE TYPE: cDNA
28     HYOTHETICAL: NO
29     ANTI-SENSE: NO
30     ORIGINAL SOURCE:
31     ORGANISM: Gossypium hirsutum
32     STRAIN: Coker 312
33     DEVELOPMENTAL STAGE: 10 day old fiber cells
34     TISSUE TYPE: fiber cells
35     IMMEDIATE SOURCE:
36     LIBRARY: CCKP10
37     CLONE: B12
38     US-07-885-970A-6

```

Query Match	26.5%	Score 262.6;	DB 1;	Length 727;
Best Local Similarity	72.5%;	Pred. No. 4.5e-70;		
Matches 340;	Conservative 0;	Mismatches 129;	Indels 0;	Gaps 0

Oy	442	TTTAGGGACACTGGCCACCACCAATTTTGGCCCTCCCAACTTTGGCTCTCCCTTAACAACAACTGGT	501
Db	1	ATAACCGTGACAGCCACCACCACTTTTGTCCACCTTAACCTAATGCTTTATCTAGTGACCAATGGC	60
Oy	502	GGATGGTGACCCCTCTCTCCAAACACTTTCGACATGGCTGAGGCTCGCTCTTCAATC	561
Db	61	GGGTGGTGCAATCCCCCAACGAGAACCTTTGATTTGGCCGGAACCGGCAATCTTGGGGATA	120
Oy	562	GCTCAATACCGAGCTGGTATCGTCCCGCTCTCTTTGTAAGGATACATGATGAGAGAA	621
Db	121	GCAGATATATCGAGCTGGATCGCTCCCTGTTATGTTACAGAAAGGCTGTCATGTGGAAGAA	180
Oy	622	GGTGAGTGAGGTTTATACATCAATGCCCACCTACTATTCAACCTCGTTTGTGACACAAAC	681
Db	181	GGAGGCAATCAGGTATACCCATGAAATGACATTTGTACTTCAACATGGTGTGATTAACGAAC	240
Oy	682	GTCCGTGGCGCAGCGGACGTCACACTCTGTGTCGATTAAGGGGCTCGAACTGGATGGCA	741
Db	241	GTGGAGGGGGCAGGGGATTAACGTACGTGTCATCAAGGGTTCCAGAACAGATGGCTA	300
Oy	742	TTCATGTCTAGAAATTTGGGGCCAAAACCTGGCAAGCAACAACTATCTCAATGGCCAAAGC	801
Db	301	CCTAATGTCAGAAATTTGGGGCCAAAACCTGGCAGAGCAATGCTTAACCTTAACGACAAAGC	360
Oy	802	CTTTCCTTTCAAGTCACTCTTATGTAAGTGTGCGACTCTCACTGCTCTATAATCTCGTTCT	861
Db	361	CTCTCTTTTAAGTGACTGCCAGCCGATGGCAGGACTATCAACAAGCTTAATGTAAGTCT	420
Oy	862	TCCATTGGCAATTTGGCCAAACCTATGAAGGCGCTCAATTTCAAAACA	910

Db 421 GCTGGTTGGCAATTCCGACAAACTTTGAAGGAGGCCAGTTTAAAGACA 469

```

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60
61
62
63
64
65
66
67
68
69
70
71
72
73
74
75
76
77
78
79
80
81
82
83
84
85
86
87
88
89
90
91
92
93
94
95
96
97
98
99
100
101
102
103
104
105
106
107
108
109
110
111
112
113
114
115
116
117
118
119
120
121
122
123
124
125
126
127
128
129
130
131
132
133
134
135
136
137
138
139
140
141
142
143
144
145
146
147
148
149
150
151
152
153
154
155
156
157
158
159
160
161
162
163
164
165
166
167
168
169
170
171
172
173
174
175
176
177
178
179
180
181
182
183
184
185
186
187
188
189
190
191
192
193
194
195
196
197
198
199
200
201
202
203
204
205
206
207
208
209
210
211
212
213
214
215
216
217
218
219
220
221
222
223
224
225
226
227
228
229
230
231
232
233
234
235
236
237
238
239
240
241
242
243
244
245
246
247
248
249
250
251
252
253
254
255
256
257
258
259
260
261
262
263
264
265
266
267
268
269
270
271
272
273
274
275
276
277
278
279
280
281
282
283
284
285
286
287
288
289
290
291
292
293
294
295
296
297
298
299
300
301
302
303
304
305
306
307
308
309
310
311
312
313
314
315
316
317
318
319
320
321
322
323
324
325
326
327
328
329
330
331
332
333
334
335
336
337
338
339
340
341
342
343
344
345
346
347
348
349
350
351
352
353
354
355
356
357
358
359
360
361
362
363
364
365
366
367
368
369
370
371
372
373
374
375
376
377
378
379
380
381
382
383
384
385
386
387
388
389
390
391
392
393
394
395
396
397
398
399
400
401
402
403
404
405
406
407
408
409
410
411
412
413
414
415
416
417
418
419
420
421
422
423
424
425
426
427
428
429
430
431
432
433
434
435
436
437
438
439
440
441
442
443
444
445
446
447
448
449
450
451
452
453
454
455
456
457
458
459
460
461
462
463
464
465
466
467
468
469
470
471
472
473
474
475
476
477
478
479
480
481
482
483
484
485
486
487
488
489
490
491
492
493
494
495
496
497
498
499
500
501
502
503
504
505
506
507
508
509
510
511
512
513
514
515
516
517
518
519
520
521
522
523
524
525
526
527
528
529
530
531
532
533
534
535
536
537
538
539
540
541
542
543
544
545
546
547
548
549
550
551
552
553
554
555
556
557
558
559
560
561
562
563
564
565
566
567
568
569
570
571
572
573
574
575
576
577
578
579
580
581
582
583
584
585
586
587
588
589
590
591
592
593
594
595
596
597
598
599
600
601
602
603
604
605
606
607
608
609
610
611
612
613
614
615
616
617
618
619
620
621
622
623
624
625
626
627
628
629
630
631
632
633
634
635
636
637
638
639
640
641
642
643
644
645
646
647
648
649
650
651
652
653
654
655
656
657
658
659
660
661
662
663
664
665
666
667
668
669
670
671
672
673
674
675
676
677
678
679
680
681
682
683
684
685
686
687
688
689
690
691
692
693
694
695
696
697
698
699
700
701
702
703
704
705
706
707
708
709
710
711
712
713
714
715
716
717
718
719
720
721
722
723
724
725
726
727
728
729
730
731
732
733
734
735
736
737
738
739
740
741
742
743
744
745
746
747
748
749
750
751
752
753
754
755
756
757
758
759
760
761
762
763
764
765
766
767
768
769
770
771
772
773
774
775
776
777
778
779
780
781
782
783
784
785
786
787
788
789
790
791
792
793
794
795
796
797
798
799
800
801
802
803
804
805
806
807
808
809
810
811
812
813
814
815
816
817
818
819
820
821
822
823
824
825
826
827
828
829
830
831
832
833
834
835
836
837
838
839
840
841
842
843
844
845
846
847
848
849
850
851
852
853
854
855
856
857
858
859
860
861
862
863
864
865
866
867
868
869
870
871
872
873
874
875
876
877
878
879
880
881
882
883
884
885
886
887
888
889
890
891
892
893
894
895
896
897
898
899
900
901
902
903
904
905
906
907
908
909
910
911
912
913
914
915
916
917
918
919
920
921
922
923
924
925
926
927
928
929
930
931
932
933
934
935
936
937
938
939
940
941
942
943
944
945
946
947
948
949
950
951
952
953
954
955
956
957
958
959
960
961
962
963
964
965
966
967
968
969
970
971
972
973
974
975
976
977
978
979
980
981
982
983
984
985
986
987
988
989
990
991
992
993
994
995
996
997
998
999
1000
1001
1002
1003
1004
1005
1006
1007
1008
1009
1010
1011
1012
1013
1014
1015
1016
1017
1018
1019
1020
1021
1022
1023
1024
1025
1026
1027
1028
1029
1030
1031
1032
1033
1034
1035
1036
1037
1038
1039
1040

```

Query March	26.5%	Score 263.6	DB 1	Length 727
Best Local Similarity	72.5%	Pred. No. 4.5e-70		
Matches 340; Conservative	0	Mismatches 129	Indels 0	Gaps 0

QY 442 ATTAGGGTACAGCCACCAACCTTTGGCCCTCTAACTTTGGCTCCCTAACACAAAGT 501

Db 1 ATACCGTACAGCCACCAACCTTTGGCTCAGCTAACTATGCTTATCTAGACAAATGCG 60

QY 502 GGAATGTGCAACCCCTCTCTCCACACTTGCAGATAGTGAAGCTGCTCTTCAAAATC 561

Db 61 GGGTGTGCAATCCCCACAGAAACACTTTGATTTGGCGGAACGGCACTTTTCCGATA 120

QY 562 GCTCAATACCGAGCTGTATGCTCCCCGCTCTCTTCTGATAGGTACATGTATGAAGAA 621

APPLICANT: Brill, Winston J.
TITLE OF INVENTION: GENETICALLY ENGINEERED COTTON PLANTS
TITLE OF INVENTION: FOR ALTERED FIBER
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSEE: Quarles and Brady
STREET: P.O BOX 2113
STREET: FIRST WISCONSIN PLAZA
CITY: MADISON
STATE: WISCONSIN
COUNTRY: U.S.A.
ZIP: 53701
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette - 3.50 inch, 800Kb storage
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh
SOFTWARE: Microsoft Word 4.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/787,335
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/530,797
FILING DATE:
APPLICATION NUMBER: US 07/253,243
FILING DATE: 04-OCT-88
ATTORNEY/AGENT INFORMATION:
NAME: Nicholas J. Seay

REFERENCE/DOCKET NUMBER: 1122990245
INFORMATION FOR SEQ ID NO: 5
SEQUENCE CHARACTERISTICS:
SEQUENCE: 107

```

? TYPE: nucleic acid
? STRANDEDNESS: single
? TOPOLOGY: linear
? MOLECULE TYPE: cDNA to mRNA
? HYPOTHETICAL: no
? ANTI-SENSE: no
? ORIGINAL SOURCE:
? ORGANISM: Goseyplum hireutum
? STRAIN: Coker 312
? DEVELOPMENTAL STAGE: 10 day old fiber cells
? TISSUE TYPE: fiber cells
? IMMEDIATE SOURCE:
? LIBRARY: CKEB10
? CLONE: B12
? US-08-787-335-5

Query Match      26.5%   Score 262.6;  DB 2;   Length 727;
Best Local Similarity 72.5%;  Fred. No. 4.5e-70;
Matches 340;  Conservative 0;  Mismatches 129;  Indels 0;  Gaps 0

442 ATTAGGGTCATCGCACCAACCTTTGGCCCTCCCTACTTTCCTCCCTCAACAACAATGCT 501
|||
Db      1 ATPACCGTAGACGCCACCACTTTGTTCACCTTAACATGCTTATATATAGCAANTGC 60

502 GGATGGTCGACCCCTCTCTCTCCACACTTGCACATGGCTGAGCTGCTTCTTCAATC 561
|||
Db      61 GGGTGGTCGAAATCCCCCAGCAACACTTTGATTTGGCCGACCGGCAATCTTGGCGATA 120

QY      562 GCTCAATATCCGAGCTGATGTCGTCGCCGTCCTTTGTGAGGGAGCATTATGAAAGAA 621
|||
Db      121 GGAGATATATCGAGCTGGAATGTCCTCTGTTATGTTCCAAAGGGTGTCATGTGAAAGAA 180

```

Db 181 GGAGCATCAGGTACCCCTGATGAGATTCGTCTTCAACATGTTTATATACCAAC 244

Qy 682 GTCCGTGGCGCAGGGGAGCGTCCACTCTGTGTGATTAAGGGAGTCCGAATCGATGGCAA 744

Db 241 GTGGGAGGGGCAAGGGATTTAACTGTCACTGTCCATCAAGGTTCCAGAAACAGATGGCTA 304

QY 742 TCATGCTAGAAATTTGGGGCCAAACTGGCAAGCAACTATCTCAATGGCCAAAGC 801
DB 301 CCTATGTCAGAAATTTGGGGCCAAACTGGCAAGCAACTATCTCAATGGCCAAAGC 360
QY 802 CTTTCCTTTGAAGCAGCTTAGAGTGTGGCACTGCTCACTGCTTAATCTGTTCT 861
DB 361 CTCTCTTTTAAGGATGCTGCGAGGAGGAGCACTATACAGGCTCAATGATGTGCT 420
QY 862 TCCAAATGGCAATTTGGCCAAACTATGAAAGGCCCTCAATCTTAACCA 910
DB 421 GCTGTTGGCAATTCGAGCAAACTTTGAAGAGGCCAGTTTAAAGACA 469

RESULT 10
US-07-885-970A-26
Sequence 26, Application US/07885970A
Patent No. 5495070
GENERAL INFORMATION:
APPLICANT: John, Maliyakal E.
TITLE OF INVENTION: GENETICALLY ENGINEERING COTTON
NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS:
ADDRESSEE: Nicholas J. Seay, Charles & Brady
STREET: P.O. Box 2113, First Wisconsin Plaza
CITY: Madison
STATE: Wisconsin
COUNTRY: USA
ZIP: 53701
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Microsoft Word
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/885,970A
FILING DATE: 19920518
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/617,239
FILING DATE: 21-NOV-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/253,243
FILING DATE: 04-OCT-1988
ATTORNEY/AGENT INFORMATION:
NAME: Seay, Nicholas J.
REGISTRATION NUMBER: 27,386
TELECOMMUNICATION INFORMATION:
TELEPHONE: (608) 283-2478
TELEFAX: (608) 251-5139
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
LENGTH: 2415 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHEtical: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Gossypium barbadense
STRAIN: Sea Island
IMMEDIATE SOURCE:
LIBRARY: EMBL SI
CLONE: STB12
US-07-885-970A-26

Query Match 25.9%; Score 256.6; DB 1; Length 2415;
Best Local Similarity 64.6%; Pred. No. 5.9e-68;
Matches 458; Conservative 0; Mismatches 174; Indels 77; Gaps 2;

QY 279 TGGCAACATGGGAGGAGCTTGTGGGATTTGGAATTTATACAGCCAGGATGGACGAA 338
DB 976 TGTATTATAGGGGAGGAGCTTGTGTATGAAACCTGTACAGTCAGGATATGGAACGAG 1035

QY 339 CACGCTGGCCCTGAGCAGCTGCGATTTTAACAATGATTAAGTGTGTGC-TTGCTTGC 397
DB 1036 CAGAGCAGCTTTAGAGCATGCTCATTTTCAACATGCTTAGCTGCGGTGACGCTACG 1095
QY 398 AAATGACTTTTACAAAGCAGCTTAATAGTGCTTCCGGAACTTATAGGATCACTGCA 457
DB 1096 AGCTCGGATCAACAATGATCTCAATGATGATTAAGTCAACCAATACCGTGAACGCA 1155
QY 458 CCAACTTTTGGCTTCTTCAATTTGCTTCTCCCTTAACAACATGATGATGATGCAACCTC 517
DB 1156 CCAACTTTTGGCTTCTTCAATTTGCTTCTCCCTTAACAACATGATGATGATGCAACCTC 1215
QY 518 CTCTCCAACTTTCGACATGCTGAGCTGCTGCTTCTTCAATAGCTCAATACGAGCTG 577
DB 1216 CAGAGAACCTTTGATTTTGGCCGAAACGCGATTTCTGAGATCGCGAAATTCGACTG 1275
QY 578 GATTCGTCCCG-----TCTCTTTGTTGGGTACATGATGACAA 589
DB 1276 GAATCGTCCCTGTTATGTTGAGAGGAGTGAATTAACATCAATCATCACACTC 1335
QY 590 -----TCTCTTTGTTGGGTACATGATGACAA 621
DB 1336 TTTAAGGATATGTTAACTGTGGGTGTTTAACTTTTGGAGGTGTCATGTGAGAA 1395
QY 622 GGTGAGTGAAGTTTCAATCAATGAGCACTCAATCAACCTGTTTGTATGACAAAC 681
DB 1396 GAGAGCATGAGTACACATGATGATGATGATGATGATGATGATGATGATGATGATG 1455
QY 682 GTGAGTGGCGCAGGCGACGTCACCTGTGTGATGAAGGGGTCTCGAATGATGACAA 741
DB 1456 GTGAGGAGGGCAGGGGATATTAACGTAGTGTTCATCAAGTGTCAAAAACGATGCTA 1515
QY 742 TCATGCTTGAATTTGGGGCCAAACTGGCAAGCAACTATCTCAATGGCCAAAGC 801
DB 1516 CCTATGTCAGAAATTTGGGGCCAAACTGGCAAGCAACTATCTCAATGGCCAAAGC 1575
QY 802 CTTTCCTTTCAAGTCACTTAGTATGATGATGATGATGATGATGATGATGATGATGATG 861
DB 1576 CTCTCTTTTCAAGTCACTTAGTATGATGATGATGATGATGATGATGATGATGATGATG 1635
QY 862 TCCAAATGGCAATTTGGCCAAACTATGAAAGGCCCTCAATCTTAACCA 910
DB 1636 GCTGTTGGCAATTCGAGCAAACTTTGAAGAGGCCAGTTTAAAGACA 1684

RESULT 11
US-08-298-687A-26
Sequence 26, Application US/08298687A
Patent No. 5521078
GENERAL INFORMATION:
APPLICANT: John, Maliyakal E.
TITLE OF INVENTION: GENETICALLY ENGINEERING COTTON
NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS:
ADDRESSEE: Nicholas J. Seay, Charles & Brady
STREET: P.O. Box 2113, First Wisconsin Plaza
CITY: Madison
STATE: Wisconsin
COUNTRY: USA
ZIP: 53701
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Microsoft Word
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/298,687A
FILING DATE:
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/617,239

FILING DATE: 21-NOV-1990
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/253,243
 FILING DATE: 04-OCT-1988
 ATTORNEY/AGENT INFORMATION:
 NAME: Seay, Nicholas J.
 REGISTRATION NUMBER: 27,386
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (608) 283-2478
 TELEFAX: (608) 251-5139
 INFORMATION FOR SEQ ID NO: 26:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 2415 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: double
 TOPOLOGY: linear
 MOLECULE TYPE: DNA (genomic)
 HYPOTHETICAL: NO
 ANTI-SENSE: NO
 ORIGINAL SOURCE:
 ORGANISM: Gossypium barbadense
 STRAIN: Sea Island
 IMMEDIATE SOURCE:
 LIBRARY: EMBL-SI
 CLONE: SIB12
 US-08-298-687A-26

Query Match 25.9%; Score 256.6; DB 1; Length 2415;
 Best Local Similarity 64.6%; Pred. No. 5.9e-68;
 Matches 458; Conservative 0; Mismatches 174; Indels 77; Gaps 2;

279 TGGACCATGGGTGAGCTTGGGTATGGAATTATACAGCCAGGATGACGAA 338
 976 TGTTCATAGAGGGGAGCTTGTGTATGGAACCTGTACAGCAAGGATGGAACGAG 1035
 339 CACGGTGGGGCTGAGAGCTGCGCTATTTAACATGATTAAGTGTGGTGC-TTGGCTGG 397
 1036 CACAGAGCTTTGAGAGCTGACCTTTTCAACAAATGGCTGAGCTGGGCTGACTGCTAGC 1095
 398 AATGACTGTACAAACGACCTTAAATGTGCTCCGGGAACTATTAGGGTCACTGCCA 457
 1096 AGCTCGGGGACAAATGATTCCTCAATGGTCAATTAGTGAACCATTAACGCTGACGCA 1155
 458 CCAACTTTTGGCCCTCTAACTTTGCTCTCCCTTACAAACAATGGTGAATGCAACCCCTC 517
 1156 CCAACTTTTGGCCCTCTAACTTTGCTCTCCCTTACAAACAATGGTGAATGCAACCCCTC 517
 518 CTCTCAACACTGACATGGGTGAGCTGCGCTCCCTTCAAAATCGCTCAATACGAGCTG 577
 1216 CACGAGAACCTTTGATTTGGCCGAACCGGCAATTCCTGACATCGGGAATATGAGCTG 1275
 578 GTATCGTCCCG-----589
 1276 GAATGCTCCCTGTATGTTGAGAGGTGATTAACATCAATCAATCATCACATC 1335
 590 -----TCTCTTTCGTAGGTACCATGTATGAAGAA 621
 1336 TTTAAGTATGTTAACTGTGGGTGTTTAACTTTTGGCGGGTGTGATGTGAAGAAA 1395
 622 GTGGAGTGGGTTTCAATCAATGAGCACTCACTCACTCACTCACTCACTCACTCACTCA 681
 1396 GAGAGGATCAGGTACACCAATGAGCACTTCTACTTCAACAGGTGTTGATTAACAC 1455
 682 GTGCGTGGCGCAGGCGACGTCCACTGTGTGATTAAGGGGTCTCGAATGAGTGA 741
 1456 GTGGAGGGGCGAGGAGTATTAAGTCACTGATTCATCAAGTGTCCAAAACAGGATGGCTA 1515
 742 TCCATGCTAGAAATTGGGGCCAAAACCTGGCAAGCAACATATCTCAATGCGCAAGC 801
 1516 CCAATGCTCAGAAATTGGGGCCAAAACCTGGCAAGCAACATATCTCAATGCGCAAGC 1575
 802 CTTTCTTTCAATCACTTATGATGATGATGATGATGATGATGATGATGATGATGATGAT 861

Db 1576 CTCTCTTCAAGTACGTCCAGGATGAGCAAGTATACAAACTATGATGCT 1635
 QY 862 TCCAAATGGCAATTTGGCCAAACCTATGAGCCCTCAATTATTAACCA 910
 Db 1636 GCTGTTGCAATTCGACAACTTTGAAGAGGCGCAGTTTAAAGACA 1684

RESULT 12
 US-08-298-829-26
 Sequence 26, Application US/08298829
 Patent No. 5620882.

GENERAL INFORMATION:
 APPLICANT: John, Maliyakal E.
 TITLE OF INVENTION: GENETICALLY ENGINEERING COTTON
 TITLE OF INVENTION: PLANTS FOR ALTERED FIBER
 NUMBER OF SEQUENCES: 33
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Nicholas J. Seay, Charles & Brady
 STREET: P.O. Box 2113, First Wisconsin Plaza
 CITY: Madison
 STATE: Wisconsin
 COUNTRY: USA
 ZIP: 53701

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Microsoft Word
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/298,829
 FILING DATE: 19-OCT-1994

CLASSIFICATION: 800
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/885,970
 FILING DATE: 18-MAY-1992
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/617,239
 FILING DATE: 21-NOV-1990
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/253,243

REGISTRATION NUMBER: 27,386
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (608) 283-2478
 TELEFAX: (608) 251-5139
 ATTORNEY/AGENT INFORMATION:
 NAME: Seay, Nicholas J.

INFORMATION FOR SEQ ID NO: 26:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 2415 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: double
 TOPOLOGY: linear
 MOLECULE TYPE: DNA (genomic)
 HYPOTHETICAL: NO

ANTI-SENSE: NO
 ORIGINAL SOURCE:
 ORGANISM: Gossypium barbadense
 STRAIN: Sea Island
 IMMEDIATE SOURCE:
 LIBRARY: EMBL-SI
 CLONE: SIB12
 US-08-298-829-26

Query Match 25.9%; Score 256.6; DB 1; Length 2415;
 Best Local Similarity 64.6%; Pred. No. 5.9e-68;
 Matches 458; Conservative 0; Mismatches 174; Indels 77; Gaps 2;

279 TGGACCATGGGTGAGCTTGGGTATGGAATTATACAGCCAGGATGACGAA 338
 976 TGTTCATAGAGGGGAGCTTGTGTATGGAACCTGTACAGTCAAGGATGGAACGAG 1035
 339 CACGGTGGGGCTGAGAGCTGCGCTATTTAACATGATTAAGTGTGGTGC-TTGGCTGG 397

Db	1036	CACAGCAGCTTTGAGCACTTGCACTTTTCAACAATGGCTTGAAGCTGCGGTGCACTGCTACG	10955
Qy	398	AAATGACTTGTACAAACGACCCTTAATAGTGTGCTTCCGGGAACATAATGAGGTCACTGGCA	457
Db	1096	AGCTCCGGTGCAACAATGATCCTCAATGGTGATTAATGCAACATAACCGTGAAGCA	11555
Qy	458	CCAACTTTTGGCCCTCTTAACCTTTGCTTCCTCAACAACAATGGTGGATGGTGAACCTTC	517
Db	1156	CCAACTTTTGGCCCTCTTAACCTTTGCTTCCTCAACAACAATGGTGGTGGTGAACCTTC	12155
Qy	518	CTTCCCAACACTTGGACATGGGTGAGCGTGCCTTCCTCAATGAGTCTCAATACGAGTGT	577
Db	1216	CACGAGAACACTTTGATTTTGGCCGACCGGCAATCTTGCAGATCGCGGAATATGAGCTG	12755
Qy	578	GTATCGTCCCG-----	589
Db	1276	GAATCGTCCCTGTTATGTTCAAGAGTGTGTGAATAAATCAATTCATCATCACTC	13355
Qy	590	-----TTCCTCTTTCGTAGGGTACCATGATATGAGAA	621
Db	1336	TTTAAGTATGTATAACTGTGTGGGTGTATACTTTTGACGGGTGTCACTGTGTAAGAA	13955
Qy	622	GGTAGAGTGTATTAACAATGAATGGCCACTCATCTCAACCTCGTTTATCAACAAC	681
Db	1396	GGAGGATCAAGTACACCATGAATGAATGCAATTCGATCTTCAACATGATTTAATAAC	14555
Qy	682	GTCGGTGGCGAGCGAGCGTCACTCTGTGTCGATTAAGGGGTCTCGAATGTGACAA	741
Db	1456	GTGGAGGGGGGAGGGGATATTAACGTCAAGTGTCACTCAAGTGTCCAAACAGATGGCTA	15155
Qy	742	TCCATGTCTAAGAAATTTGGGGCCAAATCTGGCAAGAACAACTATCTCAATGGCCAAAGC	801
Db	1516	CCATATGTCAGAAATTTGGGGCCAAATCTGGCAAGAACAACTATCTCAATGGCCAAAGC	15755
Qy	802	CTTTCCTTTCAAGTCACTCTTAATGATGTGTGCACTCTCACTGCTTAATCTGTTCT	861
Db	1576	CTCTCTTTCAAGTCACTCTTAATGATGTGTGCACTCTCACTGCTTAATCTGTTCT	16355
Qy	862	TCCATTTGGCAATTTGGCCAAACCTATGAAGGCTCTCAATCTTAACCA	910
Db	1636	GCTGTTGGCAATTTGGCCAAACCTATGAAGGCTCTCAATCTTAACCA	1684

RESULT 13
 US-08-845-539-1
 : Sequence 1, Application US/08845539
 : Patent No. 5929303
 : GENERAL INFORMATION:
 : APPLICANT: Bennett, Alan B.
 : APPLICANT: Rose, Jocelyn K.C.
 : TITLE OF INVENTION: Fruit-Specific and Ripening-Regulation
 : TITLE OF INVENTION: Expandin Genes to Control Fruit Texture and Softening
 : NUMBER OF SEQUENCES: 8
 : CORRESPONDENCE ADDRESS:
 : ADDRESSEE: Townsend and Townsend and Crew LLP
 : STREET: Two Embarcadero Center, Eighth Floor
 : CITY: San Francisco
 : STATE: California
 : COUNTRY: USA
 : ZIP: 94111-3834
 : COMPUTER READABLE FORM:
 : MEDIUM TYPE: Floppy disk
 : COMPUTER: IBM PC compatible
 : OPERATING SYSTEM: PC-DOS/MS-DOS
 : SOFTWARE: Patentin Release #1.0, Version #1.30
 : CURRENT APPLICATION DATA:
 : APPLICATION NUMBER: US/08/845,539
 : FILING DATE: 25-APR-1997
 : CLASSIFICATION: 435
 : ATTORNEY/AGENT INFORMATION:
 : NAME: Baastian, Kevin L.
 : REGISTRATION NUMBER: 34,774

```

; REFERENCE/DOCKET NUMBER: 023070-078200US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 702 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 28..702
; OTHER INFORMATION: /product= "tomato Lxex1"
US-08-845-539-1

Query Match 25.4%; Score 251.6; DB 2; Length 702;
Best Local Similarity 67.2%; Pred.No. 9.8e-67;
Matches 391; Conservative 0; Mismatches 179; Indels 12; Gaps 2

Oy 229 GGTGGCTGGCGAGACGGCCAGCCACCTTTATGATGTGTGTGACGATCTGGCACATG 288
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Oy 118 GGTTCATGGGAACTGCACATGCTACATTTTACGGCGGAAGTATGCTTCTGGAACAATG 177
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Oy 289 GGTGAGCTTGTGGGATATGGGAATTTATACAGCCAAAGGATATGACAGCAACGCTGCG 348
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Oy 178 GGCAGTGCTGTGTATATGAAATTTATACAGCCAAAGATACGGAGTTACACAGCACGA 237
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Oy 349 CTGAGCACTGGCTATTTACATATGATTAAGTTGTGTGCTTGCTTGAATAACTTGT 408
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Oy 238 CTGAGTACTGCTTTGTTTAAACAAATGATTAAGTTGTGAGCTCTTTTGAACCTTAATGT 297
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Oy 409 ACAACGACCCCT-----AATGGTGCTTCGGGAA-----CTATTAGGGTCACTGGCC 456
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Oy 298 ACAATATCTCTTAATGGAAATGATGTCTTCTGAAACCTTCATTTTAATCACAGCT 357
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Oy 457 ACCAATTTTGGCCCTCTTAATCTTTGCTCTCCCTAACAACAATGATGATGTGCACCCCT 516
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Oy 358 ACCAATTTTGGCCCAACAAATTAAGCGGTGCCAATGACATGGTGCTGTGTAACCT 417
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Oy 517 CCTCTCCAACTTGCACATGAGCTGAGCTGCTCTTCTTCAAATGCTCAATACCGAGCT 576
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Oy 418 CCTGCGCCCTCACTTGTGACCTGCTATGCTTAATGTTCTCAAACTTGCTCACTACCGCCT 477
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Oy 577 GGTATGTCGCCCGCTCCTTTCGTAAGGGATCATGATGAAGAAAGGTGAGTGAAGT 636
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Oy 478 GGCAATGTCTCTGTAACCTTAATGCGAGATCCCAATGCCGAAGCAAGGAGATCAGATTT 537
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Oy 637 ACAATCAATGGCCACTCATATCTTCAACTCGTTTGTATCACAAAAGTGTGAGCGCAGGC 696
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Oy 538 ACCATCAATGGATTCGTTACTTCACTTAAGTGTGATCAAGAAATGATGACAGGTGACGG 597
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Oy 697 GACGTCACCTGTGTGATTAAGGGGCTTCGAACCTGATGCAATCCATGTCTAAGAAAT 756
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Oy 598 GATATTATTAAAGTTTGGGTAAAGGAACAAGCAAAATTTGGAATTCATTGAGCGGTAT 657
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Oy 757 TGGGGCCAAACTGGCAAGCAACACTATCTCAATAGGCCAA 798
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Oy 658 TGGGGAACAATTTGGCAATCAAAATGCGGTTTAACTGTCA 699
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

RESULT 14
US-09-362-642-1
; Sequence 1, Application US/09362642
; Patent No. 6350935
; GENERAL INFORMATION:
; APPLICANT: Bennet, Alan B.
; APPLICANT: Rose, Jocelyn K.C.
; TITLE OF INVENTION: The Regents of the University of California
; TITLE OF INVENTION: Fruit-Specific and Ripening Regulation Expansin Genes
; FILE REFERENCE: 023070-078210US

```


Fri Dec 19 09:37:21 2003

us-09-383-579c-9.rml

Page 11

Search completed: December 18, 2003, 22:33:40
Job time : 91 secs

1

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Comugen Ltd.

OM nucleic - nucleic search, using bw model

Run on: December 18, 2003, 19:50:59 ; Search time 314 Seconds
(without alignments)
8528.161 Million cell updates/sec

Title: US-09-383-579C-9

Perfect score: 992
Sequence: 1 gaataactaacacaactgc.....aacacaaacgcgaacgac 992

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2552756 seqs, 1349719017 residues

Total number of hits satisfying chosen parameters: 5105512

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

1: N_Geneseq_19Jun03.*
2: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1980.DAT.*
3: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1981.DAT.*
4: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1982.DAT.*
5: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1983.DAT.*
6: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1984.DAT.*
7: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1985.DAT.*
8: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1986.DAT.*
9: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1987.DAT.*
10: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1988.DAT.*
11: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1989.DAT.*
12: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1990.DAT.*
13: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1991.DAT.*
14: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1992.DAT.*
15: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1993.DAT.*
16: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1994.DAT.*
17: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1995.DAT.*
18: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1996.DAT.*
19: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1997.DAT.*
20: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1998.DAT.*
21: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1999.DAT.*
22: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA2000.DAT.*
23: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA2001A.DAT.*
24: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA2001B.DAT.*
25: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA2002.DAT.*
26: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA2003.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	684	69.0	684	24	ABA97161
2	681	68.6	681	17	AA133320
3	676.2	68.2	681	24	ABA97162
4	404.4	40.8	1144	24	AA032964
5	398.8	40.2	1015	21	AA048712
6	398.8	40.2	1016	21	AA040777
7	394.2	39.7	762	24	AB213283
8	377.8	38.1	780	21	AA050628

9	377.8	38.1	1198	21	AA033521	Arabidopsis thalia
10	377.8	38.1	1233	21	AA050633	Arabidopsis thalia
11	366.8	37.0	1236	21	AA040035	Arabidopsis thalia
12	361.8	36.5	687	24	ABA97164	N. tabacum DNA enc
13	360.6	36.4	753	24	AB212286	Arabidopsis thalia
14	360.4	36.3	747	24	AB213264	Arabidopsis thalia
15	360.4	36.3	1324	21	AA047530	Arabidopsis thalia
16	354	35.7	1326	21	AA040169	Arabidopsis thalia
17	351.4	35.4	1212	21	AA045165	Arabidopsis thalia
18	351.4	35.4	1262	21	AA047991	Arabidopsis thalia
19	341.6	34.4	1366	21	AB212284	Arabidopsis thalia
20	341.6	34.4	1319	21	AA044930	Arabidopsis thalia
21	338.4	34.1	1205	21	AA033121	Arabidopsis thalia
22	338.2	34.1	1167	22	AA003713	Tomato seed expans
23	332	33.5	1201	21	AA044975	Arabidopsis thalia
24	321.8	32.4	1276	24	AA032963	Pear expansin 1/2
25	316.6	31.9	1236	21	AA034714	Arabidopsis thalia
26	313.6	31.6	488	21	AA029325	Expansin gene sequ
27	313.4	31.6	824	21	AA042473	Arabidopsis thalia
28	312.8	31.5	1213	22	AA003711	Tomato seed expans
29	301.8	30.4	1293	21	AA037064	Arabidopsis thalia
30	301.2	30.4	774	24	AB213037	Arabidopsis thalia
31	301.2	30.4	1037	21	AA042618	Arabidopsis thalia
32	298.8	30.1	893	24	AB098723	Arabidopsis thalia
33	298.6	30.1	1291	21	AA050400	Arabidopsis thalia
34	287.6	29.0	475	21	AA029326	Expansin gene sequ
35	276.4	27.9	537	20	AA068448	Melon expansin CME
36	270	27.2	410	25	ABX21914	Human GDP-mannose
37	264.8	26.7	1103	22	AA003712	Tomato seed expans
38	262.6	26.5	727	17	AA030255	Cotton fibre cell-
39	262.6	26.5	727	17	AA013037	Cotton fibre-spect
40	262.6	26.5	727	18	AA070044	Cotton fibre spect
41	262.6	26.5	727	18	AA062613	Cotton fibre spect
42	262.6	26.5	727	21	AA035549	CDNA sequence a co
43	256.6	25.9	2415	17	AA030268	Cotton fibre clone
44	256.6	25.9	2415	17	AA013053	Cotton fibre-spect
45	256.6	25.9	2415	18	AA070039	Cotton B12 gene an

ALIGNMENTS

RESULT 1	ABA97161	standard; DNA; 684 BP.
ID	ABA97161	
AC	ABA97161	
XX		
DT	19-APR-2002	(first entry)
XX		
DE	C. sativus DNA encoding S1 expansin homologue.	
XX		
KW	Expansin; S1; cellulose-based textile; cotton; paper recycling;	
KM	paper pulp; plant tissue; papermaking; gene; cucumber; ds.	
XX		
OS	Cucumis sativus.	
PH		
FT	Key	Location/Qualifiers
FT	CDS	1..684
FT		/*tag= a
FT		/partial
FT		/product= "S1 expansin homologue"
FT		/note= "No start codon given"
PN	DE10032630-A1.	
XX		
PD	22-NOV-2001.	
XX		
PF	05-JUL-2000; 2000DE-1032630.	
PR		
PR	16-MAY-2000; 2000DE-1023561.	
XX		
PA	(PARB) BAYER AG.	

FOR (DB)

us-09-3834-506-9.rng

XX Berendes F, Rast HG, Vogt U, Gouloudis C;
 DR WPI; 2002-155755/21.
 DR P-PSDB; AAG80768.

PT Vector encoding an expansin, useful in treatment of cellulosic
 materials for paper recycling, providing large-scale production
 PS Claim 2; Page 11-14; 22pp; German.

CC This invention describes a novel vector (A) comprising (i) nucleic acid
 CC (II) encoding an expansin (II) and (ii) coupled sequences that allow
 CC expression of (I) in microorganisms. The recombinant expansins described
 CC in the invention are used in preparation, treatment and finishing of
 CC cellulose-based textiles (e.g. cotton) or in recycling of paper or for
 CC preparation of pulp from plant tissue, as a substitute for corrosive
 CC chemicals currently used in papermaking. Recombinant methods make
 CC possible large scale production of extensin possible. This sequence
 CC encodes the Cucumis sativus (cucumber) SI extensin homologue described in
 CC the invention.

XX Sequence 684 BP; 163 A; 179 C; 164 G; 178 T; 0 other;

Query Match 69.0%; Score 684; DB 24; Length 684;
 Best Local Similarity 100.0%; Pred. No. 2e-184;
 Matches 684; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX 223 GACTACGGTGGTGGGAGAGCGGCGACGACCTTTATGATGGTGGTGGTGGTGGC 282
 DB 1 GACTACGGTGGTGGGAGAGCGGCGACGACCTTTATGATGGTGGTGGTGGTGGC 60
 XX 283 ACCATGGTGGAGCTTGGGATATGGAATTATACGCAAGGATATGCGACGACG 342
 DB 61 ACCATGGTGGAGCTTGGGATATGGAATTATACGCAAGGATATGCGACGACG 120
 XX 343 GTGGGCTGAGACCTGGCTATTTACATGATTAAGTTGGTGGTGGTGGTGGTGG 402
 DB 121 GTGGGCTGAGACCTGGCTATTTACATGATTAAGTTGGTGGTGGTGGTGGTGG 180
 XX 403 ACTTGTACAAAGACCTTAAATGATGCTTCCGGGAACTATTAAGGCTACGACCA 462
 DB 181 ACTTGTACAAAGACCTTAAATGATGCTTCCGGGAACTATTAAGGCTACGACCA 240
 XX 463 TTTTGGCTCTTACTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 522
 DB 241 TTTTGGCTCTTACTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 300
 XX 523 CAACCTTGGAGATGGCTGAGCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 582
 DB 301 CAACCTTGGAGATGGCTGAGCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 360
 XX 583 GTTCCCGTCTCTTCTGATAGGATACATGATGAAAGAGTGAAGTGTATACATC 642
 DB 361 GTTCCCGTCTCTTCTGATAGGATACATGATGAAAGAGTGAAGTGTATACATC 420
 XX 643 AATGGCACTCACTTCAACCTGTTTGTATCAAAAGCTGGTGGCGGCGAGCTGC 702
 DB 421 AATGGCACTCACTTCAACCTGTTTGTATCAAAAGCTGGTGGCGGCGAGCTGC 480
 XX 703 CACTCTGTGTGATTAAGGGGTCTGAATGATGATGCAATGCTCTGAAATTTGGGG 762
 DB 481 CACTCTGTGTGATTAAGGGGTCTGAATGATGATGCAATGCTCTGAAATTTGGGG 540
 XX 763 CAATACTGGCAAGCAAACTATCTCAATGGGCAAGGCTTTCTTTCAAGTCACTTT 822
 DB 541 CAATACTGGCAAGCAAACTATCTCAATGGGCAAGGCTTTCTTTCAAGTCACTTT 600
 XX 823 AGTATGATGTCGCACTCTCACTGGCTATTAATCTGTTCTTCAATTTGGGCA 882
 DB 601 AGTATGATGTCGCACTCTCACTGGCTATTAATCTGTTCTTCAATTTGGGCA 660
 XX 883 ACCTATGAAGGCGCTCAATTTCTTA 906

DB 661 ACCTATGAAGGCGCTCAATTTCTTA 684

RESULT 2
 AAT13320
 ID AAT13320 standard; DNA; 681 BP.

XX AAT13320;

XX 25-MAR-2003 (updated)
 DT 08-JUL-1996 (first entry)

XX Cucurbit expansin-29 cDNA.

XX Expansin-29; plant cell wall; cellulose; paper recycling; de-inking;
 KW polysaccharide; cucumber; ss.

XX Cucumis sativus var. Burpee Pickler.

XX AUA9540262-A.

XX 04-APR-1996.

XX 06-DEC-1995; 95AU-0040262.

XX 12-MAY-1993; 93US-0060944.

XX 12-MAY-1995; 95US-0440517.

XX 12-MAY-1994; 94AU-0068320.

XX (PENN-) PENN STATE RES FOUND.

XX Cosgrove DJ, McQueen-Mason S;

XX WPI; 1996-201150/21.

XX P-PSDB; AAR94527.

XX Expansin proteins which alter the mechanical strength of

XX poly:saccharide(s) - useful in paper mfr. and recycling

XX Disclosure; Page 30; 60pp; English.

XX A cDNA clone (AAT13320) codes for cucumber expansin-29 (AAR94527),

XX a member of a novel class of proteins that catalyze the extension of

XX plant cell walls and the weakening of the hydrogen bonds in pure

XX cellulose. It was obt. by PCR amplification of cucumber seedling

XX cDNA using primers based on isolated peptide fragments of the protein.

XX The gene can be expressed in bacterial or other systems for use in

XX recombinant expansin prodn. Expression of the gene in transgenic

XX plants may allow alteration of plant growth characteristics, such

XX as useful chemicals.

XX (Updated on 25-MAR-2003 to correct PR field.)

XX (Updated on 25-MAR-2003 to correct PR field.)

XX Sequence 681 BP; 161 A; 179 C; 164 G; 177 T; 0 other;

Query Match 68.6%; Score 681; DB 17; Length 681;
 Best Local Similarity 100.0%; Pred. No. 1.4e-183;
 Matches 681; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX 223 GACTACGGTGGTGGGAGAGCGGCGACGACCTTTATGATGGTGGTGGTGGTGGC 282
 DB 1 GACTACGGTGGTGGGAGAGCGGCGACGACCTTTATGATGGTGGTGGTGGTGGC 60
 XX 283 ACCATGGTGGAGCTTGGGATATGGAATTATACGCAAGGATATGCGACGACG 342
 DB 61 ACCATGGTGGAGCTTGGGATATGGAATTATACGCAAGGATATGCGACGACG 120
 XX 343 GTGGGCTGAGACCTGGCTATTTACATGATTAAGTTGGTGGTGGTGGTGGTGG 402
 DB 121 GTGGGCTGAGACCTGGCTATTTACATGATTAAGTTGGTGGTGGTGGTGGTGG 180

QY 403 ACTGTGACAAAGCAACCTTAATGTCCTTCGGGAACTATTAGGTCACCTCCACCAAC 462
 Db 181 ACTGTGACAAAGCAACCTTAATGTCCTTCGGGAACTATTAGGTCACCTCCACCAAC 240
 QY 463 TTTGGCCCTCTTAATGTCCTTCCTCCCTAACAAATGTCATGTCGAACCTCTCTC 522
 Db 241 TTTGGCCCTCTTAATGTCCTTCCTCCCTAACAAATGTCATGTCGAACCTCTCTC 300
 QY 523 CAACACTTGCACATGTCGTCGACCTGCTCCTTCAATGTCATACCGAGTCGTATC 582
 Db 301 CAACACTTGCACATGTCGTCGACCTGCTCCTTCAATGTCATACCGAGTCGTATC 360
 QY 583 GTCCCGCTCTCTTTCGTAGGATACCATGATGAAAGAGTGAAGTGAAGTTTACATC 642
 Db 361 GTCCCGCTCTCTTTCGTAGGATACCATGATGAAAGAGTGAAGTGAAGTTTACATC 420
 QY 643 AATGGCACTGATCTTCAACCTGTTTGTATCAAAACGTCGGTGGGCGGAGGAGTC 702
 Db 421 AATGGCACTGATCTTCAACCTGTTTGTATCAAAACGTCGGTGGGCGGAGGAGTC 480
 QY 703 CACTGTGTGATTAAGGGGTCTGAACTGGATGGCAATCATGTCATAGAAATTTGGGCG 762
 Db 481 CACTGTGTGATTAAGGGGTCTGAACTGGATGGCAATCATGTCATAGAAATTTGGGCG 540
 QY 763 CAAAACTGGCAAGCAACCACTATCTCAATGCGCAAGGCTTTCCTTCAAGTCACTCTT 822
 Db 541 CAAAACTGGCAAGCAACCACTATCTCAATGCGCAAGGCTTTCCTTCAAGTCACTCTT 600
 QY 823 AGTATGATGTCGACCTTCATCTGCTATATCTGTTCTTCAATTGGCAATTTGGCCAA 882
 Db 601 AGTATGATGTCGACCTTCATCTGCTATATCTGTTCTTCAATTGGCAATTTGGCCAA 660
 QY 883 ACCTATGAAGGCTCAATTC 903
 Db 661 ACCTATGAAGGCTCAATTC 681

RESULT 3
 ID ABA97162 standard; DNA; 681 BP.
 XX ABA97162;
 XX 19-APR-2002 (first entry)
 DT C. sativus DNA encoding expansin csexp1a.
 XX
 DE C. sativus DNA encoding expansin csexp1a.
 XX
 KM Expansin; cellulose-based textile; cotton; paper recycling; csexp1a;
 KW paper pulp; plant tissue; papermaking; gene; cucumber; ds.
 XX
 OS Cucumis sativus.
 XX
 FH Key Location/Qualifiers
 FT CDS 1..681
 FT /*tag= a
 FT /partial
 FT /product= "csexp1a"
 FT /note= "No start or stop codon given"
 XX
 XX DE10032630-A1.
 XX
 XX PD 22-NOV-2001.
 XX
 XX PF 05-JUL-2000; 2000DE-1032630.
 XX
 XX PR 16-MAY-2000; 2000DE-1023561.
 XX
 XX (FARB) BAYER AG.
 XX
 XX PA Berendes F, Raet HG, Vogt U, Gouloudis C;
 XX WPI; 2002-155755/21.
 XX P-PSDB; AAG80769.
 DR

XX Vector encoding an expansin, useful in treatment of cellulosic
 PT materials for paper recycling, providing large-scale production
 PR
 XX Claim 2; Page 14-16; 22pp; German.
 XX
 CC This invention describes a novel vector (A) comprising (i) nucleic acid
 CC (1) encoding an expansin (II) and (ii) coupled sequences that allow
 CC expression of (i) in microorganisms. The recombinant expansins described
 CC in the invention are used in preparation, treatment and finishing of
 CC cellulose-based textiles (e.g. cotton) or in recycling of paper or for
 CC preparation of pulp from plant tissue, as a substitute for corrosive
 CC chemicals currently used in papermaking. Recombinant methods make
 CC possible large scale production of extensins possible. This sequence
 CC encodes the Cucumis sativus (cucumber) extensin, csexp1a, described in
 CC the invention.
 XX
 SQ Sequence 681 BP; 161 A; 178 C; 164 G; 178 T; 0 other;
 Query Match 68.2%; Score 676.2; DB 24; Length 681;
 Best Local Similarity 99.6%; Pred. No. 3,3e-182;
 Matches 678; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 223 GACTACGGGTGGCTGGAGACGGCGACGCCACCTTTATGTCGTGTCGATGTCGTC 282
 Db 1 GACTACGGGTGGCTGGAGACGGCGACGCCACCTTTATGTCGTGTCGATGTCGTC 60
 QY 283 ACCATGGGTGGAGCTTGGGTATGGAAATTTATACGCCAAGGTATGCGACAAACG 342
 Db 61 ACCATGGGTGGAGCTTGGGTATGGAAATTTATACGCCAAGGTATGCGACAAACG 120
 QY 343 GTGGCGGTGAGCACTGGCTATTATTAACATGATGATGTCGTGCTTGGTATG 402
 Db 121 GTGGCGGTGAGCACTGGCTATTATTAACATGATGATGTCGTGCTTGGTATG 180
 QY 403 ACTGTGACAAAGCAACCTTAATGTCCTTCGGGAACTATTAGGTCACCTCCACCAAC 462
 Db 181 ACTGTGACAAAGCAACCTTAATGTCCTTCGGGAACTATTAGGTCACCTCCACCAAC 240
 QY 463 TTTGGCCCTCTTAATGTCCTTCCTCCCTAACAAATGTCATGTCGAACCTCTCTC 522
 Db 241 TTTGGCCCTCTTAATGTCCTTCCTCCCTAACAAATGTCATGTCGAACCTCTCTC 300
 QY 523 CAACACTTGCACATGTCGTCGACCTGCTCCTTCAATGTCATACCGAGTCGTATC 582
 Db 301 CAACACTTGCACATGTCGTCGACCTGCTCCTTCAATGTCATACCGAGTCGTATC 360
 QY 583 GTCCCGCTCTCTTTCGTAGGATACCATGATGAAAGAGTGAAGTGAAGTTTACATC 642
 Db 361 GTCCCGCTCTCTTTCGTAGGATACCATGATGAAAGAGTGAAGTGAAGTTTACATC 420
 QY 643 AATGGCACTGATCTTCAACCTGTTTGTATCAAAACGTCGGTGGGCGGAGGAGTC 702
 Db 421 AATGGCACTGATCTTCAACCTGTTTGTATCAAAACGTCGGTGGGCGGAGGAGTC 480
 QY 703 CACTGTGTGATTAAGGGGTCTGAACTGGATGGCAATCATGTCATAGAAATTTGGGCG 762
 Db 481 CACTGTGTGATTAAGGGGTCTGAACTGGATGGCAATCATGTCATAGAAATTTGGGCG 540
 QY 763 CAAAACTGGCAAGCAACCACTATCTCAATGCGCAAGGCTTTCCTTCAAGTCACTCTT 822
 Db 541 CAAAACTGGCAAGCAACCACTATCTCAATGCGCAAGGCTTTCCTTCAAGTCACTCTT 600
 QY 823 AGTATGATGTCGACCTTCATCTGCTATATCTGTTCTTCAATTGGCAATTTGGCCAA 882
 Db 601 AGTATGATGTCGACCTTCATCTGCTATATCTGTTCTTCAATTGGCAATTTGGCCAA 660
 QY 883 ACCTATGAAGGCTCAATTC 903
 Db 661 ACCTATGAAGGCTCAATTC 681

RESULT 4

ID	Accession	Standard	CDNA	BP
AA032964	AA032964	standard	CDNA	1144 BP
XX	AA032964			
AC	AA032964			
XX				
DT	01-JUL-2002	(first entry)		
XX				
DE	Pear expansin 2 (Exp2) CDNA			
XX				
KM	Pear, cell wall hydrolase; beta-galactosidase; pectin methylesterase;			
KM	PM; beta-Gal; polygalacturonase; PG; expansin; Exp1; expansin2; Exp2;			
KM	fruit ripening; gene expression; transgenic plant; transgenic enzyme;			
XX	gene; ss.			
OS	Pyrus communis			
XX				
TH	Key	Location/Qualifiers		
FT	CDS	83..340		
FT		/*tag= a		
FT		/product= "Pear expansin 2 protein #2"		
FT	CDS	83..850		
FT		/*tag= a		
FT		/product= "Pear expansin 2 protein #1"		
FT		/transl_except= (pos:335..343, aa:leu-asn)		
FT		/transl_except= (pos:353..361, aa:glu-pro)		
FT		/transl_except= (pos:413..421, aa:ser-leu)		
FT		/transl_except= (pos:479..487, aa:gly-ala)		
FT		/transl_except= (pos:767..775, aa:glu-arg)		
FT		/transl_except= (pos:773..781, aa:arg-asn)		
FT		/transl_except= (pos:806..814, aa:trp-leu)		
FT		/note= "All the translational exceptions comprise an in-frame stop codon; CDS does not include stop codon"		
FT		/partial		
XX				
PN	WO200216613-A2			
XX				
PD	28-FEB-2002			
XX				
PF	20-AUG-2001; 2001WO-PT00021			
XX				
PR	22-AUG-2000; 2000PT-0102511			
XX				
PA	(ICAT-) ICAT INST CIENCIA APLICADA E TECNOLOGIA			
XX				
PI	Macias Fonseca SC, Balde A, Soares Pais MS;			
XX				
DR	WPI; 2002-280942/32			
XX				
DR	P-PSDB; AAE20571, AAE20578			
XX				
PT	New beta-galactosidase, pectin methylesterase, polygalacturonase,			
PT	expansin1, and expansin2 proteins and nucleic acids, useful for			
PT	regulating fruit ripening or creating transgenic plants			
XX				
XX	Claim 14; Page 38-39; 45pp; English			
XX				
CC	The present invention relates to novel genes which encode cell wall			
CC	hydrolases such as beta-galactosidase (beta-Gal), pectin methylesterase			
CC	(PME), polygalacturonase (PG) and cell wall proteins such as expansin			
CC	(Exp1) and expansin2 (Exp2) proteins from pear fruit. The nucleic acids			
CC	are useful for regulating fruit ripening and for suppressing endogenous			
CC	beta-Gal, PME, PG, Exp1 and Exp2 genes in any fruit or other plant			
CC	organs, thus modifying the structure of the cell walls of the fruit or			
CC	plant and providing for ripe yet firm fruit and vegetables. The genes			
CC	may be used to screen a cDNA library or a genomic library from any			
CC	species, to inhibit or enhance gene expression or to produce transgenic			
CC	plants. The present sequence is a cDNA encoding pear expansin 2 protein.			
XX				
SQ	Sequence 1144 BP; 325 A; 258 C; 242 G; 319 T; 0 other;			
XX				
Query Match	40.8%; Score 404.4; DB 24; Length 1144;			
Matches	553; Similarity 73.9%; Pred. No. 1e-104; Indels 4; Gaps 3;			

Oy		180	CFTCTCCTTCTCTTCCTTTCTTCTTGCTTCAACCTTCCGCTACTAGCGGTGGCA	233
Dd		121	CTCTGTGTTCTCTTAATCTAACACTGCAGTGTGTAAATTGCTCTTTATGCTACTGGGA	180
Oy		240	GAGCGGCCAACGCCACCTTTATGTGTGTGTGACGCACTTGGCAACAATGGGTAGCTTG	299
Dd		181	AGGCGCTCAAGCCACATTTTACGGTGGCGGTGATGCTTCTGGCAATAAGGAGGACATG	240
Oy		300	TGGGTATGAGGAATTTATACGCCAAGGGTATAGGCAACGAACAGGTGGCGGTAGCAC-TG	350
Dd		241	TGGTATATGGAATTTGTATACGCAAGGAGGTATAGGAACCAACCTCAGCTTTGACACAAG	300
Oy		359	CGGTATTTTAACANTGGATTAAAGTTGTGGTGGCTTGCTTGAATGACTTTGTACAACAGC	418
Dd		301	CATTGTTCACAANTGGCTTTAGCTGTGGTCTTGTGTATGAATAGATGCAACATBACC	360
Oy		419	CTAATATGTGCTCTCCGGGAACATATTAGGGTCACTGCCAACCATTTTGGCTCTTAAT	478
Dd		361	CGAGATATGTGCGCTCCTGGATGCATCATTTGTAAGTGTACAAACTTTTGGCTCTTAAT	420
Oy		479	TTGCTCTCCCTTAACAACAATGSGATGSGTGCACCTCTCTCCAACAATTGCAACTGG	538
Dd		421	TTGCTCAATCCACAACGACATGGCGGATGTGCAATCTCTCTCAGCATTTTGCATTTGG	480
Oy		539	CTGAGCGTCCCTCTCTCAAATCGTCAATACC-GAGCTGGTATC--GTCCCCTCTCT	599
Dd		481	CTGAGCTCTCTCTTCTTGCAAAATGGCCAAATACAGATGTGSAATACAGTCCAGTTTTCT	540
Oy		596	TTGCTATGGGTACCATGTATGAAGAAGGTGAGTGAAGTTTACATCAATAGGCCACTAT	655
Dd		541	TCGAAGAATTAACCTTGTGTGAAGAAAGGAAATTAAGTTTCAACATCAAGGCCACTCT	600
Oy		656	ACTTCAACTCGTTTTGATCACAACGTCGCTGGCGCAGGCGAGTCACTCTGTGTGCA	715
Dd		601	ACTTCAACTCGTTTTGATCACAACGTCGCTGGCGCAGGCGAGTCACTCACTTTTCAA	660
Oy		716	TAAAGGGGTCTGGAACCTGSAATGSCAATCATGTCTAGAAATTTGGGGCCAAAACGTGGCAA	775
Dd		661	TCAAAGGGGTCTGGAACAGGGTGGCAACCATGTCAAGAAATCTGGGGTCAAAACTGGSCAGA	720
Oy		776	GCAACAACATATCTCAATGGCCCAAGGCTTTTCTTTCAAGTCACTCTTAGTATGATGGCA	835
Dd		721	GCAACTCTTAACCTCAATGGCCCAAGGCTCTCTCTTCCAAAGTCAACACAGTGAACGTGAA	780
Oy		836	CTCTCACTGCTATAAATCTGTTCTTCCAAATGGCAATTTGGCCAAACCTATGAGGCC	895
Dd		781	CCGTCAACGAGCTACAACGTCGCGCTGTGTAATGGCAGATTGTGCAGACATTTCCGGGG	840
Oy		896	CTCAATTTCAAAACATATAGCCACAAT 923	
Dd		841	GTCAACTTATAGATATTTCTCTACATT 868	

RESULT 5
 AAC48712
 ID AAC48712 standard; DNA; 1015 BP.

AAC48712;
 18-OCT-2000 (first entry)

Arabidopsis thaliana DNA fragment SEQ ID NO: 58484.
 Arabidopsis thaliana DNA fragment SEQ ID NO: 58484.
 Hybridisation assay; genetic mapping; gene expression control;
 protein identification; signal transduction pathway;
 metabolic pathway; promoter; termination sequence; ss.
 Arabidopsis thaliana.
 EP1033405-AZ.
 06-SEP-2000.

PF 25-FEB-2000; 2000EP-0301439.
PR 25-FEB-1999; 99US-0121825.
PR 05-MAR-1999; 99US-0123180.
PR 09-MAR-1999; 99US-0123548.
PR 23-MAR-1999; 99US-0125788.
PR 25-MAR-1999; 99US-0126266.
PR 29-MAR-1999; 99US-0126785.
PR 01-APR-1999; 99US-0127462.
PR 06-APR-1999; 99US-0128234.
PR 08-APR-1999; 99US-0128714.
PR 16-APR-1999; 99US-0129845.
PR 19-APR-1999; 99US-0130077.
PR 21-APR-1999; 99US-0130449.
PR 23-APR-1999; 99US-0130510.
PR 28-APR-1999; 99US-0130891.
PR 30-APR-1999; 99US-0132048.
PR 30-APR-1999; 99US-0132407.
PR 04-MAY-1999; 99US-0132484.
PR 06-MAY-1999; 99US-0132485.
PR 07-MAY-1999; 99US-0132487.
PR 11-MAY-1999; 99US-0132863.
PR 14-MAY-1999; 99US-0134256.
PR 14-MAY-1999; 99US-0134218.
PR 14-MAY-1999; 99US-0134221.
PR 14-MAY-1999; 99US-0134370.
PR 18-MAY-1999; 99US-0134766.
PR 19-MAY-1999; 99US-0134941.
PR 20-MAY-1999; 99US-0135124.
PR 21-MAY-1999; 99US-0135353.
PR 24-MAY-1999; 99US-0135629.
PR 25-MAY-1999; 99US-0136021.
PR 27-MAY-1999; 99US-0136392.
PR 28-MAY-1999; 99US-0136782.
PR 01-JUN-1999; 99US-0137222.
PR 03-JUN-1999; 99US-0137528.
PR 04-JUN-1999; 99US-0137502.
PR 07-JUN-1999; 99US-0137724.
PR 08-JUN-1999; 99US-0138094.
PR 10-JUN-1999; 99US-0138540.
PR 10-JUN-1999; 99US-0138647.
PR 14-JUN-1999; 99US-0139119.
PR 16-JUN-1999; 99US-0139452.
PR 17-JUN-1999; 99US-0139453.
PR 17-JUN-1999; 99US-0139492.
PR 18-JUN-1999; 99US-0139454.
PR 18-JUN-1999; 99US-0139455.
PR 18-JUN-1999; 99US-0139456.
PR 18-JUN-1999; 99US-0139457.
PR 18-JUN-1999; 99US-0139458.
PR 18-JUN-1999; 99US-0139459.
PR 18-JUN-1999; 99US-0139460.
PR 18-JUN-1999; 99US-0139461.
PR 18-JUN-1999; 99US-0139462.
PR 18-JUN-1999; 99US-0139463.
PR 18-JUN-1999; 99US-0139750.
PR 18-JUN-1999; 99US-0139763.
PR 21-JUN-1999; 99US-0139817.
PR 22-JUN-1999; 99US-0139899.
PR 23-JUN-1999; 99US-0140353.
PR 23-JUN-1999; 99US-0140354.
PR 24-JUN-1999; 99US-0140635.
PR 28-JUN-1999; 99US-0140823.
PR 29-JUN-1999; 99US-0140991.
PR 30-JUN-1999; 99US-0141287.
PR 01-JUL-1999; 99US-0141842.
PR 01-JUL-1999; 99US-0142154.
PR 02-JUL-1999; 99US-0142055.
PR 06-JUL-1999; 99US-0142390.
PR 08-JUL-1999; 99US-0142803.

PR 09-JUL-1999; 99US-0142920.
PR 12-JUL-1999; 99US-0142977.
PR 13-JUL-1999; 99US-0143542.
PR 14-JUL-1999; 99US-0143624.
PR 15-JUL-1999; 99US-0144005.
PR 16-JUL-1999; 99US-0144085.
PR 16-JUL-1999; 99US-0144086.
PR 19-JUL-1999; 99US-0144325.
PR 19-JUL-1999; 99US-0144331.
PR 19-JUL-1999; 99US-0144332.
PR 19-JUL-1999; 99US-0144333.
PR 19-JUL-1999; 99US-0144334.
PR 19-JUL-1999; 99US-0144335.
PR 20-JUL-1999; 99US-0144352.
PR 20-JUL-1999; 99US-0144632.
PR 20-JUL-1999; 99US-0144884.
PR 21-JUL-1999; 99US-0144814.
PR 21-JUL-1999; 99US-0145086.
PR 21-JUL-1999; 99US-0145088.
PR 22-JUL-1999; 99US-0145085.
PR 22-JUL-1999; 99US-0145087.
PR 22-JUL-1999; 99US-0145089.
PR 22-JUL-1999; 99US-0145192.
PR 23-JUL-1999; 99US-0145145.
PR 23-JUL-1999; 99US-0145218.
PR 26-JUL-1999; 99US-0145224.
PR 27-JUL-1999; 99US-0145276.
PR 27-JUL-1999; 99US-0145913.
PR 27-JUL-1999; 99US-0145918.
PR 27-JUL-1999; 99US-0145919.
PR 28-JUL-1999; 99US-0145951.
PR 28-JUL-1999; 99US-0146386.
PR 02-AUG-1999; 99US-0146388.
PR 02-AUG-1999; 99US-0146389.
PR 03-AUG-1999; 99US-0147038.
PR 04-AUG-1999; 99US-0147204.
PR 04-AUG-1999; 99US-0147302.
PR 05-AUG-1999; 99US-0147192.
PR 05-AUG-1999; 99US-0147260.
PR 06-AUG-1999; 99US-0147303.
PR 06-AUG-1999; 99US-0147416.
PR 09-AUG-1999; 99US-0147493.
PR 09-AUG-1999; 99US-0147935.
PR 10-AUG-1999; 99US-0148171.
PR 11-AUG-1999; 99US-0148319.
PR 12-AUG-1999; 99US-0148341.
PR 13-AUG-1999; 99US-0148565.
PR 16-AUG-1999; 99US-0148684.
PR 16-AUG-1999; 99US-0149368.
PR 17-AUG-1999; 99US-0149175.
PR 18-AUG-1999; 99US-0149426.
PR 20-AUG-1999; 99US-0149722.
PR 20-AUG-1999; 99US-0149723.
PR 20-AUG-1999; 99US-0149929.
PR 23-AUG-1999; 99US-0149902.
PR 23-AUG-1999; 99US-0149930.
PR 25-AUG-1999; 99US-0150566.
PR 26-AUG-1999; 99US-0150884.
PR 27-AUG-1999; 99US-0151065.
PR 27-AUG-1999; 99US-0151066.
PR 27-AUG-1999; 99US-0151080.
PR 30-AUG-1999; 99US-0151303.
PR 31-AUG-1999; 99US-0151438.
PR 01-SEP-1999; 99US-0151930.
PR 07-SEP-1999; 99US-0152363.
PR 10-SEP-1999; 99US-0153070.
PR 13-SEP-1999; 99US-0153758.
PR 15-SEP-1999; 99US-0154018.
PR 16-SEP-1999; 99US-0154709.
PR 20-SEP-1999; 99US-0154779.
PR 22-SEP-1999; 99US-0155139.
PR 23-SEP-1999; 99US-0155486.
PR 24-SEP-1999; 99US-0155659.

PR	28-SEP-1999;	99US-0156458.
PR	29-SEP-1999;	99US-0156596.
PR	04-OCT-1999;	99US-0157117.
PR	05-OCT-1999;	99US-0157753.
PR	06-OCT-1999;	99US-0157865.
PR	07-OCT-1999;	99US-0158029.
PR	08-OCT-1999;	99US-0158232.
PR	12-OCT-1999;	99US-0158369.
PR	13-OCT-1999;	99US-0159293.
PR	13-OCT-1999;	99US-0159294.
PR	13-OCT-1999;	99US-0159295.
PR	14-OCT-1999;	99US-0159329.
PR	14-OCT-1999;	99US-0159330.
PR	14-OCT-1999;	99US-0159331.
PR	14-OCT-1999;	99US-0159637.
PR	14-OCT-1999;	99US-0159638.
PR	18-OCT-1999;	99US-0159584.
PR	21-OCT-1999;	99US-0160741.
PR	21-OCT-1999;	99US-0160767.
PR	21-OCT-1999;	99US-0160768.
PR	21-OCT-1999;	99US-0160770.
PR	21-OCT-1999;	99US-0160814.
PR	21-OCT-1999;	99US-0160815.
PR	22-OCT-1999;	99US-0160980.
PR	22-OCT-1999;	99US-0160981.
PR	22-OCT-1999;	99US-0160989.
PR	25-OCT-1999;	99US-0161404.
PR	25-OCT-1999;	99US-0161405.
PR	25-OCT-1999;	99US-0161406.
PR	26-OCT-1999;	99US-0161355.
PR	26-OCT-1999;	99US-0161360.
PR	26-OCT-1999;	99US-0161361.
PR	28-OCT-1999;	99US-0161920.
PR	28-OCT-1999;	99US-0161992.
PR	28-OCT-1999;	99US-0161993.
PR	29-OCT-1999;	99US-0162142.

Query Match	40.2%;	Score 398.8;	DB 21;	Length 1015;
Best Local Similarity	73.0%;	Pred. No. 3.8e-103;		
Matches 527;	Conservative 0;	Mismatches 192;	Indels 3;	Gaps 1

QY	199	TTCTTCTTTGCTTTCACCTTGCGTCACTACAGGTGGCTGGACAGGGGCCACGCCACCTTT	258
Db	137	TTATTCTCCCAAGAACCTCATGGAACGACGAGGTTGGCAAGGTGTGTCAGCCACGTTT	196
QY	259	TATGTTGTGTGTCAGCATCTGGACCAATGGGTGAGCTTGTGGTATGGGAATTTATAC	318
Db	197	TACGGCGCGAAGATGCTTCCGGCACATGGCGCGAGCTGTGGCTATGGAATTTGTAT	256
QY	319	AGCCAAAGGTATNGACAGCAACGGGTGGCGCTGAGACACTGGCGTATTTTAACAATGATTA	378
Db	257	GGCCAAGGTTACGGGACGAAACACGGCGGTTTAAGTAGGCTCTATATCAACAGGACTC	316
QY	379	AGTTGTGTGCTTGCTTGGAAATGACTTGTACAAACGACCTTAATNGTGCCTTCCGGA	438
Db	317	ACGTGTGCGGCTGTGATGAGATGAAGTAAACATGACCGAGGTGGTGTCTCGGATCA	376
QY	439	ACTATTAGGGTCACTGCGCACCACTTTTGGCCCTCTAACTTTGCTCTCCCTTAACAACAT	498
Db	377	ACCATCAACGGTACAGCTCAAACTTTTGGCCACCTTAACCTCGGCTCTCCAAACATAT	436
QY	499	GATGATGATGATCAACCTCTCTCTCCAAACACTTCGACATGGGTGACCTGGCTTCCCTCA	558
Db	437	GGAGTTGTGCAATCTCTCTCTTCAAGATTTGACCTCGCGAGCCAGCTTTTCTTCA	496
QY	559	ATCGCTCAATACCGAGCTGTATGTCCCGTCTCTCTTTCGATGGGTACCATGATGAAG	618
Db	497	ATCGCTCAGTATCGGCGCGGCAATGTCTCTGCTCTTTCGGAAGATACCAATGATGAAG	556
QY	619	AAAGGTGAGTGAAGTTTAAATCAATGACCACTATCACTTCAACCTGTTTGTATCA	678
Db	557	AAAGGAGGAATTAAGTTTACATCAAGCAACCTATCACTTCAACCTGTTTGTATCTCC	616

Qy	679	AAAGTCGTGGGCGCAGGCGACGCTCAGCTCTGTGTGATAAAGGGGCTCTCGAAC---TGA	735
Db	617	AAAGTGAAGGAGCAGGAGAGCTAACGCCCGCTTCAATCAAAAGCTCAAAAACAAGTGC	676
Qy	736	TGGCAATTCATGCTTGAATAATTGGGGCCAAAATGCGAAGCAACACTATCTCAATGGC	759
Db	677	TGGCAAGCANTGTCTAGAAACTGGGGGCAAAAATGCGCAGACCAATTCATCATGTAAGAC	738
Qy	796	CAGGCGCTTCCCTTCAAGTCACTCTTAGTAGTAGTGCGCACTCTCAGTCCCTATATATCTC	855
Db	737	CAAGCGCTTCTCTTCAGGTAAACGACACGAGCATGCTGTCACACTCGTTAGCAAGACGTG	796
Qy	856	GTTCTCTTCAATTGGCATTTGGCCAAACCTATGAGGCCCTCAATTCTTAACCATATCA	915
Db	797	GCTCTCTTAATTGGCAGGTTCGACAAACCTACCAAGGTGTGCACTTCTGATCCAAACCA	856
Qy	916	GC	917
Db	857	TC	858

RESULT 6
AAC40777
ID AAC40777 standard; DNA; 1016 BP

DT 17-OCT-2000 (First entry)

DE Arabidopsis thaliana DNA fragment SEQ ID NO: 29509

KM Hybridisation assay; genetic mapping; gene expression control.
KM protein identification; signal transduction pathway;
KM metabolic pathway; promoter; termination sequence; ss.

OS Arabidopsis thaliana

PN EP1033405-A2.

PD 06-SEP-2000.

PF 25-FEB-2000; 2000EP-0301439.

PR 25-FEB-1999; 99US-0121825-

PR 09-MAR-1999; 99US-0123548.

PR	25-MAR-1999;	99US-0126264.
DD	20 MAR 1999	00115-0126278E

PR	01-APR-1999;	99US-0127462.
DD	01-APR-1999	00US-0128234

PR 08-APR-1999; 99US-0128714.
15 APR 1999; 99US-0128945

PR	19-APR-1999;	99US-0130077.
ED	21 APR 1999.	60US-0130048.

PR 23-APR-1999; 99US-0130510.

PR 28-APR-1999; 99US-0131449.

PR	30-APR-1999;	99US-0132407.
DD	04 MAY 1999	00US-0132484

PR 05-MAY-1999; 99US-0132485.
OC MAY 1999 0015 0132485

PR	06-MAY-1999;	99US-0132487.
DD	07 MAY 1999	0011S-0132963

PR	11-MAY-1999;	99US-0134256.
DE	14 MAY 1999	0011C 0134218

PR 14-MAY-1999; 99US-0134219.
14 MAY 1999 0015 0134231

PR	14-MAY-1999;	99US-0134370.
DE	19 MAY 1999	00115-01343768

PR	19-MAY-1999;	99US-0134941.
DE	20 MAY 1999	99US-0135134

PR 20-MAY-1999; 99US-0135124.

PR	21-MAY-1999;	99US-0135353.
PR	24-MAY-1999;	99US-0135629.
PR	25-MAY-1999;	99US-0136021.
PR	27-MAY-1999;	99US-0136392.
PR	28-MAY-1999;	99US-0136782.
PR	01-JUN-1999;	99US-0137222.
PR	03-JUN-1999;	99US-0137528.
PR	04-JUN-1999;	99US-0137502.
PR	07-JUN-1999;	99US-0137724.
PR	08-JUN-1999;	99US-0138094.
PR	10-JUN-1999;	99US-0138540.
PR	10-JUN-1999;	99US-0138847.
PR	14-JUN-1999;	99US-0139119.
PR	16-JUN-1999;	99US-0139452.
PR	17-JUN-1999;	99US-0139453.
PR	18-JUN-1999;	99US-0139454.
PR	18-JUN-1999;	99US-0139455.
PR	18-JUN-1999;	99US-0139456.
PR	18-JUN-1999;	99US-0139457.
PR	18-JUN-1999;	99US-0139458.
PR	18-JUN-1999;	99US-0139459.
PR	18-JUN-1999;	99US-0139460.
PR	18-JUN-1999;	99US-0139461.
PR	18-JUN-1999;	99US-0139462.
PR	18-JUN-1999;	99US-0139463.
PR	18-JUN-1999;	99US-0139750.
PR	21-JUN-1999;	99US-0139763.
PR	22-JUN-1999;	99US-0139817.
PR	23-JUN-1999;	99US-0139899.
PR	24-JUN-1999;	99US-0140353.
PR	24-JUN-1999;	99US-0140354.
PR	28-JUN-1999;	99US-0140695.
PR	29-JUN-1999;	99US-0140823.
PR	30-JUN-1999;	99US-0140991.
PR	01-JUL-1999;	99US-0141287.
PR	02-JUL-1999;	99US-0142154.
PR	06-JUL-1999;	99US-0142055.
PR	08-JUL-1999;	99US-0142390.
PR	09-JUL-1999;	99US-0142803.
PR	12-JUL-1999;	99US-0142920.
PR	13-JUL-1999;	99US-0142977.
PR	14-JUL-1999;	99US-0143542.
PR	15-JUL-1999;	99US-0143624.
PR	16-JUL-1999;	99US-0144005.
PR	16-JUL-1999;	99US-0144085.
PR	19-JUL-1999;	99US-0144325.
PR	19-JUL-1999;	99US-0144331.
PR	19-JUL-1999;	99US-0144332.
PR	19-JUL-1999;	99US-0144333.
PR	19-JUL-1999;	99US-0144344.
PR	19-JUL-1999;	99US-0144352.
PR	20-JUL-1999;	99US-0144352.
PR	20-JUL-1999;	99US-0144632.
PR	21-JUL-1999;	99US-0144884.
PR	21-JUL-1999;	99US-0144884.
PR	21-JUL-1999;	99US-0145086.
PR	22-JUL-1999;	99US-0145088.
PR	22-JUL-1999;	99US-0145085.
PR	22-JUL-1999;	99US-0145087.
PR	22-JUL-1999;	99US-0145089.
PR	22-JUL-1999;	99US-0145192.
PR	23-JUL-1999;	99US-0145145.
PR	23-JUL-1999;	99US-0145218.
PR	23-JUL-1999;	99US-0145224.
PR	26-JUL-1999;	99US-0145276.
PR	27-JUL-1999;	99US-0145913.
PR	27-JUL-1999;	99US-0145918.
PR	28-JUL-1999;	99US-0145919.
PR	02-AUG-1999;	99US-0145951.
PR	02-AUG-1999;	99US-0146386.
PR	02-AUG-1999;	99US-0146388.
PR	02-AUG-1999;	99US-0146389.
PR	03-AUG-1999;	99US-0147038.
PR	04-AUG-1999;	99US-0147204.
PR	04-AUG-1999;	99US-0147302.
PR	05-AUG-1999;	99US-0147392.
PR	05-AUG-1999;	99US-0147260.
PR	06-AUG-1999;	99US-0147303.
PR	06-AUG-1999;	99US-0147416.
PR	09-AUG-1999;	99US-0147493.
PR	09-AUG-1999;	99US-0147935.
PR	10-AUG-1999;	99US-0148171.
PR	11-AUG-1999;	99US-0148319.
PR	12-AUG-1999;	99US-0148341.
PR	13-AUG-1999;	99US-0148565.
PR	13-AUG-1999;	99US-0148684.
PR	16-AUG-1999;	99US-0149368.
PR	17-AUG-1999;	99US-0149175.
PR	18-AUG-1999;	99US-0149426.
PR	20-AUG-1999;	99US-0149722.
PR	20-AUG-1999;	99US-0149723.
PR	20-AUG-1999;	99US-0149929.
PR	23-AUG-1999;	99US-0149902.
PR	23-AUG-1999;	99US-0149930.
PR	25-AUG-1999;	99US-0150566.
PR	26-AUG-1999;	99US-0150884.
PR	27-AUG-1999;	99US-0151065.
PR	27-AUG-1999;	99US-0151066.
PR	27-AUG-1999;	99US-0151080.
PR	30-AUG-1999;	99US-0151303.
PR	31-AUG-1999;	99US-0151438.
PR	01-SEP-1999;	99US-0151930.
PR	07-SEP-1999;	99US-0152363.
PR	10-SEP-1999;	99US-0153070.
PR	13-SEP-1999;	99US-0153758.
PR	15-SEP-1999;	99US-0154039.
PR	16-SEP-1999;	99US-0154018.
PR	20-SEP-1999;	99US-0154779.
PR	22-SEP-1999;	99US-0155139.
PR	23-SEP-1999;	99US-0155486.
PR	24-SEP-1999;	99US-0155659.
PR	28-SEP-1999;	99US-0156458.
PR	29-SEP-1999;	99US-0156596.
PR	04-OCT-1999;	99US-0157117.
PR	05-OCT-1999;	99US-0157753.
PR	06-OCT-1999;	99US-0157865.
PR	07-OCT-1999;	99US-0158029.
PR	08-OCT-1999;	99US-0158369.
PR	12-OCT-1999;	99US-0159293.
PR	13-OCT-1999;	99US-0159294.
PR	13-OCT-1999;	99US-0159295.
PR	14-OCT-1999;	99US-0159329.
PR	14-OCT-1999;	99US-0159330.
PR	14-OCT-1999;	99US-0159331.
PR	14-OCT-1999;	99US-0159637.
PR	14-OCT-1999;	99US-0159638.
PR	18-OCT-1999;	99US-0159584.
PR	21-OCT-1999;	99US-0160741.
PR	21-OCT-1999;	99US-0160767.
PR	21-OCT-1999;	99US-0160768.
PR	21-OCT-1999;	99US-0160770.
PR	21-OCT-1999;	99US-0160814.
PR	21-OCT-1999;	99US-0160815.
PR	22-OCT-1999;	99US-0160980.
PR	22-OCT-1999;	99US-0160981.
PR	22-OCT-1999;	99US-0160989.
PR	25-OCT-1999;	99US-0161404.
PR	25-OCT-1999;	99US-0161405.
PR	25-OCT-1999;	99US-0161406.
PR	26-OCT-1999;	99US-0161359.
PR	26-OCT-1999;	99US-0161360.
PR	26-OCT-1999;	99US-0161361.

PR 28-OCT-1999; 99US-0161920.
 PR 28-OCT-1999; 99US-0161992.
 PR 28-OCT-1999; 99US-0161993.
 PR 29-OCT-1999; 99US-0162142.

Query Match 40.2%; Score 398.8; DB 21; Length 1016;
 Best Local Similarity 73.0%; Pred. No. 3.8e-103;
 Matches 527; Conservative 0; Mismatches 192; Indels 3; Gaps 1;

QY 199 TTCCTCTTGTCTTCACTTCGCTGACTACGCTGCTGCAAGCGCGCCACGCACTTT 258
 DB 137 TTATTCCTCCAGGAAGCTATGAGAGACGAGGCTTGCAAGGTGTACCGCAGCTTT 196
 QY 255 TATGTGTGTGAGCCATCTGCGACCATGAGTGTGAGCTTTGGGTATGGAAATTATAC 318
 DB 197 TAGCGGGGGAAGATGCTTCCGACCATAGGGGGAGCTTGTGGCTATGGAATTGTAT 256
 QY 319 AGCCAAAGGTATGGCAAGAACGCGTGGGCTGAGCACTGCGCTATTAAATGATTA 378
 DB 257 GGCAGAGGTACGGAGCAACGCGGCTTTAAGTACGCTTATTCACAAACGACTC 316
 QY 379 AGTTGTGTCTTCTTCCAAATGACTGTACAAACGACCTTAATGTGCTTCCGGA 438
 DB 317 AGGTGTGGCGGCTGCTATGATGAGTGAAGTGAAGATGACCCGAGTGTCTCGGCTCA 376
 QY 439 ACTATTAGGCTCACTGCCAACATTTTGGCCCTCTTAACCTTGGCTCTCCCTAACAAAT 498
 DB 377 ACCATCACGCTACACAGCTCAAACTTTTCCCACTTACCTGCTCTTCCAAAGTATAT 436
 QY 499 GGTGATGTGGAACCTCTCTCCCAACTTTCGACATGGCTGAGCGCTTCTCTTCA 558
 DB 437 GGAAGTGTGCAATCTCTCTTCCAGATTTGACCTGCGGAGCAAGTTCCTTCA 496
 QY 559 ATGCTCAATACGAGCTGTATCTGCTCCGCTCTCTTCTGTAAGGTACATGATGAAG 618
 DB 497 ATGCTCAATGCTGCGGCAATGTTCTCTGCTCTTTCGAAAGATACATGATGAAG 556
 QY 619 AAGGTGAGTGAAGTTTACATCAATGCGCACTTACTTCACTCTGTTTATGATCA 678
 DB 557 AAGGAGGAATTAAGTGTATGATCAACGACACTCACTTCACTCTGTTGATCTCC 616
 QY 679 AACGTGAGGCGCAGGACGCTGCTGTGTGATTAAGGGGCTGGAAC--TGA 735
 DB 617 AACGTGAGGAGAGCAGAGACGTAACGCGTCTCAATCAAAAGCTCAAAACACAGTGC 676
 QY 736 TGGCAATCCATGCTTGAATTTGGGCGCAAACTGCGCAAGCAACATATCTCAATGCG 795
 DB 677 TGGCAAGCATGTCTGAATTTGGGCAAACTGCGCAAGCAATTCATATGAAACGAC 736
 QY 796 CAAGGCTTCTCTTCAAGTCACTTGAATGATGTGCACTTCACTGCTATTAATTC 855
 DB 737 CAAGGCTTCTCTTCAAGTCACTTGAATGATGTGCACTTCACTGCTATTAATTC 796
 QY 856 GTTCCCTCAATTTGGCAATTTGGCAAACTTGAAGGCGCTCAATTTAAACCATATCA 915
 DB 797 GCTCTTCAATTTGGCAATTTGGCAAACTTGAAGGCGCTCAATTTAAACCATATCA 856
 QY 916 GC 917
 DB 857 TC 858

RESULT 7
 AB213283
 ID AB213283 standard; DNA; 762 BP.
 XX
 AC AB213283;
 XX
 DT 21-JAN-2003 (first entry)
 XX
 DE Arabidopsis thaliana stress regulated gene SEQ ID NO 1088.
 XX
 KW Arabidopsis thaliana; plant; gene; stress; transgenic; ds.

XX Arabidopsis thaliana.
 OS Arabidopsis thaliana.
 PN WO200216655-A2.
 XX
 XX 28-FEB-2002.
 XX
 XX 24-AUG-2001; 2001WO-US26685.
 PF
 XX 24-AUG-2000; 2000US-227866P.
 PR 26-JAN-2001; 2001US-264647P.
 PR 22-JUN-2001; 2001US-300111P.
 XX
 PA (SCRI) SCRIPPS RES. INST.
 PA (SYGN) SYNGENTA PARTICIPATIONS AG.
 XX
 PI Harper JF, Kreps J, Wang X, Zhu T;
 PI WPI; 2002-304127/34.
 DR
 XX
 PT Identifying a stress condition to which a plant cell has been exposed
 PT and producing plants with increased tolerance to these abiotic stresses
 PT
 XX
 PS Claim 144; SEQ ID NO 1088; 577bp + Sequence Listing; English.
 CC The invention relates to identifying a stress condition to which a plant
 CC cell has been exposed, comprising:
 CC (a) contacting nucleic acid representative of expressed polynucleotides
 CC in the plant cell with an array or probes representative of the plant
 CC cell genome; and
 CC (b) detecting a profile of expressed polynucleotides in the plant cell
 CC characteristic of a stress response. The method is useful in the
 CC production of transgenic plants, cells and seeds and in producing plants
 CC with increased tolerance to abiotic stress. The present sequence is that
 CC of an Arabidopsis thaliana stress regulated gene (AB212196-AB21574) used
 CC in methods of the invention.
 CC Note: The sequence data for this patent is not represented in the printed
 CC specification but is based on sequence information supplied to Derwent by
 CC the European Patent Office.
 XX
 XX Sequence 762 BP; 202 A; 196 C; 184 G; 180 T; 0 other;
 QY
 Query Match 39.7%; Score 394.2; DB 24; Length 762;
 Best Local Similarity 73.1%; Pred. No. 6.9e-102;
 Matches 520; Conservative 0; Mismatches 188; Indels 3; Gaps 1;
 QY 199 TTCCTCTTGTCTTCACTTCGCTGACTACGCTGCTGCAAGCGCGCCACGCACTTT 258
 DB 52 TTATTCCTCCAGGAAGCTATGAGAGACGAGGCTTGCAAGGTGTACCGCAGCTTT 111
 QY 255 TATGTGTGTGAGCCATCTGCGACCATGAGTGTGAGCTTGGTATGGAATTATAC 318
 DB 112 TAGCGGGGGAAGATGCTTCCGCAACATGGCGGAGCTTGTGCTATGGAATTGTAT 171
 QY 319 AGCCAAAGGTATGAGCAAGAACGCGTGGCGCTGAGCACTGCGCTATTAACAATGATTA 378
 DB 172 GGCAGAGTTAGGAGCAACACGCGGCTTTAAGTACGGCTCTATTAACAAACGACTC 231
 QY 379 AGTTGTGTGCTTGTGGAATGACTGTACAAACGACCTTAATGAGTGTGCTTCCGGA 438
 DB 232 AGGTGTGGCGCTGCTATGATGAGTGAAGTGAAGTGAACGAGGTGTGTCTCGGCTCA 291
 QY 439 ACTATTAGGCTCACTGCCAACATTTTGGCCCTCTTAACCTTGTCTCTCTTAACAACAT 498
 DB 292 ACCATCACGCTACAGCTTAAATTTTGGCCACTTAACCTTGGCTCTTCCAAAGTATAT 351
 QY 499 GGTGATGTGCAACCTCTCTTCCAAACATTTGACATGAGTGTGAGCTTGTCTTCTTCA 558
 DB 352 GGAAGTGTGCAACCTCTCTTCCAAACATTTGACATGAGTGTGAGCTTGTCTTCTTCA 411
 QY 559 ATGCTCAATACGAGCTGTGATGCTGCTCCGCTCTCTTGTGAGGTATCATGATGAAG 618

Db	412	ATCGCTAGTATCGTCCGCGATTGTTCTCTCTTCCGAGAGTACATGATGAG	471	PR	19-MAY-1999;	99US-0134941.
Qy	619	AAAGTGGAGTGGATTATCAATCAATGCGCATCATATCTCAACCTGGTTTGATCACA	678	PR	20-MAY-1999;	99US-0135124.
Db	472	AAAGGAGGAATAGGTTTACATCAACGACATCATATCTTCAACCTGGTTTGATCACC	531	PR	21-MAY-1999;	99US-0135353.
Qy	679	AACGTGGTGGCGAGCGACGTCCTCTCTGTGATTAAGGGGTCGAAAC--TGGA	735	PR	24-MAY-1999;	99US-0135629.
Db	532	AACGTAGGAGGAGGAGGAGTACACGCCCTCTCAATCAAGGCTCAAAACACAGTCG	591	PR	25-MAY-1999;	99US-0136021.
Qy	736	TGGCAATCCAGTCTAGAAATTTGGGGCCAAATGGGCAACCACTATCTCAATGCG	795	PR	27-MAY-1999;	99US-0136392.
Db	592	TGGCAAGGATGTCTAGAACTGGGACAAACTGGGAGACCAATTCATCATGAAACGAC	651	PR	28-MAY-1999;	99US-0136782.
Qy	796	CAAGGACCTTCTCTTCAAGTCACTCTTGTAGTGGTCGACCTCTCACTGCTATATCTC	855	PR	01-JUN-1999;	99US-0137222.
Db	652	CAAGGACCTTCTCTTCCAGTACGACCGCATGTCGCACTGCTTAGCAACGACGCTG	711	PR	03-JUN-1999;	99US-0137528.
Qy	856	GTTCTCTTCCATTGGCAATTTGGCCAAACCTATGAAAGGCTCTCAATTCTAA	906	PR	04-JUN-1999;	99US-0137502.
Db	712	GCTCTCTTATTTGGCAGTTGCGACAAACCTACCAAGGTGTCAGTTCTGA	762	PR	07-JUN-1999;	99US-0137724.

RESULT 8
AAC50628
ID AAC50628 standard; DNA; 780 BP.

XX	AAC50628;	
AC	AAC50628;	
XX	18-OCT-2000 (first entry)	
DT	18-OCT-2000 (first entry)	
XX	Arabidopsis thaliana DNA fragment SEQ ID NO: 65548.	
DE	Arabidopsis thaliana DNA fragment SEQ ID NO: 65548.	
XX	Hybridisation assay; genetic mapping; gene expression control;	
KM	protein identification; signal transduction pathway;	
KM	metabolic pathway; promoter; termination sequence; ss.	
XX	Arabidopsis thaliana.	
OS	Arabidopsis thaliana.	
XX	EP1033405-A2.	
PN	EP1033405-A2.	
XX	06-SEP-2000.	
PD	06-SEP-2000.	
XX	25-FEB-2000; 2000EP-0301439.	
PF	25-FEB-2000; 2000EP-0301439.	
XX	25-FEB-1999;	99US-0121825.
PR	05-MAR-1999;	99US-0123180.
PR	09-MAR-1999;	99US-0123548.
PR	23-MAR-1999;	99US-0125788.
PR	25-MAR-1999;	99US-0126264.
PR	29-MAR-1999;	99US-0126785.
PR	01-APR-1999;	99US-0127462.
PR	06-APR-1999;	99US-0128234.
PR	08-APR-1999;	99US-0128714.
PR	16-APR-1999;	99US-0129845.
PR	19-APR-1999;	99US-0130077.
PR	21-APR-1999;	99US-0130449.
PR	23-APR-1999;	99US-0130510.
PR	23-APR-1999;	99US-0130891.
PR	28-APR-1999;	99US-0131449.
PR	30-APR-1999;	99US-0132048.
PR	30-APR-1999;	99US-0132407.
PR	04-MAY-1999;	99US-0132484.
PR	05-MAY-1999;	99US-0132485.
PR	06-MAY-1999;	99US-0132486.
PR	06-MAY-1999;	99US-0132487.
PR	07-MAY-1999;	99US-0132863.
PR	11-MAY-1999;	99US-0134256.
PR	14-MAY-1999;	99US-0134219.
PR	14-MAY-1999;	99US-0134221.
PR	14-MAY-1999;	99US-0134370.
PR	18-MAY-1999;	99US-0134768.

PR	19-MAY-1999;	99US-0134941.
PR	20-MAY-1999;	99US-0135124.
PR	21-MAY-1999;	99US-0135353.
PR	24-MAY-1999;	99US-0135629.
PR	25-MAY-1999;	99US-0136021.
PR	27-MAY-1999;	99US-0136392.
PR	28-MAY-1999;	99US-0136782.
PR	01-JUN-1999;	99US-0137222.
PR	03-JUN-1999;	99US-0137528.
PR	04-JUN-1999;	99US-0137502.
PR	07-JUN-1999;	99US-0137724.
PR	08-JUN-1999;	99US-0138094.
PR	10-JUN-1999;	99US-0138540.
PR	10-JUN-1999;	99US-0138847.
PR	14-JUN-1999;	99US-0139119.
PR	16-JUN-1999;	99US-0139452.
PR	16-JUN-1999;	99US-0139453.
PR	17-JUN-1999;	99US-0139492.
PR	18-JUN-1999;	99US-0139454.
PR	18-JUN-1999;	99US-0139455.
PR	18-JUN-1999;	99US-0139456.
PR	18-JUN-1999;	99US-0139457.
PR	18-JUN-1999;	99US-0139458.
PR	18-JUN-1999;	99US-0139459.
PR	18-JUN-1999;	99US-0139460.
PR	18-JUN-1999;	99US-0139461.
PR	18-JUN-1999;	99US-0139462.
PR	18-JUN-1999;	99US-0139463.
PR	18-JUN-1999;	99US-0139750.
PR	18-JUN-1999;	99US-0139763.
PR	21-JUN-1999;	99US-0139817.
PR	22-JUN-1999;	99US-0139899.
PR	23-JUN-1999;	99US-0140353.
PR	23-JUN-1999;	99US-0140354.
PR	24-JUN-1999;	99US-0140695.
PR	28-JUN-1999;	99US-0140823.
PR	29-JUN-1999;	99US-0140991.
PR	30-JUN-1999;	99US-0141287.
PR	01-JUL-1999;	99US-0141842.
PR	01-JUL-1999;	99US-0142154.
PR	02-JUL-1999;	99US-0142055.
PR	06-JUL-1999;	99US-0142305.
PR	08-JUL-1999;	99US-0142803.
PR	09-JUL-1999;	99US-0142920.
PR	12-JUL-1999;	99US-0142977.
PR	13-JUL-1999;	99US-0143542.
PR	14-JUL-1999;	99US-0143624.
PR	15-JUL-1999;	99US-0144005.
PR	16-JUL-1999;	99US-0144085.
PR	16-JUL-1999;	99US-0144086.
PR	19-JUL-1999;	99US-0144334.
PR	19-JUL-1999;	99US-0144335.
PR	20-JUL-1999;	99US-0144352.
PR	20-JUL-1999;	99US-0144632.
PR	20-JUL-1999;	99US-0144884.
PR	21-JUL-1999;	99US-0144814.
PR	21-JUL-1999;	99US-0145086.
PR	22-JUL-1999;	99US-0145088.
PR	22-JUL-1999;	99US-0145085.
PR	22-JUL-1999;	99US-0145087.
PR	22-JUL-1999;	99US-0145089.
PR	22-JUL-1999;	99US-0145192.
PR	23-JUL-1999;	99US-0145145.
PR	23-JUL-1999;	99US-0145218.
PR	23-JUL-1999;	99US-0145224.
PR	26-JUL-1999;	99US-0145276.
PR	27-JUL-1999;	99US-0145913.
PR	27-JUL-1999;	99US-0145918.
PR	27-JUL-1999;	99US-0145919.

```

PR 28-JUL-1999; 99US-0145591.
PR 02-AUG-1999; 99US-0146386.
PR 02-AUG-1999; 99US-0146388.
PR 02-AUG-1999; 99US-0146389.
PR 03-AUG-1999; 99US-0147038.
PR 04-AUG-1999; 99US-0147204.
PR 04-AUG-1999; 99US-0147302.
PR 05-AUG-1999; 99US-0147192.
PR 06-AUG-1999; 99US-0147260.
PR 06-AUG-1999; 99US-0147303.
PR 06-AUG-1999; 99US-0147416.
PR 09-AUG-1999; 99US-0147493.
PR 09-AUG-1999; 99US-0147935.
PR 10-AUG-1999; 99US-0148171.
PR 11-AUG-1999; 99US-0148319.
PR 12-AUG-1999; 99US-0148341.
PR 13-AUG-1999; 99US-0148565.
PR 13-AUG-1999; 99US-0148584.
PR 16-AUG-1999; 99US-0149368.
PR 17-AUG-1999; 99US-0149175.
PR 18-AUG-1999; 99US-0149426.
PR 20-AUG-1999; 99US-0149722.
PR 20-AUG-1999; 99US-0149723.
PR 20-AUG-1999; 99US-0149829.
PR 23-AUG-1999; 99US-0149802.
PR 23-AUG-1999; 99US-0149930.
PR 25-AUG-1999; 99US-0150566.
PR 26-AUG-1999; 99US-0150884.
PR 27-AUG-1999; 99US-0151065.
PR 27-AUG-1999; 99US-0151066.
PR 27-AUG-1999; 99US-0151080.
PR 30-AUG-1999; 99US-0151303.
PR 31-AUG-1999; 99US-0151308.
PR 01-SEP-1999; 99US-0151930.
PR 07-SEP-1999; 99US-0152363.
PR 10-SEP-1999; 99US-0153070.
PR 13-SEP-1999; 99US-0153758.
PR 15-SEP-1999; 99US-0154018.
PR 16-SEP-1999; 99US-0154039.
PR 20-SEP-1999; 99US-0154779.
PR 22-SEP-1999; 99US-0155139.
PR 23-SEP-1999; 99US-0155486.
PR 24-SEP-1999; 99US-0156559.
PR 28-SEP-1999; 99US-0156458.
PR 29-SEP-1999; 99US-0156596.
PR 04-OCT-1999; 99US-0157117.
PR 05-OCT-1999; 99US-0157753.
PR 06-OCT-1999; 99US-0157865.
PR 07-OCT-1999; 99US-0158029.
PR 08-OCT-1999; 99US-0158232.
PR 12-OCT-1999; 99US-0158369.
PR 13-OCT-1999; 99US-0159293.
PR 13-OCT-1999; 99US-0159294.
PR 13-OCT-1999; 99US-0159295.
PR 14-OCT-1999; 99US-0159329.
PR 14-OCT-1999; 99US-0159330.
PR 14-OCT-1999; 99US-0159331.
PR 14-OCT-1999; 99US-0159637.
PR 14-OCT-1999; 99US-0159638.
PR 18-OCT-1999; 99US-0159584.
PR 21-OCT-1999; 99US-0160741.
PR 21-OCT-1999; 99US-0160767.
PR 21-OCT-1999; 99US-0160768.
PR 21-OCT-1999; 99US-0160770.
PR 21-OCT-1999; 99US-0160814.
PR 21-OCT-1999; 99US-0160815.
PR 22-OCT-1999; 99US-0160980.
PR 22-OCT-1999; 99US-0160981.
PR 22-OCT-1999; 99US-0160989.
PR 25-OCT-1999; 99US-0161404.
PR 25-OCT-1999; 99US-0161405.
PR 25-OCT-1999; 99US-0161406.
PR 26-OCT-1999; 99US-0161359.

```

```

PR 26-OCT-1999; 99US-0161360.
PR 26-OCT-1999; 99US-0161361.
PR 28-OCT-1999; 99US-0161920.
PR 28-OCT-1999; 99US-0161922.
PR 28-OCT-1999; 99US-0161993.
PR 29-OCT-1999; 99US-0162142.

```

```

Query Match 38.1%; Score 377.8; DB 21; Length 780;
Best Local Similarity 72.0%; Pred. No. 3.2e-97;
Matches 493; Conservative 0; Mismatches 192; Indels 0; Gaps 0;

```

```

QY 219 CGCTGCTAACGGTGGTGGCGACAGCGGCGCCACCTTTATGSGTGGTGAAGCATC 278
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 90 CGGCTACGGTGGCGGTTGGATTCACGCTACGCCACTTTTACGGTGGTGGATGCTTC 149
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 279 TGGCACCAATGGATGGAGCTTGTGGTATGGAAATTTATACGCCAAGGATAGCAGCA 338
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 150 CGGCACATGGGTGGTGGTGTGTGGATATGGTATATATATAGCCAGGCTACGGGACG 209
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 339 CACGGTGGCGCTGAGCACTGCGCTATTTAACATGGATTAAGTTGTGCTTGTGCA 398
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 210 CACGGCGGCTTAACACAGACTCTCTTCACACATGACTTGAAGTGTGCTTGTGGA 269
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 399 AATGACTGTACAAACGACCCCTTAATGGGCTTCGGGAACTATTAGGTCACGCCAC 458
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 270 GATTAAGATGTGAAACGATGTGAATGGTGTATCTGCTCAATGCTGTACCGCTAC 329
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 459 CACTTTTGCCTCCTTAATCTTGTCTCCCTTAACAACATGGTGGATGGTCAACCTTC 518
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 330 AATCTTGTGCGCGCAATTAACGCGTGTAGCGAACATATGGCGGTGTGTATCTCC 389
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 519 TCTTCAACACTTGCACATGAGCTGAGCTGCTTCTTCAATGCTCAATACCGAGCTGG 578
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 390 TCTTGAACACTTGTGACTGTGCTGACGCTGTTTTCACGCAATGCTCAATGACAGCTGG 449
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 579 TATGCTCCCGCTCCTTTGTAAGGATCAATGTATGAAGAAGGTGAGTGGATTAC 638
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 450 AATGCTCCCTGTTCTTACAGAGGTTCTTTCAGAGAGAGAGAGATTAAGTTAC 509
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 639 AATCAATGGCCACTGATCTTCACTTCACTGTTTGTATCAAAACGTGGTGGCGCAGCGA 698
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 510 GATTAACGGCCACTGATCTTCACTTGTGTGTATCAAAACGTGGTGGCGCAGCGA 569
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 699 CGTCACTGTGTGTGATTAAGGGGTCTGAACTGGAATGGCAATCAATGCTTAAGAAATTG 758
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 570 CATTCACTCGGGGAGATCAAGGTTCAAGAACATGTGCGCAAGTATGTCAAGAACGTG 629
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 759 GGGCCAAAACGGCAAGCAACAATATCTCAATGAGCCACTTCCCTTCAAGTAC 818
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 630 GGGGCAAAATGGCAAGCAACTTACCTCAACGCTCAAGCATTTCTTTAAGTAC 689
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 819 TCTTAGTATGATGCTGACACTGCTCATATATCTGTTCTTCCATATGGCAATTTGG 878
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 690 CACGACGACGCGCCGACAGTGTCTCTTCAACGCCGCTCTGCGGTTGCTTATAG 749
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 879 CCAAACTATGAAGCCCTCAATTC 903
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 750 CCAGACTTTTGGCGGTGACAGTTTC 774
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

RESULT 9
AAC33521
ID AAC33521 standard; DNA; 1198 BP.
XX AAC33521;
AC AAC33521;
DT 17-OCT-2000 (first entry)
DE Arabidopsis thaliana DNA fragment SEQ ID NO: 3354.
XX
XX Hybridisation assay; genetic mapping; gene expression control;
KW protein identification; signal transduction pathway;
KW metabolic pathway; promoter; termination sequence; ss.

```

XX	Arabidopsis thaliana.	XX	25-FEB-2000; 2000EP-0301439.
OS		PR	25-FEB-1999; 99US-0121825.
XX	EP1033405-A2.	PR	05-MAR-1999; 99US-0123160.
PN		PR	09-MAR-1999; 99US-0123548.
XX	06-SEP-2000.	PR	23-MAR-1999; 99US-0125788.
PD		PR	25-MAR-1999; 99US-0126264.
XX		PR	29-MAR-1999; 99US-0126785.
PF		PR	01-APR-1999; 99US-0127462.
XX		PR	06-APR-1999; 99US-0128234.
XX		PR	08-APR-1999; 99US-0128714.
		PR	16-APR-1999; 99US-0129845.
		PR	19-APR-1999; 99US-0130077.
		PR	21-APR-1999; 99US-0130449.
		PR	23-APR-1999; 99US-0130510.
		PR	23-APR-1999; 99US-0130891.
		PR	28-APR-1999; 99US-0131449.
		PR	30-APR-1999; 99US-0132048.
		PR	30-APR-1999; 99US-0132407.
		PR	04-MAY-1999; 99US-0132484.
		PR	05-MAY-1999; 99US-0132485.
		PR	06-MAY-1999; 99US-0132486.
		PR	06-MAY-1999; 99US-0132487.
		PR	07-MAY-1999; 99US-0132863.
		PR	11-MAY-1999; 99US-0134256.
		PR	14-MAY-1999; 99US-0134218.
		PR	14-MAY-1999; 99US-0134219.
		PR	14-MAY-1999; 99US-0134221.
		PR	14-MAY-1999; 99US-0134370.
		PR	18-MAY-1999; 99US-0134768.
		PR	19-MAY-1999; 99US-0134941.
		PR	20-MAY-1999; 99US-0135124.
		PR	21-MAY-1999; 99US-0135353.
		PR	24-MAY-1999; 99US-0135629.
		PR	25-MAY-1999; 99US-0136021.
		PR	27-MAY-1999; 99US-0136392.
		PR	28-MAY-1999; 99US-0136782.
		PR	01-JUN-1999; 99US-0137222.
		PR	03-JUN-1999; 99US-0137528.
		PR	04-JUN-1999; 99US-0137502.
		PR	07-JUN-1999; 99US-0137724.
		PR	08-JUN-1999; 99US-0138094.
		PR	10-JUN-1999; 99US-0138540.
		PR	10-JUN-1999; 99US-0138847.
		PR	14-JUN-1999; 99US-0139119.
		PR	16-JUN-1999; 99US-0139453.
		PR	17-JUN-1999; 99US-0139452.
		PR	17-JUN-1999; 99US-0139454.
		PR	18-JUN-1999; 99US-0139455.
		PR	18-JUN-1999; 99US-0139456.
		PR	18-JUN-1999; 99US-0139457.
		PR	18-JUN-1999; 99US-0139458.
		PR	18-JUN-1999; 99US-0139459.
		PR	18-JUN-1999; 99US-0139460.
		PR	18-JUN-1999; 99US-0139461.
		PR	18-JUN-1999; 99US-0139462.
		PR	18-JUN-1999; 99US-0139463.
		PR	18-JUN-1999; 99US-0139750.
		PR	18-JUN-1999; 99US-0139763.
		PR	21-JUN-1999; 99US-0139817.
		PR	22-JUN-1999; 99US-0139899.
		PR	23-JUN-1999; 99US-0140353.
		PR	23-JUN-1999; 99US-0140354.
		PR	24-JUN-1999; 99US-0140695.
		PR	28-JUN-1999; 99US-0140823.
		PR	29-JUN-1999; 99US-0140991.
		PR	30-JUN-1999; 99US-0141287.
		PR	01-JUL-1999; 99US-0141842.
		PR	01-JUL-1999; 99US-0142154.
		PR	02-JUL-1999; 99US-0142055.
		PR	06-JUL-1999; 99US-0142390.
		PR	08-JUL-1999; 99US-0142803.
		PR	09-JUL-1999; 99US-0142920.
		PR	12-JUL-1999; 99US-0142977.
		PR	13-JUL-1999; 99US-0143542.
		PR	14-JUL-1999; 99US-0143624.
		PR	15-JUL-1999; 99US-0144005.
		PR	16-JUL-1999; 99US-0144086.
		PR	16-JUL-1999; 99US-0144325.
		PR	19-JUL-1999; 99US-0144331.
		PR	19-JUL-1999; 99US-0144332.
		PR	19-JUL-1999; 99US-0144333.
		PR	19-JUL-1999; 99US-0144334.
		PR	19-JUL-1999; 99US-0144335.
		PR	20-JUL-1999; 99US-0144352.
		PR	20-JUL-1999; 99US-0144632.
		PR	20-JUL-1999; 99US-0144884.
		PR	21-JUL-1999; 99US-0144884.
		PR	21-JUL-1999; 99US-0145088.
		PR	22-JUL-1999; 99US-0145085.
		PR	22-JUL-1999; 99US-0145087.
		PR	22-JUL-1999; 99US-0145089.
		PR	22-JUL-1999; 99US-0145145.
		PR	23-JUL-1999; 99US-0145218.
		PR	23-JUL-1999; 99US-0145224.
		PR	26-JUL-1999; 99US-0145276.
		PR	27-JUL-1999; 99US-0145913.
		PR	27-JUL-1999; 99US-0145918.
		PR	28-JUL-1999; 99US-0145951.
		PR	02-AUG-1999; 99US-0146386.
		PR	02-AUG-1999; 99US-0146388.
		PR	02-AUG-1999; 99US-0146389.
		PR	03-AUG-1999; 99US-0147038.
		PR	04-AUG-1999; 99US-0147204.
		PR	04-AUG-1999; 99US-0147302.
		PR	05-AUG-1999; 99US-0147192.
		PR	05-AUG-1999; 99US-0147260.
		PR	06-AUG-1999; 99US-0147303.
		PR	09-AUG-1999; 99US-0147493.
		PR	09-AUG-1999; 99US-0147935.
		PR	10-AUG-1999; 99US-0148171.
		PR	11-AUG-1999; 99US-0148319.
		PR	12-AUG-1999; 99US-0148341.
		PR	13-AUG-1999; 99US-0148565.
		PR	13-AUG-1999; 99US-0148684.
		PR	16-AUG-1999; 99US-0149368.
		PR	17-AUG-1999; 99US-0149175.
		PR	18-AUG-1999; 99US-0149426.
		PR	20-AUG-1999; 99US-0149722.
		PR	20-AUG-1999; 99US-0149723.
		PR	20-AUG-1999; 99US-0149929.
		PR	23-AUG-1999; 99US-0149902.
		PR	23-AUG-1999; 99US-0149930.
		PR	25-AUG-1999; 99US-0150566.
		PR	26-AUG-1999; 99US-0150884.
		PR	27-AUG-1999; 99US-0151065.
		PR	27-AUG-1999; 99US-0151066.
		PR	30-AUG-1999; 99US-0151080.
		PR	31-AUG-1999; 99US-0151103.
		PR	01-SEP-1999; 99US-0151138.
		PR	07-SEP-1999; 99US-0152363.
		PR	10-SEP-1999; 99US-0153070.

PR	13-SEP-1999;	99US-0153758.
PR	15-SEP-1999;	99US-0154018.
PR	16-SEP-1999;	99US-0154039.
PR	20-SEP-1999;	99US-0154779.
PR	22-SEP-1999;	99US-0155139.
PR	23-SEP-1999;	99US-0155486.
PR	24-SEP-1999;	99US-0155659.
PR	28-SEP-1999;	99US-0156458.
PR	29-SEP-1999;	99US-0156596.
PR	04-OCT-1999;	99US-0157117.
PR	05-OCT-1999;	99US-0157753.
PR	06-OCT-1999;	99US-0157865.
PR	07-OCT-1999;	99US-0158029.
PR	08-OCT-1999;	99US-0158232.
PR	12-OCT-1999;	99US-0158369.
PR	13-OCT-1999;	99US-0158293.
PR	13-OCT-1999;	99US-0159294.
PR	13-OCT-1999;	99US-0159295.
PR	14-OCT-1999;	99US-0159329.
PR	14-OCT-1999;	99US-0159330.
PR	14-OCT-1999;	99US-0159331.
PR	14-OCT-1999;	99US-0159637.
PR	14-OCT-1999;	99US-0159638.
PR	18-OCT-1999;	99US-0159584.
PR	21-OCT-1999;	99US-0160741.
PR	21-OCT-1999;	99US-0160767.
PR	21-OCT-1999;	99US-0160768.
PR	21-OCT-1999;	99US-0160770.
PR	21-OCT-1999;	99US-0160814.
PR	21-OCT-1999;	99US-0160815.
PR	22-OCT-1999;	99US-0160980.
PR	22-OCT-1999;	99US-0160981.
PR	22-OCT-1999;	99US-0160989.
PR	25-OCT-1999;	99US-0161404.
PR	25-OCT-1999;	99US-0161405.
PR	25-OCT-1999;	99US-0161406.
PR	26-OCT-1999;	99US-0161359.
PR	26-OCT-1999;	99US-0161360.
PR	28-OCT-1999;	99US-0161920.
PR	28-OCT-1999;	99US-0161921.
PR	28-OCT-1999;	99US-0161933.
PR	29-OCT-1999;	99US-0162142.

Db	475	AATGTCCTCTGTTTCTTACAGAGAGGTTTCCTTGACAGAGAAAGAGAGATAAGATTCC	534
Oy	639	AATCAATGGCCACTCATACTTCAACCTCGTTTGTATCACAAACGTGCGGACAGCGCA	698
Db	535	GATAAACGGCCACTCATCTTCACTTCACTTGTGCTGATCAACAAAGTCGGTGTCGCGAGA	594
Oy	639	CGTCACCTCTGTGTGTGATTAAGGGGTTCGAACTGATGGCAATCCATGTTCTAAGAAATG	758
Db	595	CGTTACTCTCGGGGGATTCAGGGTTCAAGAAACAGTGTGGCAAGCTATGTCAAGGAAC	654
Oy	759	GGGCAAACTGGCAACCAACCAACTATCTCATATGGCCAAAGCCTTCTTCAAGTCAC	818
Db	655	GGGCAAAATTTGGCAAAAGCACTTACTCAACGCTCAAGCACTTCTTAAAGTTCAC	714
Oy	819	TCTTAGTATGTGTGCACTCTCAGCTGCTATATCTCGTTCTTCAATTTGCAATTTGG	878
Db	715	CACGACGACGGCCGACAGTGTCTCTTCAACGCGCTCTGCGGCTGGCTTATGG	774
Oy	879	CCAAACTATGAAAGCCCTCAATTC	903
Db	775	CCAGACTTGTGCGGGTGACAGTTC	799
RESULT 10			
ID	AAC50633	standard; DNA; 1233 BP.	
AC	AAC50633;		
DT	18-OCT-2000	(first entry)	
DE	Arabidopsis thaliana DNA fragment SEQ ID NO: 65567.		
XX	Hybridisation assay; genetic mapping; gene expression control;		
XX	protein identification; signal transduction pathway;		
XX	metabolic pathway; promoter; termination sequence; 88.		
XX	Arabidopsis thaliana.		
PN	EP1033405-A2.		
XX	06-SEP-2000.		
PD			
XX	25-FEB-2000; 2000EP-0301439.		
PF			
XX	25-FEB-1999; 99US-0121825.		
PR	05-MAR-1999; 99US-0123180.		
PR	09-MAR-1999; 99US-0123548.		
PR	23-MAR-1999; 99US-0125788.		
PR	25-MAR-1999; 99US-0126264.		
PR	29-MAR-1999; 99US-0126785.		
PR	01-APR-1999; 99US-0127462.		
PR	06-APR-1999; 99US-0128234.		
PR	08-APR-1999; 99US-0128714.		
PR	16-APR-1999; 99US-0129845.		
PR	19-APR-1999; 99US-0130077.		
PR	21-APR-1999; 99US-0130449.		
PR	23-APR-1999; 99US-0130510.		
PR	23-APR-1999; 99US-0130891.		
PR	28-APR-1999; 99US-0131449.		
PR	30-APR-1999; 99US-0132048.		
PR	30-APR-1999; 99US-0132407.		
PR	04-MAY-1999; 99US-0132484.		
PR	05-MAY-1999; 99US-0132485.		
PR	06-MAY-1999; 99US-0132486.		
PR	06-MAY-1999; 99US-0132487.		
PR	07-MAY-1999; 99US-0132863.		
PR	11-MAY-1999; 99US-0133256.		
PR	14-MAY-1999; 99US-0134216.		
PR	14-MAY-1999; 99US-0134219.		
PR	14-MAY-1999; 99US-0134221.		
PR	14-MAY-1999; 99US-0134370.		

PR 18-MAY-1999;	99US-0134768.
PR 19-MAY-1999;	99US-0134941.
PR 20-MAY-1999;	99US-0135124.
PR 21-MAY-1999;	99US-0135353.
PR 24-MAY-1999;	99US-0135629.
PR 25-MAY-1999;	99US-0136021.
PR 27-MAY-1999;	99US-0136392.
PR 28-MAY-1999;	99US-0137222.
PR 01-JUN-1999;	99US-0137528.
PR 03-JUN-1999;	99US-0137502.
PR 04-JUN-1999;	99US-0137724.
PR 07-JUN-1999;	99US-0138094.
PR 08-JUN-1999;	99US-0138540.
PR 10-JUN-1999;	99US-0138847.
PR 10-JUN-1999;	99US-0139454.
PR 14-JUN-1999;	99US-0139119.
PR 16-JUN-1999;	99US-0139452.
PR 16-JUN-1999;	99US-0139453.
PR 17-JUN-1999;	99US-0139452.
PR 18-JUN-1999;	99US-0139454.
PR 18-JUN-1999;	99US-0139455.
PR 18-JUN-1999;	99US-0139456.
PR 18-JUN-1999;	99US-0139457.
PR 18-JUN-1999;	99US-0139458.
PR 18-JUN-1999;	99US-0139459.
PR 18-JUN-1999;	99US-0139460.
PR 18-JUN-1999;	99US-0139461.
PR 18-JUN-1999;	99US-0139462.
PR 18-JUN-1999;	99US-0139463.
PR 18-JUN-1999;	99US-0139750.
PR 18-JUN-1999;	99US-0139763.
PR 21-JUN-1999;	99US-0139817.
PR 22-JUN-1999;	99US-0139839.
PR 23-JUN-1999;	99US-0140353.
PR 23-JUN-1999;	99US-0140354.
PR 24-JUN-1999;	99US-0140695.
PR 28-JUN-1999;	99US-0140823.
PR 29-JUN-1999;	99US-0140991.
PR 30-JUN-1999;	99US-0141287.
PR 01-JUL-1999;	99US-0141842.
PR 01-JUL-1999;	99US-0142154.
PR 02-JUL-1999;	99US-0142055.
PR 06-JUL-1999;	99US-0142390.
PR 08-JUL-1999;	99US-0142803.
PR 09-JUL-1999;	99US-0142920.
PR 12-JUL-1999;	99US-0142977.
PR 13-JUL-1999;	99US-0143542.
PR 14-JUL-1999;	99US-0143624.
PR 15-JUL-1999;	99US-0144005.
PR 16-JUL-1999;	99US-0144085.
PR 16-JUL-1999;	99US-0144086.
PR 19-JUL-1999;	99US-0144325.
PR 19-JUL-1999;	99US-0144331.
PR 19-JUL-1999;	99US-0144332.
PR 19-JUL-1999;	99US-0144333.
PR 19-JUL-1999;	99US-0144334.
PR 19-JUL-1999;	99US-0144335.
PR 20-JUL-1999;	99US-0144352.
PR 20-JUL-1999;	99US-0144632.
PR 20-JUL-1999;	99US-0144884.
PR 21-JUL-1999;	99US-0144814.
PR 21-JUL-1999;	99US-0145086.
PR 21-JUL-1999;	99US-0145088.
PR 22-JUL-1999;	99US-0145085.
PR 22-JUL-1999;	99US-0145087.
PR 22-JUL-1999;	99US-0145089.
PR 22-JUL-1999;	99US-0145192.
PR 23-JUL-1999;	99US-0145145.
PR 23-JUL-1999;	99US-0145218.
PR 26-JUL-1999;	99US-0145224.
PR 26-JUL-1999;	99US-0145276.
PR 27-JUL-1999;	99US-0145913.
PR 27-JUL-1999;	99US-0145918.
PR 27-JUL-1999;	99US-0145919.
PR 28-JUL-1999;	99US-0145951.
PR 02-AUG-1999;	99US-0146386.
PR 02-AUG-1999;	99US-0146388.
PR 02-AUG-1999;	99US-0146389.
PR 03-AUG-1999;	99US-0147038.
PR 04-AUG-1999;	99US-0147204.
PR 04-AUG-1999;	99US-0147302.
PR 05-AUG-1999;	99US-0147192.
PR 05-AUG-1999;	99US-0147260.
PR 06-AUG-1999;	99US-0147303.
PR 06-AUG-1999;	99US-0147416.
PR 09-AUG-1999;	99US-0147493.
PR 09-AUG-1999;	99US-0147935.
PR 10-AUG-1999;	99US-0148171.
PR 11-AUG-1999;	99US-0148319.
PR 12-AUG-1999;	99US-0148341.
PR 13-AUG-1999;	99US-0148565.
PR 13-AUG-1999;	99US-0148684.
PR 16-AUG-1999;	99US-0149368.
PR 17-AUG-1999;	99US-0149175.
PR 18-AUG-1999;	99US-0149426.
PR 20-AUG-1999;	99US-0149722.
PR 20-AUG-1999;	99US-0149723.
PR 20-AUG-1999;	99US-0149929.
PR 23-AUG-1999;	99US-0149902.
PR 23-AUG-1999;	99US-0149930.
PR 25-AUG-1999;	99US-0150566.
PR 26-AUG-1999;	99US-0150884.
PR 27-AUG-1999;	99US-0151065.
PR 27-AUG-1999;	99US-0151086.
PR 30-AUG-1999;	99US-0151303.
PR 31-AUG-1999;	99US-0151438.
PR 01-SEP-1999;	99US-0151930.
PR 07-SEP-1999;	99US-0152363.
PR 10-SEP-1999;	99US-0153070.
PR 13-SEP-1999;	99US-0153758.
PR 15-SEP-1999;	99US-0154018.
PR 16-SEP-1999;	99US-0154039.
PR 20-SEP-1999;	99US-0154779.
PR 22-SEP-1999;	99US-0155139.
PR 23-SEP-1999;	99US-0155486.
PR 24-SEP-1999;	99US-0155659.
PR 26-SEP-1999;	99US-0156458.
PR 29-SEP-1999;	99US-0156586.
PR 04-OCT-1999;	99US-0157117.
PR 05-OCT-1999;	99US-0157753.
PR 06-OCT-1999;	99US-0157865.
PR 07-OCT-1999;	99US-0158029.
PR 08-OCT-1999;	99US-0158232.
PR 12-OCT-1999;	99US-0158369.
PR 13-OCT-1999;	99US-0159293.
PR 13-OCT-1999;	99US-0159294.
PR 13-OCT-1999;	99US-0159295.
PR 14-OCT-1999;	99US-0159329.
PR 14-OCT-1999;	99US-0159330.
PR 14-OCT-1999;	99US-0159331.
PR 14-OCT-1999;	99US-0159637.
PR 18-OCT-1999;	99US-0159638.
PR 18-OCT-1999;	99US-0159958.
PR 21-OCT-1999;	99US-0160741.
PR 21-OCT-1999;	99US-0160767.
PR 21-OCT-1999;	99US-0160768.
PR 21-OCT-1999;	99US-0160770.
PR 21-OCT-1999;	99US-0160814.
PR 21-OCT-1999;	99US-0160815.
PR 22-OCT-1999;	99US-0160980.
PR 22-OCT-1999;	99US-0160981.
PR 22-OCT-1999;	99US-0160989.
PR 25-OCT-1999;	99US-0161404.
PR 25-OCT-1999;	99US-0161405.
PR 25-OCT-1999;	99US-0161406.

PR 26-OCT-1999; 99US-0161359.
PR 26-OCT-1999; 99US-0161360.
PR 26-OCT-1999; 99US-0161361.
PR 28-OCT-1999; 99US-0161920.
PR 28-OCT-1999; 99US-0161921.
PR 28-OCT-1999; 99US-0161993.
PR 29-OCT-1999; 99US-0162142.

Query Match 38.1%; Score 377.8; DB 21; Length 1233;
Best Local Similarity 72.0%; Pred. No. 4e-97;
Matches 493; Conservative 0; Mismatches 192; Indels 0; Gaps 0;

QY 219 CCTGCTAGGCTGGGCTGGAGAGCGGCGACCGCTTTTATGAGGCTGAGCCATC 278
DB 153 CCGCTACGGTGGGGGTGGATCAACGCTACCGCCTTTTACGGTGGTGGATCTTC 212
QY 279 TGGCACCATTGGGTGAGCTTGTGGGTATGGAATTTATACAGCAAGGTATGCGACGAA 338
DB 213 CCGGCAATAGGGTGGTGGCTTGTGGATATGGTATATAGCGCAAGGCTACGGACGAG 272
QY 339 CACGGTGGCGCTGAGACCTGCGCTATTTAAACAATGATTAAGTTGTGGCTTGGCTTGA 398
DB 273 CACGGCGGCTTAAGACAGCTCTCTCAACAATGAGCTTAGCTGTGGTCTTCTTGA 332
QY 399 AATGACTTGTACAAAGACCTTAATGAGGCTTCGGGAACCTATTAGGGTCACTGCCAC 458
DB 333 GATAGATGTGAAGAAAGATGTAATGATGTTTACTGCTCATGCTGTGTAACCGCTAC 392
QY 459 CAACCTTTGCCCTCTTACTTGTCTCTCCCTAACAAACAATGATGATGAGTGAACCTCC 518
DB 393 AACTTCTGCCCGCCAAATAGCCGTTAGGAACAATATGGGGTGGTGTATCTCC 452
QY 519 TCTCCAACTTGTGACATGGCTGAGCTGCTCTTCAANTGCTCAATACGAGCTGG 578
DB 453 TCTTGAACACTTGAACCTTGTCTGAGCTGTTTCAACGATTTGCTCAGTACAGACTGG 512
QY 579 TATGCGCCCGCTCTCTTGTGATGAGGCTATGATGAAGAAAGGTGAGGCTTTC 638
DB 513 AATGCTCCGTTTCTTACAGAAAGGTTCTTGCAGAGAGAGGAAATTAATTCAC 572
QY 639 AATCAATGGCACTCATTAATCTTCAACCTGTTTGTATCACAAAGTGGTGGCGACGCA 698
DB 573 GATTAAGCGCCACTCATTAATCTTCAACCTTGTGCTGATCAAAAGTGGTGGTGGCGA 632
QY 699 CGTCACTGTGTGTGATAAAGGGTCTCGAAGTGAATGCAATCATGTATGAATTTG 758
DB 633 CGTTCACTCGGCGCGCATCAAGGGTCAAGAAAGTGGCAAGCTATGTCAAGGAATG 692
QY 759 GGGCCAAACTGGCAAGCAACAATATCTCAATGCGCAAGGCTTCTTCAACTCAC 818
DB 693 GGGGCAAAATGGCAAGCAACTTACCTCAAGGTCAGGCACTTCTTAAAGGTAC 752
QY 819 TCTTATGATGAGTGGCACTCTCACTGCTATTAATCTGTTCTTCAATTTGCAATTTGG 878
DB 753 CACGACGAGCGCGCGACAGTGTCTCTTCAAGCGGCTCTCGCGGCTGTATTAG 812
QY 879 CCAAACTATGAAGGCTTCAATTC 903
DB 813 CCAGACTTTTGGCGGTGACAGTTTC 837

RESULT 11

AAC40035 standard; DNA; 1236 BP.

XX AAC40035;

DT 17-OCT-2000 (first entry)

XX Arabidopsis thaliana DNA fragment SEQ ID NO: 26808.

DE Hybridisation assay; genetic mapping; gene expression control;

KM protein identification; signal transduction pathway;

KW metabolic pathway; promoter; termination sequence; ss.

XX Arabidopsis thaliana.

XX EP1033405-A2.

XX 06-SEP-2000.

XX 25-FEB-2000; 2000EP-0301439.

XX 25-FEB-1999; 99US-0121825.

XX 05-MAR-1999; 99US-0123180.

XX 09-MAR-1999; 99US-0123548.

XX 23-MAR-1999; 99US-0125788.

XX 25-MAR-1999; 99US-0126264.

XX 29-MAR-1999; 99US-0126785.

XX 01-APR-1999; 99US-0127462.

XX 08-APR-1999; 99US-0128234.

XX 16-APR-1999; 99US-0128714.

XX 19-APR-1999; 99US-0128845.

XX 21-APR-1999; 99US-0130077.

XX 23-APR-1999; 99US-0130510.

XX 28-APR-1999; 99US-0130891.

XX 30-APR-1999; 99US-0131449.

XX 04-MAY-1999; 99US-0132048.

XX 04-MAY-1999; 99US-0132407.

XX 05-MAY-1999; 99US-0132484.

XX 06-MAY-1999; 99US-0132485.

XX 06-MAY-1999; 99US-0132486.

XX 07-MAY-1999; 99US-0132487.

XX 11-MAY-1999; 99US-0132487.

XX 14-MAY-1999; 99US-0134219.

XX 14-MAY-1999; 99US-0134219.

XX 14-MAY-1999; 99US-0134221.

XX 18-MAY-1999; 99US-0134370.

XX 18-MAY-1999; 99US-0134768.

XX 19-MAY-1999; 99US-0134941.

XX 20-MAY-1999; 99US-0135124.

XX 21-MAY-1999; 99US-0135353.

XX 24-MAY-1999; 99US-0135629.

XX 25-MAY-1999; 99US-0136021.

XX 27-MAY-1999; 99US-0136392.

XX 28-MAY-1999; 99US-0136782.

XX 01-JUN-1999; 99US-0137222.

XX 03-JUN-1999; 99US-0137528.

XX 04-JUN-1999; 99US-0137502.

XX 07-JUN-1999; 99US-0137724.

XX 08-JUN-1999; 99US-0138094.

XX 10-JUN-1999; 99US-0138540.

XX 10-JUN-1999; 99US-0138847.

XX 14-JUN-1999; 99US-0139119.

XX 16-JUN-1999; 99US-0139452.

XX 16-JUN-1999; 99US-0139453.

XX 17-JUN-1999; 99US-0139492.

XX 18-JUN-1999; 99US-0139454.

XX 18-JUN-1999; 99US-0139454.

XX 18-JUN-1999; 99US-0139455.

XX 18-JUN-1999; 99US-0139456.

XX 18-JUN-1999; 99US-0139457.

XX 18-JUN-1999; 99US-0139458.

XX 18-JUN-1999; 99US-0139459.

XX 18-JUN-1999; 99US-0139460.

XX 18-JUN-1999; 99US-0139461.

XX 18-JUN-1999; 99US-0139462.

XX 18-JUN-1999; 99US-0139463.

XX 18-JUN-1999; 99US-0139750.

XX 18-JUN-1999; 99US-0139763.

XX 21-JUN-1999; 99US-0139817.

XX 22-JUN-1999; 99US-0139899.

XX 23-JUN-1999; 99US-0140353.

XX 23-JUN-1999; 99US-0140354.

XX 24-JUN-1999; 99US-0140695.

```

PR 28-JUN-1999; 99US-0140823.
PR 29-JUN-1999; 99US-0140991.
PR 30-JUN-1999; 99US-0141287.
PR 01-JUL-1999; 99US-0141842.
PR 01-JUL-1999; 99US-0142154.
PR 02-JUL-1999; 99US-0142055.
PR 06-JUL-1999; 99US-0142390.
PR 08-JUL-1999; 99US-0142803.
PR 09-JUL-1999; 99US-0142920.
PR 12-JUL-1999; 99US-0142977.
PR 13-JUL-1999; 99US-0143542.
PR 14-JUL-1999; 99US-0143624.
PR 15-JUL-1999; 99US-0144005.
PR 16-JUL-1999; 99US-0144085.
PR 19-JUL-1999; 99US-0144325.
PR 19-JUL-1999; 99US-0144331.
PR 19-JUL-1999; 99US-0144337.
PR 19-JUL-1999; 99US-0144333.
PR 19-JUL-1999; 99US-0144334.
PR 19-JUL-1999; 99US-0144335.
PR 20-JUL-1999; 99US-0144352.
PR 20-JUL-1999; 99US-0144632.
PR 20-JUL-1999; 99US-0144884.
PR 21-JUL-1999; 99US-0144814.
PR 21-JUL-1999; 99US-0145086.
PR 22-JUL-1999; 99US-0145088.
PR 22-JUL-1999; 99US-0145085.
PR 22-JUL-1999; 99US-0145089.
PR 22-JUL-1999; 99US-0145087.
PR 22-JUL-1999; 99US-0145192.
PR 23-JUL-1999; 99US-0145145.
PR 23-JUL-1999; 99US-0145218.
PR 23-JUL-1999; 99US-0145224.
PR 26-JUL-1999; 99US-0145276.
PR 27-JUL-1999; 99US-0145913.
PR 27-JUL-1999; 99US-0145918.
PR 28-JUL-1999; 99US-0145919.
PR 28-JUL-1999; 99US-0145951.
PR 02-AUG-1999; 99US-0146386.
PR 02-AUG-1999; 99US-0146388.
PR 02-AUG-1999; 99US-0146389.
PR 03-AUG-1999; 99US-0147038.
PR 04-AUG-1999; 99US-0147204.
PR 04-AUG-1999; 99US-0147302.
PR 05-AUG-1999; 99US-0147309.
PR 05-AUG-1999; 99US-0147260.
PR 06-AUG-1999; 99US-0147303.
PR 06-AUG-1999; 99US-0147416.
PR 09-AUG-1999; 99US-0147493.
PR 09-AUG-1999; 99US-0147935.
PR 10-AUG-1999; 99US-0148171.
PR 11-AUG-1999; 99US-0148319.
PR 12-AUG-1999; 99US-0148341.
PR 13-AUG-1999; 99US-0148565.
PR 13-AUG-1999; 99US-0148684.
PR 16-AUG-1999; 99US-0149368.
PR 17-AUG-1999; 99US-0149175.
PR 18-AUG-1999; 99US-0149426.
PR 20-AUG-1999; 99US-0149722.
PR 20-AUG-1999; 99US-0149723.
PR 20-AUG-1999; 99US-0149929.
PR 23-AUG-1999; 99US-0149902.
PR 23-AUG-1999; 99US-0149930.
PR 25-AUG-1999; 99US-0150566.
PR 26-AUG-1999; 99US-0150884.
PR 27-AUG-1999; 99US-0151065.
PR 27-AUG-1999; 99US-0151066.
PR 27-AUG-1999; 99US-0151080.
PR 30-AUG-1999; 99US-0151303.
PR 31-AUG-1999; 99US-0151438.
PR 01-SEP-1999; 99US-0151930.
PR 07-SEP-1999; 99US-0152363.

PR 10-SEP-1999; 99US-0153070.
PR 13-SEP-1999; 99US-0153758.
PR 15-SEP-1999; 99US-0154018.
PR 16-SEP-1999; 99US-0154039.
PR 20-SEP-1999; 99US-0154779.
PR 22-SEP-1999; 99US-0155139.
PR 23-SEP-1999; 99US-0155486.
PR 24-SEP-1999; 99US-0155659.
PR 28-SEP-1999; 99US-0156458.
PR 29-SEP-1999; 99US-0156596.
PR 04-OCT-1999; 99US-0157117.
PR 05-OCT-1999; 99US-0157753.
PR 06-OCT-1999; 99US-0157865.
PR 07-OCT-1999; 99US-0158029.
PR 08-OCT-1999; 99US-0158232.
PR 12-OCT-1999; 99US-0158369.
PR 13-OCT-1999; 99US-0159293.
PR 13-OCT-1999; 99US-0159294.
PR 13-OCT-1999; 99US-0159295.
PR 14-OCT-1999; 99US-0159329.
PR 14-OCT-1999; 99US-0159330.
PR 14-OCT-1999; 99US-0159331.
PR 14-OCT-1999; 99US-0159637.
PR 14-OCT-1999; 99US-0159638.
PR 18-OCT-1999; 99US-0159584.
PR 21-OCT-1999; 99US-0160741.
PR 21-OCT-1999; 99US-0160757.
PR 21-OCT-1999; 99US-0160768.
PR 21-OCT-1999; 99US-0160770.
PR 21-OCT-1999; 99US-0160814.
PR 21-OCT-1999; 99US-0160815.
PR 22-OCT-1999; 99US-0160980.
PR 22-OCT-1999; 99US-0160981.
PR 22-OCT-1999; 99US-0160989.
PR 25-OCT-1999; 99US-0161404.
PR 25-OCT-1999; 99US-0161405.
PR 25-OCT-1999; 99US-0161406.
PR 26-OCT-1999; 99US-0161359.
PR 26-OCT-1999; 99US-0161360.
PR 26-OCT-1999; 99US-0161361.
PR 26-OCT-1999; 99US-0161920.
PR 28-OCT-1999; 99US-0161992.
PR 28-OCT-1999; 99US-0161993.
PR 29-OCT-1999; 99US-0162142.

Query Match 37.0%; Score 366.8; DB 21; Length 1236;
Best Local Similarly 71.9%; Pred. No. 5.4e-94;
Matches 493; Conservative 0; Mismatches 192; Indels 1; Gaps 1;

QY 219 CGCTAGCTAGCGGTGGCTGGGAGAGCGGCCAGCGCACCCTTTTATGCTGTGTGACGATC 278
DB 155 CGTCTACGTGGCGGTGGATCAACGCTCAGCGCACCCTTTTACGCTGTGTGTGCTTC 214
QY 279 TGGCACCATGGGTGAGAGCTTGTGGTATGGAAATTTATACAGCCAGGATGACAGAA 338
DB 215 CGGCAATATGGGTGGTGTCTGTGGATATGTTATCTATATAGCCATAGCGGAGAG 274
QY 339 CAGGTGGCGCTGAGCACTG-CGCTATTTAACAATGATTAAGTTGTGTGCTTTCG 397
DB 275 CACGGCGGCTTGAAGCAGACGACGCTCTTCAACATGACTTAGCTGTGTCTTTCGTTTG 334
QY 398 AAATGACTTGTAAAGAGCAACCTTAATGAGCCCTCCGGAACTATAGGTCACGCCA 457
DB 335 AGATTAAGATGTAAAGAGATGTAAATGATGTATTACTGTGCTCAATGCTTTGTAACCGCTA 394
QY 458 CCAACTTTGCGCTCTTAACCTTGTCTCCCTTAACAACAATGATGTGACACCTTC 517
DB 395 CAAACTTGTGCGCGCAAAATAGCGGTATAGCAACAATATGCGGTTGTATATCTTC 454
QY 518 CTCTCAACACTTGCAGATGCTGAGCTGTGCTTCTTCAATGCTCAATACCGAGCTG 577
DB 455 CTCTTGAACACTTGTGACCTGTGACGCTGTCTTTTTCAAACGCAATGTCTCAGTACAGAGCTG 514

```

QY	578	GTATCGCCCGCCGCTCCTTTGCAAGGGATACATGATGAAGAAAGTGGAGTGAGTTTA	637
Db	515	GAATCGTCCCTGTTTCTCTACAGAGGGTTCCTTCAGAGAGAGAGAGAAATTAAGATTCA	574
QY	638	CAATCAATGGCCCACTCATPACTTCAACCTTGTTTGATCAAAACGTGGTGCGCAGGCG	697
Db	575	CGATTAACCGGCCACTCATPACTTCAACTTGTGCTGATCAAAACGTGGTGCGCGAG	634
QY	698	ACGTCCACTCTGTGTGATTAAGGGGTCTCGAACTGGATGGCAATCCATGTCTTGAATTT	757
Db	635	ACGTTCACTCGGGGGGATCAAGGGTTCAGAAACGTGTGGCAAGCTATGTCAAGGAAC	694
QY	758	GGGGGCCAAAACGTGCAAGCAACAACTATCTCAATGGCCAAAGGCGCTTCTTTCAAGTCA	817
Db	695	GGGGGCCAAAATTTGGCAAGCAACTCTTACTCTAAGCGTCAGCACTTTCTTTAAGTCA	754
QY	818	CTCTTAGTAGTGTGTCACACTCTCACTGCGCTATATCTCGTTCCTTCAATTTGGCAATTTG	877
Db	755	CCACACAGCGACGCGCCACAGTGTTGTCTCTTCAACGCGCTCTCGCGGTGCTTATG	814
QY	878	GCCAAACCTTATGAAGCGCTCAATTTC	903
Db	815	GCCAGACTTTTGGCGGTGACAGTTTC	840

RESULT 12

ABA97164	standard; DNA; 687 BP.
ABA97164;	
ABA97164;	
19-APR-2002	(first entry)
N. tabacum DNA encoding expansin nexp4a.	
Expansin; cellulose-based textile; cotton; paper recycling; csexp4a;	
paper pulp; plant tissue; papermaking; gene; tobacco; ds.	
Nicotiana tabacum.	
Key	Location/Qualifiers
FT CDS	1..687
FT	/*tag= a
FT	/partial
FT	/product= "nexp4a"
FT	/note= "No start or stop codon disclosed"
XX	
PN	DE10032630-A1.
XX	
PD	22-NOV-2001.
XX	
PF	05-JUL-2000; 2000DE-1032630.
XX	
PR	16-MAY-2000; 2000DE-1023561.
XX	
PA	(FARB) BAYER AG.
XX	
PI	Berendes F, Raet HG, Vogt U, Gouloudis C;
XX	
DR	WPI: 2002-155755/21.
XX	P-PsDB; AAG80771.
PT	Vector encoding an expansin, useful in treatment of cellulosic
XX	materials for paper recycling, providing large-scale production
PS	Claim 2; Page 19-21; 22pp; German.
CC	This invention describes a novel vector (A) comprising (i) nucleic acid
CC	(1) encoding an expansin (II) and (ii) coupled sequences that allow
CC	expression of (i) in microorganisms. The recombinant expansins described
CC	in the invention are used in preparation, treatment and finishing of
CC	cellulose-based textiles (e.g. cotton) or in recycling of paper or for
CC	preparation of pulp from plant tissue, as a substitute for corrosive.

CC	chemicals currently used in papermaking. Recombinant methods make
CC	possible large scale production of extensin possible. This sequence
CC	encodes the Lycopersicon esculentum (tomato) extensin, described
CC	in the invention.
XX	
XX	
Seq	Sequence 687 BP; 183 A; 128 C; 170 G; 206 T; 0 other;
Query Match	36.5%; Score 361.8; DB 24; Length 687;
Best Local Similarity	70.9%; Pred. No. 1,le-92;
Matches 480; Conservative	0; Mismatches 197; Indels 0; Gaps 0
Oy	229 GGTGGCTTGGCAGACGCGCACGCCACTTTATGTGTGTGTGCATCTGGCAACCATG 288
Db	10 GGAGGTGGATTAAATGCTACATGTAACCTTTATGTGTGTGTGATGTCCTGGCAAAATG 69
Oy	289 GGTGAGCTTGTGGGTATGGGAATTTATACAGCCCAAAGGTATGCAACCAACGGTGGG 348
Db	70 GGTGGGGGATGTGATATGAAATTTGTATAGCCAAAGGATATGTAACAATATCTCAGCA 129
Oy	349 CTGAGCACTGGCGCTATTATTAACATAGSATTTAAGTTGTGGTGCTTGCTTGCAGAAATGA 408
Db	130 TTAAATACAGTAAATGTTTACAAATAGGCTTGAGCTGTGTTCTTGTATTGATGATAAGTGT 189
Oy	409 ACAACAGACCTTAATGTGTGCTTCGGGAACTATTAAGGTCATCTCCACCAACTTTTGC 468
Db	190 GTGATATGATAGGAAGAAGGTGTGTGCTGTGTTCAATGTGTGATGATCAACCAATTTTTC 249
Oy	469 CCTCTTAACTTTGCTCTCTCCCPAACACAATGTGTGATGTGTCAACCTCTCTTCCAAC 528
Db	250 CCACCAATATATGATATGCTCTTAACATGACAGGGGGTGTGTATATCTCCCTTACCAT 309
Oy	529 TTGCACATGSGTGAGGCGCTTCCTTGAATTCGCTCAATCCGAGCTGTATCGCCCC 588
Db	310 TTGATATCTCTCAGCCTTAATTTTCCACACATGCTCAATACAAAGCTGGAATGTCTT 369
Oy	589 GTCTCTTTCCTTAGGGTACCATGTATGAAGAAGGTGAGTGAAGGTTTACATCAATGAGC 648
Db	370 GTTGCTTACAGAAAGGTATCCCTGCAGAAAGAGGAGGTATTAAGTTTACATCAATGSA 429
Oy	649 CACTCATATCTCOAACCTTCGTTTTGATCAAAAAGTGGTGGCGACAGGCACTCCAATT 708
Db	430 CACTCATATCTCAACCTTGTACTTGTATCAAAATGTGTGGTGGTGTGATGTATGCT 489
Oy	709 GTGTGATTAAGGGGTCTCGAATGAGATGGAATCATGTCATAGAAATTTGGGGCCAAAC 768
Db	490 GTTGTGTAAAGATCAAGAACTGGTGTGGCAACCAATGTCAAGAACTGGGGCAAAAC 549
Oy	769 TGCGAAAGCAACAATATCTCATAGCGCAAGGCTTTCTTTCAAGTCACTCTTAGTAT 828
Db	550 TGGCAAAACAACATATATCTTAATGCGCAACGCTCTCATTTAAGTTACTACAGTAT 609
Oy	829 GGTGCACTGCACTGCTTATATCTGTTCTTCAATTTGGCAATTTGGCCAAACTAT 888
Db	610 GGCGGCAATTTGATTTCTTACAAATGTTGACCTGCTCATTTGTTTGGACAGACTTAT 669
Oy	889 GAAGGCTCTCAATTTCTA 905
Db	670 ACTGGAGCTCAATTTCA 686
RESULT 13	
ABZ12286	
ID	ABZ12286 standard; DNA; 753 BP.
XX	ABZ12286;
XX	
DT	21-JAN-2003 (first entry)
XX	
DE	Arabidopsis thaliana stress regulated gene SEQ ID NO 91.
XX	
KX	Arabidopsis thaliana; plant; gene; stress; transgenic; ds.
XX	
OS	Arabidopsis thaliana.

XX WO200216655-A2.
 PN 28-FEB-2002.
 PD 24-AUG-2001; 2001MO-US26685.
 XX 24-AUG-2000; 2000US-227866P.
 XX 26-JUN-2001; 2001US-264647P.
 PR 22-JUN-2001; 2001US-300111P.
 XX (SCRI) SCRIIPS RES INST.
 PA (SYGN) SYNGENTA PARTICIPATIONS AG.
 XX Harper JF, Kreps J, Wang X, Zhu T;
 PI WPI; 2002-304127/34.
 DR Identifying a stress condition to which a plant cell has been exposed
 PT and producing plants with increased tolerance to these abiotic stresses
 PT
 XX
 XX
 PS Claim 14; SEQ ID NO 91; 577pp + Sequence Listing; English.
 CC The invention relates to identifying a stress condition to which a plant
 CC cell has been exposed, comprising:
 CC (a) contacting nucleic acid representative of expressed polynucleotides
 CC in the plant cell with an array or probes representative of the plant
 CC cell genome; and
 CC (b) detecting a profile of expressed polynucleotides in the plant cell
 CC characteristic of a stress response. The method is useful in the
 CC production of transgenic plants, cells and seeds and in producing plants
 CC with increased tolerance to abiotic stress. The present sequence is that
 CC of an Arabidopsis thaliana stress regulated gene (AB212196-AB217574) used
 CC in methods of the invention.
 CC Note: The sequence data for this patent is not represented in the printed
 CC specification but is based on sequence information supplied to Derwent by
 CC the European Patent Office.
 XX
 XX
 SO Sequence 753 BP; 196 A; 187 C; 187 G; 183 T; 0 other;
 Query Match 36.4%; Score 360.6; DB 24; Length 753;
 Best Local Similarity 71.1%; Pred. No. 2.5e-92;
 Matches 477; Conservative 0; Mismatches 194; Indels 0; Gaps 0;
 QY 229 GGTGGCTGGGAGCGGCGGCACTTTATGCTGCTGATGCGATCTGGCAGCATG 288
 DB 73 GGAAGTGGGTCAACGACGACGCACTTCTACGCTGCTGATGCTTCCGACACATG 132
 QY 289 GGTGAGCTTGTGGGTATGGAAATTTATACAGCCAAAGGTATGACGACGATGGCG 348
 DB 133 GGAAGTGGGTCAACGACGACGCACTTCTACGCTGCTGATGCTTCCGACACATG 192
 QY 349 CTGAGCACTGGCGTATTTAACAATGATTAAGTTGCTGCTTCTGGAATGACTTGT 408
 DB 193 CTAAGCAGCGGCTCATTCATTAATGCTTAAGTTGCTGCTTCTGGAATGATG 252
 QY 409 ACAAGAGACCTTAATGCTGCTTCCGGAATTTAGGCTCACTGACCAACTTTTGC 468
 DB 253 CAAAGAGATGAAATGCTGCTTCCGGAATTTAGGCTCACTGACCAACTTTTGC 312
 QY 469 CTTCTCACTTGTGCTGCTTCCGGAATTTAGGCTCACTGACCAACTTTTGC 528
 DB 313 CTTCTCACTTGTGCTGCTTCCGGAATTTAGGCTCACTGACCAACTTTTGC 372
 QY 529 TTGACATGCTGCTGCTTCCGGAATTTAGGCTCACTGACCAACTTTTGC 588
 DB 373 TTGATCTCTCTGAGCCGCTATTTCAACGATGCTCAATACAGAGCCGCAATGTC 432
 QY 589 GTTCTCTTGTGAGGCTGACCATGATTAAGAAAGTGAAGTGAAGTTTACATCAATG 648
 DB 433 GTGCTTACGGAAGTGGCTGCTGCTGGAAGAGAGGAATTAAGTTTACATCAATG 492

QY 649 CACTCACTTCAACCTCGTTTGTATCAAAAGCTGGTGGCGAGCGAGCTTCACTCT 708
 DB 493 CACTCACTTCAACCTCGTTTGTATCAAAAGCTGGTGGCGAGCGAGCTTCACTCT 552
 QY 709 GTTCTCTTGTGAGGCTGCTGCACTGATGATGCAATTCATGCTTGAATTTGGGCGAAAC 768
 DB 553 GCGATGTTTAAAGTTTCAAAAGCTGATGATGCAAGCGATGTCAGAAATCTGGGACAGAAC 612
 QY 769 TGGCAAGCAACAACATATCTCAATGAGCGGCTTCTTCAAGTCACTTTAGTAT 828
 DB 613 TGGCAAGTCACTTCACTTCACTTCAAGCAATCTTCTTCAATTCAGATTAACAGAGCAT 672
 QY 829 GGTGCACTCTCACTGCTATTAATCTGCTTCTTCAATTTGCAATTTGGCAACCTAT 888
 DB 673 GGCCAACCATGCTCTCTAACAACGTTGCTAAGCAGGCTGCTTTCGCGACGACCTTC 732
 QY 889 GAAGGCGCTCA 899
 DB 733 ACAGGTGCGCA 743

RESULT 14

AB213264
 ID AB213264 standard; DNA; 747 BP.

XX AB213264;

AC 21-JUN-2003 (first entry)

DT Arabidopsis thaliana stress regulated gene SEQ ID NO 1069.

DE Arabidopsis thaliana; plant; gene; stress; transgenic; ds.

XX Arabidopsis thaliana.

OS Arabidopsis thaliana.

XX WO200216655-A2.

PN 28-FEB-2002.

PD 24-AUG-2001; 2001MO-US26685.

PF 24-AUG-2000; 2000US-227866P.

PR 26-JUN-2001; 2001US-264647P.

PR 22-JUN-2001; 2001US-300111P.

XX (SCRI) SCRIIPS RES INST.

PA (SYGN) SYNGENTA PARTICIPATIONS AG.

XX Harper JF, Kreps J, Wang X, Zhu T;

PI WPI; 2002-304127/34.

DR Identifying a stress condition to which a plant cell has been exposed

PT and producing plants with increased tolerance to these abiotic stresses

PT
 XX
 XX
 PS Claim 14; SEQ ID NO 1069; 577pp + Sequence Listing; English.
 CC The invention relates to identifying a stress condition to which a plant
 CC cell has been exposed, comprising:
 CC (a) contacting nucleic acid representative of expressed polynucleotides
 CC in the plant cell with an array or probes representative of the plant
 CC cell genome; and
 CC (b) detecting a profile of expressed polynucleotides in the plant cell
 CC characteristic of a stress response. The method is useful in the
 CC production of transgenic plants, cells and seeds and in producing plants
 CC with increased tolerance to abiotic stress. The present sequence is that
 CC of an Arabidopsis thaliana stress regulated gene (AB212196-AB217574) used
 CC in methods of the invention.
 CC Note: The sequence data for this patent is not represented in the printed
 CC specification but is based on sequence information supplied to Derwent by
 CC the European Patent Office.
 XX

XX,

PR 29-JUN-1999; 99US-0140991


```
Db 481 AGCCGTGTTTCAAGCATTGCTCAGTACAAAAGCTGTGTGTGTCCTGTTTCTTACAGAA 540
Qy 602 GGGTACCATGTATGAGAAAGGTGAGTGAAGTTTACAAATCAATGGCCACTCATACTTCA 661
Db 541 GGGTCCGTAATGAGAAAGAGGTATATGATTCACATCAACGGTCACTCTTACTTCA 600
Qy 662 AACCTGTTTGAATCAAAAGTCCGTGGGGCAAGCGACGTCCACTCTGTGTGATPAAAG 721
Db 601 ACCTTGTCTTGGTGAACCAATGTGTGTGTGTGAGATGTTCATTCGTTGCGTTAAG 660
Qy 722 GGTTCGAACGTGATGGCAATCATGTCTAGAAAATTGGGGCCAAAACGTGGCAAGCAACA 781
Db 661 GTTCTAGAACAGGTGGCAACAATGTCAAGAACTGGGGACAGAACTGGCAAGCAACA 720
Qy 782 ACTATCTCAATGGCCAAAGGCTTTCTTCAAGTCACTCTTAGTAGATGGTGGCACTTCA 841
Db 721 ATCTCTTAAACGTCAGACATTGTCAATTAAAGTGACTCTAGTAGATGGTGGTACCGTCG 780
Qy 842 CTGCTATATCTCTGTTCTTCCATTGGCAATTTGGCCAAACCTTATGAAAGGCCCTCAT 901
Db 781 TCTCTAACAACATGTGCTCCAGCTAGTGTGTCTTGGACAAACCTTCACCGGCCGTCAAT 840
Qy 902 TC 903
Db 841 TC 842
```

Search completed: December 18, 2003, 20:56:17
Job time : 317 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 18, 2003, 21:57:27 ; Search time 362 Seconds
(without alignments)
9131.342 Million cell updates/sec

Title: US-09-383-579C-9

Perfect score: 992
1 gaataatcaacaacattgc.....aacacaaacgcgaacac 992

Scoring table: IDENTITY NUC

Gapop 10.0, Gapext 1.0

Searched: 2211978 seqs, 1666101734 residues

Total number of hits satisfying chosen parameters: 4423956

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: Published Applications NA:*
2: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:*
3: /cgn2_6/ptodata/1/pubpna/PTCT_NEW_PUB.seq:*
4: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*
5: /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:*
6: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:*
7: /cgn2_6/ptodata/1/pubpna/PTCTUS_PUBCOMB.seq:*
8: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq:*
9: /cgn2_6/ptodata/1/pubpna/US09_PUBCOMB.seq:*
10: /cgn2_6/ptodata/1/pubpna/US09_PUBCOMB.seq:*
11: /cgn2_6/ptodata/1/pubpna/US09C_PUBCOMB.seq:*
12: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:*
13: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq2:*
14: /cgn2_6/ptodata/1/pubpna/US10_PUBCOMB.seq:*
15: /cgn2_6/ptodata/1/pubpna/US10_PUBCOMB.seq:*
16: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:*
17: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:*
18: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	681	68.6	681	US-09-896-301-1	Sequence 1, Appl1
2	394.2	39.7	762	US-09-938-842A-1088	Sequence 1088, Ap
3	386.2	38.9	1153	US-10-150-559-3	Sequence 3, Appl1
4	373.8	37.7	753	US-10-409-701-8	Sequence 8, Appl1
5	360.6	36.4	753	US-09-938-842A-91	Sequence 91, Appl1
6	360.4	36.3	747	US-09-938-842A-1069	Sequence 1069, Ap
7	341.6	34.4	774	US-09-938-842A-89	Sequence 89, Appl1
8	301.2	30.1	893	US-09-938-842A-842	Sequence 842, Ap
9	298.8	29.8	9	US-09-770-445-491	Sequence 491, App
10	270	27.2	410	US-09-878-574-3973	Sequence 3973, Ap
11	251.2	25.3	768	US-09-938-842A-1046	Sequence 1046, Ap
12	251	25.3	391	US-09-878-574-62	Sequence 62, Appl1
13	169.2	17.1	366	US-09-770-791-430	Sequence 430, Ap
14	149	15.0	373	US-09-878-574-3468	Sequence 3468, Ap
15	148.6	15.0	391	US-09-878-574-1206	Sequence 1206, Ap

16	92.6	9.3	293	9	US-09-294-093B-2002	Sequence 2002, Ap
17	90	9.1	394	10	US-09-878-574-2728	Sequence 2728, Ap
18	88.8	9.0	1262	10	US-09-878-574-14926	Sequence 14926, A
19	80.8	8.1	285	10	US-09-878-574-13597	Sequence 13697, A
20	73.4	7.4	259	10	US-09-878-574-12313	Sequence 12313, A
21	50.6	5.1	352	10	US-09-867-701-7077	Sequence 7077, Ap
22	48.6	4.9	238	9	US-09-294-093B-4389	Sequence 4389, Ap
23	48	4.8	5568	13	US-10-111-455-621	Sequence 621, Ap
24	47.4	4.8	380	9	US-09-770-791-183	Sequence 183, App
25	47.2	4.8	3673778	13	US-10-312-841-1	Sequence 1, Appl1
26	46.6	4.7	12601	13	US-10-311-455-2179	Sequence 2179, Ap
27	46.2	4.7	4177	11	US-09-945-373-23	Sequence 23, Appl1
28	46.2	4.7	4177	11	US-10-035-212-23	Sequence 23, Appl1
29	46.2	4.7	4177	16	US-10-075-446-23	Sequence 23, Appl1
30	45	4.5	533	13	US-10-027-632-195881	Sequence 195881, Sequence 195881,
31	45	4.5	533	14	US-10-027-632-195881	Sequence 195881,
32	45	4.5	598	13	US-10-027-632-194545	Sequence 194545,
33	45	4.5	598	14	US-10-027-632-194545	Sequence 194545,
34	44.6	4.5	8666	13	US-10-311-455-369	Sequence 369, App
35	43.8	4.4	2774	13	US-09-814-353-20554	Sequence 20554, A
36	43.6	4.4	16668	13	US-10-311-455-294	Sequence 294, App
37	43	4.3	42533	13	US-10-004-113-43	Sequence 43, Appl1
38	42.8	4.3	593	13	US-10-027-632-158420	Sequence 158420,
39	42.8	4.3	593	13	US-10-027-632-158421	Sequence 158421,
40	42.8	4.3	593	14	US-10-027-632-158420	Sequence 158420,
41	42.8	4.3	593	14	US-10-027-632-158421	Sequence 158421,
42	42.4	4.3	5455	13	US-10-312-841-2	Sequence 34, Appl1
43	42.4	4.3	3673778	13	US-10-312-841-2	Sequence 2, Appl1
44	42	4.2	235	10	US-09-867-701-8842	Sequence 8842, Ap
45	41.8	4.2	903	13	US-10-029-386-20462	Sequence 20462, A

ALIGNMENTS

RESULT 1
US-09-896-301-1
Sequence 1, Application US/09896301
Patient No. US20020103355A1
GENERAL INFORMATION:
APPLICANT: Cosgrove, Daniel J
APPLICANT: McQueen-Mason, Simon
APPLICANT: Gullitman, Mark J
APPLICANT: Sncherban, Tatyana
APPLICANT: Shi, Jun
TITLE OF INVENTION: PURIFIED EXPANSIN PROTEINS
FILE REFERENCE: 1194/1C114US3
CURRENT FILING DATE: 2001-06-29
PRIOR APPLICATION NUMBER: 09/092,160
PRIOR FILING DATE: 1998-06-05
PRIOR APPLICATION NUMBER: 08/440,517
PRIOR FILING DATE: 1995-05-12
PRIOR APPLICATION NUMBER: 08/242,090
PRIOR FILING DATE: 1994-05-12
PRIOR APPLICATION NUMBER: 08/060,944
PRIOR FILING DATE: 1993-05-12
NUMBER OF SEQ ID NOS: 7
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 1
LENGTH: 681
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: cDNA cucumber
US-09-896-301-1

Query Match 68.6%; Score 681; DB 10; Length 681;
Best Local Similarity 100.0%; Pred. No. 2.8e-188;
Matches 681; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 223 GACTACGCTGGCTGGACGCGCACCTTTATGTGTGTGATGACGATCTGGC 282

QY	349	TTGAGCAGTCGGCATTTTAAACAATGAAATTAAGTTGTGGTGCCTTGCGAAATGACTTGT	408
Db	654	TTTANGCAGCGGCTCTGTTCAACAAATGTTTTAGCTGTGTGCTCTGTTTGAGAGCTCAAAATGT	595
QY	409	ACAAACGACCCCTAAATGATGTCCTTCCGGAAA-----CTATTAGGTCACCTGCACCAAC	462
Db	594	GCTAGTGATCCAAATATGATGTCATTCTGTGTGTGTCCTTCAATCTTCATCAGTCGCATAT	535
QY	463	TTTTGGCCCTCTTAATTTGCTGTCCCTTAACAACAATGGTGAATGGTGAACCCCTCTCTC	522
Db	534	TTGTGTCTTCGAACTTTGCTCAAGCTAAGTGAACAATGGTGGTGGTGAACCTCTTCA	475
QY	523	CAACACTTCGACATAGGCTGAGCCTGACCTTCCCTCAAAATCGCTCAATACCGAGCTGTATC	582
Db	474	CTTCACTTTGATATCTTGCTATGTCCTATGTTTCTCAAGATCGCTGATATCGTGCGGGAATC	415
QY	583	GTCGCCGTCTCTTTTCGTAGGGTACCATGATGAAAGAAAGGTGAGTGAAGTTTCAATC	642
Db	414	GTCCCGCTCTCTTCCCGCGAGTCCATGCGGGAAGAGAGAGGAATTAAGTTCAAAATC	355
QY	643	AATGGCCATCATCTTCAACCTGTTTGAATCAAAAGTCGGTGGGCGAGGCGACGTC	702
Db	354	AACGTTTCGTTATTTTAATCTGTGTCTAGTCACTAAACGNNNNNGGCGCGAAACATA	295
QY	703	CACCTGTGTGATTAAGAGGGGTCTCGAAGTGGATGGCAATCCATGCTAGAATTTGGGGC	762
Db	294	GTCGGGCTAGGTGTGAAGAAACAAATCTTCGTGATGACATATAGTCGTAACTGGGGA	235
QY	763	CAAAACTGGCAAGCAACAATATCTCATATGSCCAAGGCTTTCTTTCAAGTCACTCTT	822
Db	234	CAAAACTGGCAATTAATCACTGATTTGGTGTGTGATCAGTCACTTCTTTAGAGTCAACAAC	175
QY	823	AGTATGGTGCACCTCTCACGCCCATATATCTCGTTCCCTTCAATTTGGCAATTTGGCCAA	882
Db	174	AGTATCGTGAAGCTGACGTCGTGAAACATTTGCTCCGGCAATTTGGAATTTGGTCAG	115
QY	883	ACCT 886	
Db	114	ACTT 111	

RESULT 10
US-09-878-574-3973
; Sequence 3973, Application US/09878574
; Patent No. US20020110548A1
GENERAL INFORMATION:
APPLICANT: Byrum, Joseph R.
APPLICANT: La Rosa, Thomas J.
APPLICANT: Thompson, Michael D.
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
FILE REFERENCE: 38-21(15401)B
CURRENT APPLICATION NUMBER: US/09/878,574
CURRENT FILING DATE: 2001-12-21
PRIOR APPLICATION NUMBER: 09/333,535
PRIOR FILING DATE: 1999-06-14
NUMBER OF SEQ ID NOS: 15775
SEQ ID NO 3973
LENGTH: 410
TYPE: DNA


```

Db      61 ATTGCTGAATATAGAGCTGGAATTTGCTGCTGCTTGCAGAGGGTCTCTGTGTGAAA 120
QY      619 AAAGGTGAGTGAAGTTTAAATCAATGAGCACTCAATCTCAACTGCTTTTGTATGACA 678
Db      121 AAGGGAGGAATAGAGTTTCAATCAATGAGCACTCTTACTCTCAACTAGTTTGTATGACC 180
QY      679 AACGTGCTGGGCGGAGGCGACGCTCTGTGTGTGATTAAGGGGTCTGGAAGTGTATG 738
Db      181 AATGTGCTGAGCTGTGTATGTGAATTCATTAAGGGTCCAAACTGGGGTGG 240
QY      739 CAATCATGTCTAGAAATTTGGGGCCAAACTGGCAAGCAACAATATCTCAATGAGCCAA 798
Db      241 CAGCCCATTTCAAGAACTGGGGGCAAACTGGCAAGCAACTCATACTTCAATGAGCAA 300
QY      799 GGCCTTTCTTTCAAGTCACTTTAGTGTGTGTGAGTGTGCACTCTCACTCATATCTGTT 858
Db      301 TNCCTCTCTTTCAAGTCAACACAGTGTATGAGCAAGTGTGCAAGCTTCAATGTGGCA 360
QY      859 CCTTCAATTTGGCAATTTGGCCCAACCT 886
Db      361 CCAGCCAAATTTGGCAATTTGGCCAGACT 388

```

RESULT 13

```

US-09-770-791-430
; Sequence 430, Application US/09770791
; Patent No. US20020062014A1
; GENERAL INFORMATION:
; APPLICANT: Gorlach, Jörn
; APPLICANT: An, Yong-Qiang
; APPLICANT: Hamilton, Carol M.
; APPLICANT: Price, Jennifer L.
; APPLICANT: Raines, Tracy M.
; APPLICANT: Yu, Yang
; APPLICANT: Rameaka, Joshua G.
; APPLICANT: Page, Amy
; APPLICANT: Mathew, Abraham V.
; APPLICANT: Ledford, Brooke L.
; APPLICANT: Woessner, Jeffrey P.
; APPLICANT: Haas, William David
; APPLICANT: Garcia, Carlos A.
; APPLICANT: Kriker, Maïa
; APPLICANT: Slader, Ted
; APPLICANT: Davis, Keith R.
; APPLICANT: Allen, Keith
; APPLICANT: Hoffman, Neil
; APPLICANT: Hurlan, Patrick
; TITLE OF INVENTION: Expressed Sequences of Arabidopsis
; FILE REFERENCE: 2029 (PAPA-018PRV)
; CURRENT APPLICATION NUMBER: US/09/770,791
; PRIOR FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: 60/178,480
; NUMBER OF SEQ ID NOS: 999
; SOFTWARE: FaSTSeq for Windows Version 4.0
; SEQ ID NO 430
; LENGTH: 366
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-770-791-430

```

```

Query Match      17.1%; Score 169.2; DB 9; Length 366;
Best Local Similarity 71.7%; Pred. No. 6.6e-39;
Matches 238; Conservative 0; Mismatches 88; Indels 6; Gaps 1;

```

```

QY      228 CGGTGCTGGCAGAGCGGCGCCACCTTTATGTGTGTGTGAGCATCTGGCAACT 287
Db      35 CGGACCGGTGGCAGAAATGCAACCCCACTTCTACGGTGTGAGAGCGCTCCGCGCAAT 94
QY      288 GGGTGAAGCTTGTGGTATGGAATTTATACAGCAAGGTATGAGCAAGCAAGCGGTGGC 347
Db      95 GGGCGGCGGTGTGGTGTGAGGAACTTTATACAGCAAGGTATGAGCAAGCGGTGGC 154

```

```

QY      348 GCTGAGCACTGGCGCTATTATTAACATGATTAAGTTGTGTGCTTCTGGAATGACTTG 407
Db      155 GTTGAGCACTGGCTTTGTTCACACGATTCAGCTGTGTGTCTTTTGAATTAAGTG 214
QY      408 TACAAACGACCCCTAATGAGTGTCTCCGGGAA-----CTATTAGAGTCACTGCCACAA 461
Db      215 TACTGATGATCCGAATGAGTGTGTCTCCGGGAAATCATCTATTCTTTGTAGCGGCAAGAA 274
QY      462 CTTTGGCCCTCTTAATCTTGTCTCTCCCTAACAACAATGAGTGTGATGAGTCACTCTCT 521
Db      275 CTTTGTTCGCGGAATTTTGTCTCAGCCGAGTACGACGAGGAGGTGTGCAATCCGCGCG 334
QY      522 CCAACACTTGCACATGAGTGTGAGCTTCTCC 553
Db      335 CGAGCATTTTGTATCTCGCATCTCATATGTTCC 366

```

RESULT 14

```

US-09-878-574-3468
; Sequence 3468, Application US/09878574
; Patent No. US20020110548A1
; GENERAL INFORMATION:
; APPLICANT: Byrum, Joseph R.
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Thompson, Michael D.
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
; FILE REFERENCE: 38-21(15401) B
; CURRENT APPLICATION NUMBER: US/09/878,574
; PRIOR FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: 09/333,535
; NUMBER OF SEQ ID NOS: 15775
; SEQ ID NO 3468
; LENGTH: 373
; TYPE: DNA
; ORGANISM: Glycine max
; OTHER INFORMATION: Clone ID: LIB3028-010-Q1-B1-E9
US-09-878-574-3468

```

```

Query Match      15.0%; Score 149; DB 10; Length 373;
Best Local Similarity 74.3%; Pred. No. 5.3e-33;
Matches 188; Conservative 0; Mismatches 65; Indels 0; Gaps 0;

```

```

QY      222 TGACTACGCTGTGCTGCGCAGAGCGGCGCCACCTTTATGTGTGTGTGACGACTTGG 281
Db      65 TGGTTTGGAGGTTTGGACCAATGCAATGCACTTCTATGAGAGGGGGTGTGCTTCTGG 124
QY      282 CACCATGGGTGAGCTTGTGTGTATGGAATTTATACAGCCAAAGGTATGACGAAAC 341
Db      125 GACATGTGGGTGGGCTTGTGTGTATGGAATCTGTATAGCCAAAGTTATGAACTGATAC 184
QY      342 GGTGGCGTGAAGCACTGCGCTATTATTAACAATGATTAAGTGTGTGTGCTTGTGCAAT 401
Db      185 AACAGCACTGAGCACTGCACTTTCAACAATGAGTTAAGTGTGTGTGCTTGTGCAAT 244
QY      402 GACTGTACAAAGCAACCTTAATGTGTGCTTCCGGGAATATTAAGGTCACTGCCACAA 461
Db      245 TAAATGTGGAATGAGCAACCAATGTGTGCTTCTGCTGCTCATATGATCATGCCACAA 304
QY      462 CTTTGGCCCTCTCT 474
Db      305 TTTCTGTCCACCT 317

```

RESULT 15

```

US-09-878-574-1206
; Sequence 1206, Application US/09878574
; Patent No. US20020110548A1
; GENERAL INFORMATION:
; APPLICANT: Byrum, Joseph R.
; APPLICANT: La Rosa, Thomas J.

```


GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 18, 2003, 20:41:56 ; Search time 2062 Seconds
(without alignments)
11692.551 Million cell updates/sec

Title: US-09-383-579C-9

Perfect score: 992
Sequence: 1 gaataatcaacaacattgc.....aacacaaacgcgaacgac 992

Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 22781392 seqs, 12152238056 residues

Total number of hits satisfying chosen parameters: 45562784

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

EST:*
1: em_estbda:*
2: em_estbhum:*
3: em_estin:*
4: em_estnu:*
5: em_estoy:*
6: em_estpl:*
7: em_estro:*
8: em_hlc:*
9: gb_est1:*
10: gb_est2:*
11: gb_hlc:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: em_gss_hum:*
18: em_gss_inv:*
19: em_gss_pln:*
20: em_gss_vrt:*
21: em_gss_fun:*
22: em_gss_man:*
23: em_gss_mus:*
24: em_gss_pro:*
25: em_gss_rdg:*
26: em_gss_phg:*
27: em_gss_vrt:*
28: gb_gss1:*
29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	435.4	43.9	880	14	CD574577 UCRPT01.0
2	435.2	43.9	798	10	BG581975 EST483712
3	429.4	43.3	816	14	CD575807 UCRPT01.0
4	422.2	42.6	809	14	CB291406 UCRCS01.0

5	418.8	42.2	799	14	CB293003	CB293003 UCRCS01.0
6	418.6	42.2	838	14	CB980842	CB980842 CAB70003
7	414.2	41.8	767	12	B1932999	B1932999 EST552885
8	411.4	41.5	681	14	CD484188	CD484188 atc01-4ms
9	410	41.3	786	13	BQ165503	BQ165503 EST611372
10	406	40.9	719	14	CA785153	CA785153 bauc5c03
11	404.8	40.8	864	14	CB822230	CB822230 EST 3081
12	404.6	40.8	878	14	CD574625	CD574625 UCRPT01.0
13	403.4	40.7	770	12	BM780176	BM780176 EST590754
14	402.6	40.6	815	10	BE131139	BE131139 L48-1090T
15	401.8	40.5	735	14	CD486517	CD486517 CRH3.3F02
16	400.8	40.4	788	14	CB290960	CB290960 UCRCS01.0
17	398.2	40.1	646	9	AW574064	AW574064 EST316655
18	398	40.1	747	13	BO990338	BO990338 OCF20804
19	397.8	40.1	772	14	CB980777	CB980777 CAB70003
20	394	39.7	859	14	CD574696	CD574696 UCRPT01.0
21	391.8	39.5	843	14	CB979649	CB979649 CAB70001
22	390.2	39.3	656	13	BQ986992	BQ986992 QCF10P22
23	390.2	39.3	868	10	BG446553	BG446553 GA_EB003
24	386.6	39.0	966	10	BE055631	BE055631 GA_EB003
25	380.4	38.3	620	13	BU044752	BU044752 PP_LBa002
26	378.8	38.2	688	14	CB007302	CB007302 VC043G12
27	377.6	38.1	611	13	BU044997	BU044997 PP_LBa002
28	377	38.0	1106	11	AY104146	AY104146 Zsa_mays
29	375	37.8	741	12	B1309709	B1309709 EST531119
30	374.4	37.7	730	14	CA917809	CA917809 EST641956
31	374	37.7	685	13	BU15493	BU15493 NC42D11.P
32	373.8	37.7	617	13	BO852261	BO852261 QCB17122
33	373.6	37.7	580	13	BU763038	BU763038 aa836603
34	373.2	37.6	723	14	CB292105	CB292105 UCRCS01.0
35	371.4	37.6	775	10	BE034856	BE034856 MLO5C12.M
36	371.2	37.4	706	10	BF479593	BF479593 L48-1281T
37	370.6	37.3	699	14	CA840495	CA840495 MCT018A10
38	369.8	37.3	757	13	BU007051	BU007051 QCB13D18
39	367.2	37.0	656	13	BU892415	BU892415 P063C07.P
40	367.2	37.0	710	12	B1931078	B1931078 EST550967
41	366.6	37.0	656	13	BU893884	BU893884 P084A04.P
42	365.6	36.9	727	14	CA917661	CA917661 EST641808
43	363.8	36.7	641	13	BU046881	BU046881 PP_LBa002
44	362.8	36.6	668	9	AW776306	AW776306 EST353571
45	360.6	36.4	654	10	BE584282	BE584282 7-3E-HA.P

ALIGNMENTS

RESULT 1
CD574577
LOCUS
DEFINITION UCRPT01.06 G11.T3 Poncirus trifoliata CTV-challenged cDNA library -
Poncirus trifoliata cDNA clone UCRPT01_06.G11, mRNA sequence.
ACCESSION
VERSION CD574577.1 GI:31670479
KEYWORDS
SOURCE
ORGANISM
EST.
Poncirus trifoliata
Poncirus trifoliata
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids
; eurosids II; Sapindales; Rutaceae; Poncirus.
1 (bases 1 to 880)
Roose,M.L., Ye,X., Federici,C.F., Close,T.J., Fenton,R.D.,
Wanamaker,S., Choi,Y. and Kingan,T.
Development of EST Resources and New Genetic Markers for California
Citrus - Poncirus trifoliata CTV-challenged phloem - UCR

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
Unpublished
Contact: Mikeal Roose
Department of Botany & Plant Sciences, University of California
Riverside, CA 92521-0124, USA
Tel: 9097874137
Fax: 9097874437
Email: mikeal.roose@ucr.edu
Seq primer: T3.
Location/Qualifiers

FEATURES

1..880
/organism="Poncirus trifoliata"
/mol_type="mRNA"
/cultivar="Pomeroiy OP"
/db_xref="taxon:37690"
/clone="UCRPT01.06.511"
/tissue_type="phloem"
/dev_stage="10-30 cm shoots"
/lab_host="E. coli TUC121"
/clone_id="Poncirus trifoliata CTV-challenged cDNA library - UCR"
/note="Vector: Lambda Uni-ZAP XR, excised phagemid; Site 1: EcoRI, Site 2: XhoI. Plants were grown in the greenhouse at University of California, Riverside. The scion was open-pollinated (very probably selfed) seedling of Poncirus trifoliata cv Pomeroiy that was selected as homozygous for the CTV resistance gene. The rootstock was sweet orange infected with citrus tristeza virus (CTV) isolate TS14 over 1 year before sampling (CTV infects sweet orange, but not genotypes carrying the CTV resistance gene. Shoots 10-30 cm long were harvested in October 2000, and the green phloem (bark) was removed and frozen quickly in dry ice. Total RNA was extracted using Trizol reagent (Gibco). Poly(A) RNA was purified, a cDNA library was made, and 0.5 million primary lambda cDNA clones were in vivo excised to give a population of phagescript SK(-) phagemids. All steps to this point were performed in the ML-Rose lab at the University of California, Riverside by X. Ye. Phagemids were plated, lambda DNA purified, cDNA clones archived, and DNA sequences determined bi-directionally using an ABI3730 at the University of California Riverside Genomics Institute, Core Instrumentation Facility, (Choi, Kidman). Chromatogram files were transmitted to UC Riverside (by Choi), then processed at UC Riverside (by Wamamker) using the Harvest pipeline (<http://harvest.ucr.edu>) to remove vector and cloning oligo sequences and various contaminants, and to trim to a high quality region. Sequences that retained a phred 17 region of at least 100 bases were deposited to GenBank."

BASE COUNTY
ORIGIN

Query Match	43.9%	Score 435.4;	DB 14;	Length 880;
Best Local Similarity	75.6%	Pred. No. 1.2e-58;		
Matches 554; Conservative	0;	Mismatches 176;	Indels 3;	Gaps 1;

Oy	183	TCCTCTTCTCTCTCCCTTCTCTTGTCTTCAACCTTGCCTAGCTA --- CGGAGCGTGCA	239
Db	91	TTTGTGTTGCTCAATTTTGTGCTTTCTGTGGCACTATTGAGACTATAGGTGTGGGTGGCA	150
Oy	240	GAGCGGCACGCCACCTTTATATGAGTGTGTGTGACGCACTCTGGACCAATGGGTGAGACTTG	299
Db	151	AAGTGGCCATGCAACTTCTATAGAGAGGGGGGTGATCTTCCGGCAAAATGGGTGTGCTTG	210
Oy	300	TGGGTATGGGAATTTATACAGCCAGGATATGCAAGCAACGGTGGCGCTGAGCACTGC	359
Db	211	TGGGTATGGCAATTTGTACAGCAAGGCTATATGGACTATACACTGAGACCTTAAATACCGC	270
Oy	360	GCTATTTAACAATGGAATTAACTGTGTGTGCTTGTCTTGGAAATGACTTGTACAAAGCAACC	419
Db	271	TCTATTAACAATGGCTTAAGCTGTGTGTTCAATGCTATGAATATGAAATATGAAAAATGACCC	330
Oy	420	TAAATGTGCTTCCGGGAACATAATTAGGATCACTGCCAACCACTTTGACCCCTCTCAACTT	479
Db	331	CAAGTGTGCTCCCCGGCTCATATGTGTGACCGGCACCAACTTCTGCCCACTTAACCT	390
Oy	480	TGCTTCTCCCTAACCAACAATGGTGTGATGTGTGCAACCTCTCTTCCAAACTTGTGACATGGC	539
Db	391	TGCCCTGTCTAAACGACCAACGGGGGTGTGTGCAATCTCCCTCCAGCACTTTGACATGGC	450
Oy	540	TGAGCTTGCCTTCTTCAAAATGCTCATATCCGAGCTGTATGTGTCCTCCCGTCTCCTTTCG	599

Db	451	TGAGCCCGCTTCTTGCAAAATGGCCAAATACCGTGCAGATCGTCCCAATTTCTTCAG	510
Qy	600	TAGGATACATGTATGAAAGAAAGGTGGATGATGATTTTCAATCAATGGCCACTCATCTT	659
Db	511	AAGGATCCCGTGTGGAAAGAAAGGAGGATTAAGGTTTAAACGTCAATGGAACATCATCTT	570
Qy	660	CAACCTCGTTTGATCACAAAGTGGGAGGCGACGCGACATCTGTGCGATTA	719
Db	571	CAACCTGGTTTGGATCACAAATGTGGAGGACGAGAGATGTGATTCAGTATCAATCAA	630
Qy	720	GGGGTCTCGAATGAGATGGCAATCCATGTCTAGAATTGGGGCCAAACTGGCAAGCAA	779
Db	631	GGGTTCAAAAGACTGGATGGCAAGCAATGTCAAGGAATCGGGCCAAATTTGGCAGAGCAA	690
Qy	780	CAACTATCTCAATGGCCAAAGCCCTTTCCTTCAAGTCACTCTTAGTATGATGGCACTCT	839
Db	691	TTCTATTCTTAACGGCCAAAGCTTTCTTTCCAAGTACAGCCAGTACGGCAGAGACTGT	750
Qy	840	CATGGCTATATCTCGTTCCTTCCAAATGGCAATTTGGCCAAACCATGAAGGCCCTCA	899
Db	751	GACTAGCAACAATGTTGTGCTCGAATTTGGCAATTTGGCAAACTTTAGAGGTGTCA	810
Qy	900	ATTCTAAACATA	912
Db	811	GTTTTAGATTTTA	823

RESULT 2	
BG581975	
LOCUS	
DEFINITION	
BG581975	798 bp mRNA
EST468712 GVN	Medicago truncatula cDNA clone pgvn-66124 5' end,
mRNA sequence.	

VERSION	BG581975.1	GI:13597039
KEYWORDS	EST.	
SOURCE	Medicago truncatula (barrel medic)	
ORGANISM	Medicago truncatula	

Eukaryotes: Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eucosids I; Fabales; Fabaceae; Papilionoideae; Trifoliaceae; Medicago.

REFERENCE	AUTHORS	TITLE	JOURNAL
1 (bases 1 to 798)	Podorova, M., Pierson, B. L., Samac, D. A., Vance, C. P., Gantt, G. S., Town, C. D., Van Aken, S., Utechtack, T., Cho, J. and Fraser, C. M.	ESTs from one month old nitrogen-fixing root nodules of <i>Medicago truncatula</i> , 2001	unpublished

COMMENT

Contact: Carroll P. Vance
Department of Agronomy and Plant Genetics
University of Minnesota
411 Borlaug Hall, 1991 Upper Buford Circle, St. Paul, MN 55108 USA
Tel.: 612 625 5715
Fax: 651-649-5058
Email: Vance004@maroon.tc.umn.edu
University of Minnesota name: M83038 TIGR sequence name:
MDCBE07K More information is available at: <http://www.medicago.org>
Seq primer: Skmdd (CTA gaa CTA gtc gat CC).

FEATURES
SOURCE

```

/organism="Medicago truncatula"
/mol_type="mRNA"
/cultivar="genotype Al7"
/db_xref="taxon:3880"
/clone="pGVN-66124"
/tissue_type="N2-fixing root nodules"
/dev_stage="effective root nodules harvested one month post inoculation with Sinorhizobium meliloti"
/lab_host="E. coli strain XL04R"
/clone_lib="GVN"
/note="vector: pBluescript SK-; Site_1: EcoRI; Site_2: XhoI; cDNA was prepared from polyA+ enriched RNA from effective root nodules harvested one month post inoculation with Sinorhizobium meliloti. The cDNA was

```


Db 582 CAACCTGGTTTGGATCACAAATGTGGAGGACGAGAGTATGACTTACGTATCAATCA 641
 QY 720 GGGGCTTCGAATCGATGAGCAATCCATGCTTAGAAATTGGGCCCCAAATCGCCAAAGCA 779
 Db 642 GGGTTCAAGAAGCTGGATGACCAAGCATGTCAAGAAAGCTGGGGCCAAAATTGGCAGAGCA 701
 QY 780 CAACATATCTAATGGCCAAAGGCGTTCTTCCTTTCAGTCACTTATGATGATGCGACTCT 839
 Db 702 TTCTTATTTTAACGGGCAAAAGCTTTCTTTCCAAATTGACAGCGACTGACGCGAGACTGT 761
 QY 840 CACTGCGCTATAATCTGTTCTTCCTTCCAAATGGCAATTTGGCCAAACCT 886
 Db 762 GACTAGCAACAATGTTGTGCTCGGAAATTGGCAATTTGGGCAAACT 808

RESULT 5	CB293003	LOCUS	DEFINITION
	CB293003	799 bp	mRNA linear EST 28-FEB-2003
	UCCCS01_05bf07	g1	Washington Navel orange cold acclimated flavdo & albedo cDNA library Citrus sinensis cDNA clone UCCCS01_05bf07, mRNA
			sequence

ACCESSION	CB293003
VERSION	CB293003.1
KEYWORDS	GI:28618460
SOURCE	EST.
ORGANISM	<i>Citrus sinensis</i>
	<i>Citrus sinensis</i>

REFERENCE	AUTHORS	TITLE
1 (bases 1 to 799)	Close, T.J., Collura, K., Fenton, R.D., Feuerbacher, O., Kim, H.R., Kridina, D., Wamalakera, S., Wing, R. and Yu, Y.	Development of EST Resources and New Genetic Markers for California Citrus

Unpublished
Contact: Timothy Close
Department of Botany & Plant Sciences, University of California
Riverside, CA, 92521-0124
Tel.: 9097873318
Fax: 9097874437
Email: timothy.close@ucr.edu
Seq primer: T3.

FEATURES	Location/Qualifiers
source	1. .799

```

/organism="Citrus sinensis"
/mol_type="mRNA"
/cultivar="Washington Navel"
/db_xref="taxon:711"
/clone="UCRCS01.05b07"
/tissue_type="Rind containing flavedo and albedo"
/dev_stage="Mature fruit"
/lab_host="E. coli TUC121"
/clone_lib="Washington Navel orange cold acclimated
flavedo and albedo cDNA library"
/notes="Vector: lambda Uni-Zap XR, excised phagemid;
Site 1: EcoRI; Site 2: XhoI; Plants were grown in the
field at University of California, Riverside Agricultural
Operations since 1993. The scion was Washington Navel
orange and the rootstock Carizzo Citrange. Tissue from
mature fruit was harvested at mid-day in January 2002
during a cold spell, when pre-dawn temperatures were
approximately -2 to 2 degree C. Approximately 2 cm median
sections of the rind were excised in the field from
several fruits, then wrapped in aluminum foil and frozen
quickly in dry ice. Total RNA was extracted using a phenol
extraction procedure described in J. Japanese Soc. Hort.
Sci. (1996) 64:809-814. Poly(A) RNA was purified, a cDNA
library was made, and 1 million primary lambda cDNA clones
were in vivo excised to give a population of plasmid
SK(-) phagemids. All steps to this point were performed in
the Tu Closes lab at the University of California,
Riverside (Fenton). Phagemids were plated, plaemid DNA

```

purified, cDNA clones archived, and DNA sequences determined bi-directionally using an ABI3530 at the Arizona Genomics Institute, University of Arizona (Collura, Feuerbacher, Kim, Kudrna, Wang, Yu). Chromatogram files were transferred to UC Riverside (by Yu), then processed at UC Riverside (by Manamaker) using the Harvest pipeline (<http://harvest.ucr.edu>) to remove vector and cloning oligo sequences and various contaminants, and to trim to a high quality region. Sequences that retained a phred 17 region of at least 100 bases were deposited to Genbank." 208 a 195 c 189 g 207 t

Query Match	42.2%	Score 418.8	DB 14	Length 799
Best Local Similarity	75.8%	Pred. No.5,1e-56		
Matches 532, Conservative	0	Mismatches 167	Indels 3	Gaps 1

[illegible]

RESULT	6
CBS980842	
LOCUS	838 bp mRNA linear EST 01-MAY-2003
DEFINITION	CAB70003_1TAR_A03 Cabernet Sauvignon Berry Post-Version - CAB7
ACCESSION	Vitis_vh1iera cDNA clone CAB70003_1tar_A03 3' mRNA sequence.
VERSION	CBS980842 GI:30304048

KEYWORDS	EST.
SOURCE	Vitis vinifera
ORGANISM	Vitis vinifera
REFERENCE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; Vitaceae; Vitis.
AUTHORS	1 (bases 1 to 838) Goes da Silva, F., Tandolino, A., Lim, H., Baek, J., Jones, K. and Cook, D.
TITLE	Expressed sequence tags from cabernet sauvignon berries at various developmental stages
JOURNAL	Unpublished
COMMENT	Contact: Douglas Cook, PhD CAES Genome Facility UC Davis, Plant Pathology One Shields Ave, Davis, CA 95616, USA Tel: 530 754 6561 Fax: 530 754 6617 Email: drccook@ucdavis.edu Seq primer: GCCAACGATGCTAG.
FEATURES	Location/Qualifiers
SOURCE	1..838

		<pre> /organism="Vitis vinifera" /mol_type="mRNA" /cultivar="Cabernet Sauvignon" /db_xref="taxon:29760" /clone="CAB70003:_1A03" /bex="Hermaphrodite" /dev_stage="Post-Veraison, 18-19 brix" /lab_host="DH5alpha" /note="Organ: Berry; Vector: pDNR; Site 1: SfiI; Site 2: SfiI; CAB7 is a cDNA library of Cabernet Sauvignon from field-grown vines during stage III of berry growth at 89 days after full bloom. Berries soluble solid concentration ranged between 18-19 brix. Sampled vines were located at the University of California, Davis, Experimental Vineyard. cDNAs were made by oligo-dT priming and directly cloned. 5' and 3' adaptors were used in cloning as follows: 5'-AAGCATGTGATCAACGAGAAGTCATTACGGCGG-3' and 5'-ATTCTAGAGCCGACGCCGCACATG-T(30)NN-3'. Library was constructed using the Clonech Creator SMART kit and size-selected to contain the 0.5-3 kb size fraction." </pre>			
BASE COUNT	192 a	233 c	219 g	194 t	
ORIGIN					
Query Match	42.2%; Score 418.6; DB 14; Length 838;				
Best Local Similarity	70.5%; Pred. No. 5.3e-56;				
Matches	559; conservative	0; mismatches	234; indels	0; gaps	
Dy	146	CCATCTTATGGCTTTTCTTA	CACCCCTCTCCTCTCTTCTCTCTCT	205	
Db	38	CAATGGCTACGACGACATTTCTTACTCTCTTGCCCTCTTCTCTGTCATGCC	97		
Dy	206	TTCGCTTACCTTGCGCTAC	TACGSGTGCGTCGACAAGCGCACCGCACCTTTATGSGTG	265	
Db	98	TCCAAGGACAAATGATGACTATG	TGTGGTGGGAAGTGGGCGATCCACATTCATATGGCG	157	
Dy	266	GTCGTGACGACCTTGGGCA	CCATGGGTGGAGCTTGGGATATGGGAATTTATACAGCCNAG	325	
Db	158	GTCGTGAGGCGCTCAGGCA	CAATGGGTGGGCGCTTGGGATATGGCAACTGTACAGCCNAG	217	
Dy	326	GGTATGGACGNAACA	CGGTGGCGCTGACACACTGCGCTATTTAAACATGATTAAGTTGTG	385	
Db	218	GGTATGGGACCAAC	ACTGACGCTCTCAGCACCGGCTCTCTTCAACAGTGGGCTGACGCTGTG	277	
Dy	386	GTCCTTGCTTGAATA	TGACTGTACAAACGACCCTTAATGSGTGCCTTCGGGAACATATTA	445	
Db	278	GCGGCACTTTACGAGAT	GAATGCAACGATGACCCCAAATGSGTGCCTCCAGGAGACCTTAA	337	
Dy	446	GCGTACCTGCACCA	ACTTTTGCCCTCCTA	CTTGTGCTCTCCCTTAACAACATGTTGAT	505

[illegible]

QY 542 AGCGTCCTTCTTCAATGCTCAATACCGAGCTGTATCGTCCCGTCTCTTTCGTA 601
 DB 330 AACCTGCTCTTCTGCAAAATGCTCAAGAGGCTGAAATGCGCTTGCGCTTATGAA 389
 QY 602 GGGTACCATGTAATGAGAAAGGAGTGAAGTTTCAATCAATGGCCACTACTTCA 661
 DB 390 GGAATCCCTGTGTGAAGAAAGGTGAATAGTTTCAATCAATGGCCACTACTTCA 449
 QY 662 ACCCTGTTTGAATACAAACGTGCTGCGCAGCCAGCTCACTGTGTGCTATTAAG 721
 DB 450 ACTGTGTGCTAATCAATATGATGTGGCGCGGTGACATCCACGCGTGTCAATGA 509
 QY 722 GGTCTGAACGTGATGGCAATCCATGTCTGAATTTGGGCGCAAACTGGCAAGCA 781
 DB 510 GATCCACCGGTGATGGCAGCCCATGTCCAGAACTGGGCGCCAAACTGGCAGAGCA 569
 QY 782 ACTATCTCAATGGCCAAAGGCTTCTTCAAGTCACTGTAGTATGATGGCACTCTCA 841
 DB 570 CTTACTCTCAATGGCCAGAGCTTCTCTTCAAGTAAACACAGTGAAGCGCCGACCTCA 629
 QY 842 CTGCTCTAATCTCTTCTTCCATTTGGCAATTTGGCCAACT 886
 DB 630 CAAGTTACAAAGTGGCGCTTCCCAATTTGGCAGTTGGCGCAACT 674

RESULT 9
 BQ165503 786 bp mRNA linear EST 25-APR-2002
 LOCUS BQ165503 KVKC Medicago truncatula cDNA clone pKVKC-9F12, mRNA
 DEFINITION

ACCESSION BQ165503
 VERSION BQ165503.1 GI:20307978
 KEYWORDS EST.
 SOURCE Medicago truncatula (barrel medic)
 ORGANISM

REFERENCE 1 (bases 1 to 786)
 Vandenbosch, K., Endre, G., Silverstein, K., Town, C.D., Van Aken, S.,
 Uterback, T., Cheung, F. and Fraser, C.M.
 The Medicago truncatula 'Xiloclone' set; ESTs selected and
 re-arrayed from various libraries
 Unpublished
 Contact: Vandenbosch K
 Department of Plant Biology
 University of Minnesota
 220 Biosci Center, 1445 Gortner Ave, St. Paul, MN 55108, USA
 Tel: 612 624 2755
 Fax: 612 625 1738
 Email: kvandenb@tbs.umn.edu
 TIGR sequence name: MTNAT172TK Alias clone name: GVN-51CS More
 information is available at: www.medicago.org
 Seq primer: SKmod (CTA gaa cta gtc gat cc).
 Location/Qualifiers

FEATURES
 source

1.786
 /organism="Medicago truncatula"
 /mol_type="mRNA"
 /cul_tivar="A17"
 /db_xref="taxon:3880"
 /clone="pKVKC-9F12"
 /tissue_type="mixed tissues"
 /dev_stage="various stages"
 /lab_host="XLOLR"
 /clone_lib="KVKC"
 /note="Vector: pBluescript SK-, Site 1: EcoRI, Site 2:
 XhoI; cDNA was prepared from polyA+ enriched RNA. The cDNA
 was directionally ligated into the Unipap XR vector from
 Stratagene and packaged using Gigapack III Gold packaging
 extracts. Plasmids containing cDNA inserts were excised
 from the recombinant lambda-zap phage using Ex-aseIst

BASE COUNT 235 a 146 c 186 g 219 t
 ORIGIN

Query Match 41.3%; Score 410; DB 13; Length 786;
 Best Local Similarity 78.2%; Pred. No. 1.2e-54;
 Matches 505; Conservative 0; Mismatches 140; Indels 1; Gaps 1;

QY 260 ATGTGTGTGTGATGACGATCTGGACCATGGTGAAGCTTGTGGATATGGAATTATACA 319
 DB 1 ATGTGTGTGAGGATGATCATGACGACACATGGAGGGGCTTGTGTATGAAATTTGTATA 60
 QY 320 GCCAAGGGATGACGACGAAACAGGTGGCGGTGAGACTGGCTATTTAATGATTTA 379
 DB 61 GCCAAGGGCTATGAAACCAACACTGCTGACATGAGACTGTCT-TTTAACAATGATTTA 119
 QY 380 GTTGTGTGCTGCTTCCGAATGACTTTGTACAAAGACCTTAATAGTGTCTTCCGGAA 439
 DB 120 GTTGTGTGCTTGTCTACGAGATGAATGTACAGTGAACCTTAATGTGTCTTCCGTGA 179
 QY 440 CTATTAGGATCACTGACCAACTTTTGGCTTCTTACTTGTCTTCCCTAACACATAG 499
 DB 180 GCATATGTGTACTGTCAAAACTTCTGCCCCCAAACTTTCAGATCTAATACCAATG 239
 QY 500 GTGATGTGTGCAACCTCTCTCCAAACTTGTGACATGTGAGCTGCTTCTTCAAA 559
 DB 240 GTGATGTGTGCAACCTCTCTCCAAACTTGTGACATGTGAGCTGCTTCTTCAAA 299
 QY 560 TCGCTCAATACCGAGCTGTATGTCCTCCGCTCTTGTGATGAGGATCATGATGAGA 619
 DB 300 TTGCTCAATACAAAGTGAATTTGTTCTATTTCTTGAAGAGTCCCTGTATGAGA 359
 QY 620 AAGTGTGATGAGTTTACATCAATATGSCCACTATCTTCAACTCGTTTGTATACA 679
 DB 360 AAGAGGATCATGATTTCAATTAATGACACTCACTTCAACTTGTGTTGTGCACA 419
 QY 680 AGTGTGTGTGCGCCAGCGCCTCTCTGTGTGATTAAGGGGTCTGAATGAGTGC 739
 DB 420 ATGTGTGTGTGACTGTAGATTTCAATTTCTGTCTCAATCAAGGATCAAAAGCTGATGC 479
 QY 740 AATCATGTCTTGAATTTGGGCGCAAACTGSCAAAGCAACAATCTCAATGCGCAAG 799
 DB 480 AAGCTATGTCTTGAAGTCTGGGCGCAAGTGGCAAGCAATATCTCAATGCTCAAA 539
 QY 800 GCTTCTCTTCAAGTCACTCTTATGATGTGTGCACTCTCACTGCTTATATCTGCTTC 859
 DB 540 GCTCTCATTTCAAGTCACTTACAGATGATGATGATGATGATGATGATGATGATGATG 599
 QY 860 CTTCAATTTGGCAATTTGGCCAAACCTATGAAGGCGCTCAATTTCA 905
 DB 600 CTGGCAATTTGGCAATTTGGCCAAACCTATTTACAGGGGGGACATTTTA 645

RESULT 10
 CA785153 719 bp mRNA linear EST 04-DEC-2002
 LOCUS CA785153
 DEFINITION

ACCESSION CA785153
 VERSION CA785153.1 GI:26048700
 KEYWORDS EST.
 SOURCE Glycine max (soybean)
 ORGANISM

REFERENCE 1 (bases 1 to 719)
 Shoemaker, R., Keim, P., Vodkin, L., Erpelting, J., Corryell, V., Khanna,
 A., Bolla, B., Matra, M., Hillier, L., Kucaba, T., Martin, J., Beck, C.,
 Wylie, T., Underwood, K., Stepien, M., Theising, B., Allen, M., Bowers,
 Y., Person, B., Swaller, T., Gibbons, M., Page, D., Harvey, N., Schurk

[illegible]

```

1..770
/organism="Medicago truncatula"
/mol_type="mRNA"
/cultivar="genotype A17"
/db_xref="taxon:3880"
/clone="PKV2-54C20"
/tissue_type="Seedling roots"
/dev_stage="2 days post-inoculation with Sinorhizobium
mellotii"
/lab_host="E. coli strain SOLR"
/clone_id="KV2"
/notes="Vector: pBluescript SK -; Site 1: EcoRI; Site 2:
XhoI; cDNA was prepared from polyA+ enriched RNA. The
cDNA was directionally ligated into the Unizap XR vector
from Stratagene and packaged using Gigapack III Gold

```

packaging extracts. Plasmids containing cDNA inserts were excised from the recombinant lambda-Zap phage using Ex-assist helper phage and propagated in SOLR cells."

Query Match	40.7%;	Score 403.4;	DB 12;	Length 770;
Best Local Similarity	76.7%;	Pred. No. 1.3e-53;		
Matches 507; Conservative	0;	Mismatches 151;	Indels 3;	Gaps 1;

Query Match	40.7%;	Score 403.4;	DB 12;	Length 770;
Best Local Similarity	76.7%;	Pred. No. 1.3e-53;		
Matches 507;	Conservative 0;	Mismatches 151;	Indels 3;	Gaps 1;
Qy	183	TCTCTTTCTTCTTCCTTCTTCTTCTTGTGCTTACCTTGCCTGACTAC--GCTGCTGCA	239	
Db	110	TTTCTTTGTCTTAGCTTATGCTTATGCTTAAAGCACCTTTTGTGTACTACGAGGTGATGGA	169	
Qy	240	GAGCGGCCACGCCACCTTTTATGGTGTGTGACGCATCTGGCACCATGGGTGAGCTTG	299	
Db	170	AAATGCTCATGCCACATTTATGTGTGAGGAGATGATCAAGGCACAAATGGGAGGTCTTG	229	
Qy	300	TGGGTATGGGAATTTATACAGCCAAAGGATATGGACGAAACGGTGGCGCTGACACCTGC	359	
Db	230	TGCTTATGGAATTTGATATACCAAGCTATAGAACCACTCTGTCACTTAAGTACTGC	289	
Qy	360	GCTATTTAACATGATTTAAGTTGTGTGCTTCTTGAAATGACTTGTACAAAGCACCC	419	
Db	290	TCTTTCAACATGATTTGAGTTGTGGTCTGTCTAGAGATGAATGTAAACATGACCC	349	
Qy	420	TAAATGTGCTTTCGGGAACATAATTAAGGTCACTGCCAACCACTTTTGCCCTCTAATT	479	
Db	350	TAAATGTGCTTCTCTGTAGCATATTTGTTACTGTACAAACTTTCGCCCAACTT	409	
Qy	480	TGCTCTCCCTTAACAACATGGTGTGATGGTGCAACCTCTGTCACAACTTGACATGGC	539	
Db	410	TGCGAGCTTATATCCAAATGGTGTGATGGTGCAACCTCTCTTACGACTTTGATCTTGC	469	
Qy	540	TGAGCTGCTCTTCCCTTCAAAATCGCTCAATACCGAGCTGTATCGTCCCGCTCTCTTGC	599	
Db	470	TGAGCTGCTTCTTCAAAATGCTCAATACAAAGCTGAATGTCTTATTTCTTCTAG	529	
Qy	600	TAGGTATCATGTATGAAGAAAGGTGATGAGGTTTAAATCAATGAGCCACTATCTT	659	
Db	530	AAGAGTCCCCCTGTGTGAAGAAAGGAAATCAGATTTCAATTAATGAGCACTATCTT	589	
Qy	660	CAACTGCTTTGATTCACAAACGTGGGTGGGCGCAGGGAGGTCCACTGTGTGATTA	719	
Db	590	CAACTGTGTTTGTGTCACAAATGTGTGGAGCTGTGAGATGTATCTTGTGTCTATCAA	649	
Qy	720	GGGCTTCGAATGTGATGCAATCATGTCTAGAAATTTGGGGCCAAACTGGCAAGCAA	779	
Db	650	GGGATCAAAAGCTGGATGGCAAGCTATGTCTAGGAACTGGGGGCGAAGACTGGCAAGAA	709	
Qy	780	CACTATCTCAATGGCCAAAGGCTTTTCTTCAAGTCACTCTTAATGATGTGCACTCT	839	
Db	710	TAACTATCTCAATGTCAAAAGCTCTCATTTCCAGTCACTACATGATGTGATGACTAT	769	
Qy	840	C 840		
Db	770	C 770		

[illegible]

Qy	723	GTCTCAACATGGATGGCAATCCATCTCTAAGAAATTTGGGGCCAAAATCTGGCAAGCA	CAA	782
Db	599	TTTGAAGACCGGGTGGCAAAACATCTCAAGAAACTGGGGCCAAAACCTGGCAAGTA	CTC	658
Qy	783	CTATCTCAATGGCCAAAGCCTTTTCTCTTCAAGTACTCTTATGATGCTGGCACTCT	CAC	842
Db	659	TTTACTTCAACGGCCAAAGCCCTGTCC-TTTAGGTTAACGCTTGACACCGACGGAC	CCCTGAC	717
Qy	843	TGGCTTAAATCTGTCTCTTCCATTTGGCAATTTTGGCCAAACCTATGAAGGCCCTCA	ATT	902
Db	718	TAGC-ACAAATGTTCTCTCTCATATGGCAATTTTGGGAGACAAATTTGGGTTGGCA	ATT	776
Qy	903	CTAAACCAT	911	
Db	777	CTAAACCT	785	

RESULT 15
CD486517

LOCUS	CD486517	736 bp	mRNA	linear	EST 04-JUN-2003
DEFINITION	CRH3.1F02 Cotton Root and Hypocotyl Lambda ZIPPOX Library (CRH)				
ACCESSION	Gossypium hirsutum cDNA clone CRH3.1F02 5'				similar to expansin,
VERSION	CD486517				
KEYWORDS	CD486517.1	GI:31407482			
SOURCE	EST.				
ORGANISM	Gossypium hirsutum (upland cotton)				
	Gossypium hirsutum				

REFERENCE

AUTHORS Dowd, C., Wilson, J., and McFadden, H.
TITLE Different Gene Expression Responses in Cotton Root and Hypocotyl tissues during infection with Fusarium Wilt Disease
JOURNAL Unpublished (2003)
COMMENT Contact: Calitrona Dowd, Helen McFadden

Tel: 61 2 6246 4914, 6246 5311
 Fax: 61 2 6246 5000
 Email: Caltriona.Dowd@csiro.au, Helen.McFadden@csiro.au
 Vector clipped sequences Bases 1-17 (GTGCACCCACCGTCG) : Sall
 adapter
 Seq primer: M13 reverse primer
 High quality sequence stop: 736.

FEATURES
source

```

/organism="Gossypium hirsutum"
/mol_type="mRNA"
/cultivar="DeltaEMERALD"
/db_xref="taxon:3635"
/clone="CRH3_3F02"
/tissue_type="Root and hypocotyl tissues"
/dev_stage="5 day old seedlings"
/lab_host="Y1090(ZL)"
/clone_1db="Cotton Root and Hypocotyl Lambda ZIPLOX
Library (CRH)"
/notes="Vector: Lambda ZIPLOX; Site 1: SalI; Site 2: NotI;
rRNA was prepared from root and hypocotyl tissues of the
cotton cultivar DeltaEMERALD. cDNA was synthesized from a
NotI-oligodT primer/adaptor using the manufacturers
protocols (Life Technologies) and then ligated to a SalI
adaptor to facilitate directional cloning. The cDNA was
cloned into the SalI and NotI sites of the Lambda ZIPLOX
phase vector (Life Technologies). Constructed by Catriona
Dowd and Helen McFadden."

```


GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 18, 2003, 19:52:30 ; Search time 3651 Seconds

(without alignments)
11115.407 Million cell updates/sec

Title: US-09-383-579c-9

Perfect score: 992

Sequence: 1 gaataaatacaacaacatgc.....aacacaacacgcgaacgac 992

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 2888711 seqs, 2045481386 residues

Total number of hits satisfying chosen parameters: 5777422

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : GenEmbl:*

1: gb_ba:*

2: gb_htg:*

3: gb_in:*

4: gb_om:*

5: gb_ov:*

6: gb_pac:*

7: gb_ph:*

8: gb_pl:*

9: gb_pr:*

10: gb_ro:*

11: gb_stb:*

12: gb_sy:*

13: gb_un:*

14: gb_vi:*

15: em_ba:*

16: em_fun:*

17: em_hum:*

18: em_in:*

19: em_mu:*

20: em_or:*

21: em_ov:*

22: em_ph:*

23: em_pac:*

24: em_pl:*

25: em_ro:*

26: em_stb:*

27: em_sy:*

28: em_un:*

29: em_vi:*

30: em_htg_hum:*

31: em_htg_inv:*

32: em_htg_other:*

33: em_htg_mus:*

34: em_htg_pln:*

35: em_htg_rnd:*

36: em_htg_man:*

37: em_htg_vtc:*

38: em_sy:*

39: em_htg_hum:*

40: em_htg_mus:*

41: em_htg_other:*

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	992	100.0	992	8	CSU30382	U30382 Cucumis sat
2	684	69.0	684	6	AX306490	U306490 Sequence
3	681	68.6	681	6	AR076514	AR076514 Sequence
4	681	68.6	681	6	AR161478	AR161478 Sequence
5	676.2	68.2	681	6	AX306492	U306492 Sequence
6	453	45.7	1109	8	PAU93167	U3167 Prunus arme
7	448.4	45.2	1177	8	AF049354	AF049354 Nicotiana
8	445.2	44.9	1153	8	AB093028	AB093028 Pyrus com
9	444.6	44.8	1243	8	AB093028	AB093028 Pyrus com
10	443.2	44.7	1118	8	AB093030	AB093030 Pyrus com
11	442	44.6	1109	8	AF350937	AF350937 Prunus ce
12	439.2	44.3	1048	8	AF297521	AF297521 Prunus av
13	438.8	44.2	1035	8	CAR291817	CAR291817 Cicer art
14	435	43.9	1108	8	AY083166	AY083166 Malus x d
15	431	43.4	1262	8	AY079206	AY079206 Mirabilis
16	429	43.2	1142	8	AF428174	AF428174 Rumex pal
17	428.6	43.2	1147	8	AF096776	AF096776 Lycopersi
18	424.2	42.8	1233	8	AF350936	AF350936 Prunus ce
19	423.6	42.7	1180	8	AF159563	AF159563 Fragaria
20	421.8	42.5	1195	8	AB104444	AB104444 Vitis lab
21	420.6	42.4	1169	8	AY299692	AY299692 Sambucus
22	420.2	42.4	1169	8	AB104443	AB104443 Vitis lab
23	417.8	42.1	1088	8	AF230332	AF230332 Zinnia el
24	416	41.9	1220	8	AB029083	AB029083 Prunus pe
25	415.2	41.6	1070	8	AY079208	AY079208 Mirabilis
26	412.6	41.2	1252	8	AF038815	AF038815 Prunus ar
27	409.2	41.2	1173	8	AF167360	AF167360 Rumex pal
28	405.6	40.9	1191	8	AY079205	AY079205 Mirabilis
29	404.4	40.8	1144	6	AX392019	AX392019 Sequence
30	401.8	40.5	1098	8	AY083168	AY083168 Musa acum
31	401	40.4	1175	8	AB104445	AB104445 Vitis lab
32	398.8	40.2	1016	8	AY086770	AY086770 Arabidops
33	394.2	39.7	762	6	AX506393	AX506393 Sequence
34	394.2	39.7	740	6	AX651951	AX651951 Sequence
35	390.2	39.3	740	6	AX654546	AX654546 Sequence
36	390.2	39.3	1219	8	OSU85246	OSU85246 Oryza sativ
37	388.6	39.1	1340	8	AB093031	AB093031 Pyrus com
38	388.2	38.9	1172	8	AF350938	AF350938 Prunus ce
39	387.6	39.1	1117	8	AF428175	AF428175 Rumex pal
40	386.2	38.9	1102	8	AF043284	AF043284 Gossypium
41	386	38.9	756	6	AX653643	AX653643 Sequence
42	385.2	38.8	1323	8	OSU0477	OSU0477 Oryza sativ
43	383.8	38.7	1419	8	AF448467	AF448467 Prunus ce
44	383	38.6	1250	8	AY189969	AY189969 Gossypium
45	382.6	38.6	891	8	PTU64893	U64893 Pinus taeda

ALIGNMENTS

RESULT 1

CSU30382

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Cucumis sativus (cucumber)

Cucumis sativus

992 bp mRNA linear PLN 04-DEC-1996

U30382.1 GI:1040874

U30382.1 Cucumis sativus expansin (Cs-Exp1) mRNA, complete cds.

REFERENCE

AUTHORS

Shcherban,I.Y., Shi,J., Durachko,D.M., Gultinan,M.J., McQueen-Mason,S.J., Shieh,M. and Cosgrove,D.J.,

Pred. No. is the number of results predicted by chance to have a

TITLE Molecular cloning and sequence analysis of expansins--a highly conserved, multigene family of proteins that mediate cell wall extension in plants

JOURNAL Proc. Natl. Acad. Sci. U.S.A. 92 (20), 9245-9249 (1995)

MEDLINE 96016146

PUBMED 7568110

REFERENCE 2 (bases 1 to 992)

AUTHORS Shcherban,T., Shi,J., Durachko,D.M., Gultinan,M.J., McQueen-Mason,S.J., Shieh,M. and Cosgrove,D.J.

TITLE Direct Submission

JOURNAL Submitted (27-JUN-1995) Daniel J. Cosgrove, Biology, Pennsylvania State University, 208 Mueller Laboratory, University Park, PA 16802, USA

FEATURES

source location/Qualifiers

1..992 /organism="Cucumis sativus"

/mol_type="mRNA"

/strain="Burpee Pickler"

/db_xref="taxon:3659"

gene 1..992 /gene="Cs-EXPI"

CDS 154..906 /gene="Cs-EXPI"

/note="similar to pollen allergen lol pl, Lolium perenne, Swiss-Pro Accession Number P14946; former gene name CUEX1; expansin-29 (Ex29) protein"

/codon_start=1

/product="expansin S1 precursor"

/protein_id="AAB37746.1"

/db_xref="GI:1040875"

/translation="MAFSYSPSSFLPLPFVPTPADYGMQSGHATPGGDAAGT MCGACGYLVISQGTNTVALFNNGLSCAGFEMTCNDRCLEGTIRVAT NCSPNFALPNNNGWCPNPLDHPMAEPALQIAQYRAGIVPVSFRVPCMKKGVF PINHGFENLVLTINVGAGDVSVISIKSRTGMQSMGRNGOMWSNNYINLGGQLS FQVTLSDGRTLVLYNLVPSNMQFGQYBGPQ"

mat_peptide 223..903 /gene="Cs-EXPI"

/product="expansin S1"

/function="induces extension (creep) in plant cell walls"

polyA_site 992 /gene="Cs-EXPI"

/note="17 A nucleotides"

BASE COUNT 259 a 277 c 177 g 279 t

ORIGIN

Query Match 100.0%; Score 992; DB 8; Length 992;

Best Local Similarity 100.0%; Pred. No. 2,5e-261;

Matches 992; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 361 CTAATTAACAATNGATTAAGTTGTGCTGCTTGCAGAAATGACTTGTACAAAGACCT 420

DB 361 CTAATTAACAATNGATTAAGTTGTGCTGCTTGCAGAAATGACTTGTACAAAGACCT 420

QY 421 AAATGTCCTTCCGGGAAGTATTAAGGTCACCTGACCAACTTTGGCCTCTTAATTT 480

DB 421 AAATGTCCTTCCGGGAAGTATTAAGGTCACCTGACCAACTTTGGCCTCTTAATTT 480

QY 481 GCTTCCTTACCAACAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 540

DB 481 GCTTCCTTACCAACAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 540

QY 541 GAGCCTGCTTCTCAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 600

DB 541 GAGCCTGCTTCTCAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 600

QY 601 AGGATACCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 660

DB 601 AGGATACCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 660

QY 661 AACCTGCTTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 720

DB 661 AACCTGCTTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 720

QY 721 GGGTTCGCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 780

DB 721 GGGTTCGCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 780

QY 781 AACTATCTCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 840

DB 781 AACTATCTCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 840

QY 841 ACTGCTTATATCTGCTTCTTCAATGATGATGATGATGATGATGATGATGATGATGAT 900

DB 841 ACTGCTTATATCTGCTTCTTCAATGATGATGATGATGATGATGATGATGATGATGAT 900

QY 901 TTCTAACCATATCTGCTTCTTCAATGATGATGATGATGATGATGATGATGATGATGAT 960

DB 901 TTCTAACCATATCTGCTTCTTCAATGATGATGATGATGATGATGATGATGATGATGAT 960

QY 961 AAACAACAACAACAACAACAACAACAACAACAACAACAACAACAACAACAACAACAACA 992

DB 961 AAACAACAACAACAACAACAACAACAACAACAACAACAACAACAACAACAACAACAACA 992

RESULT 2

AX306490 684 bp DNA linear PAT 11-DEC-2001

LOCUS AX306490

DEFINITION Sequence 1 from Patent WO0188163.

ACCESSION AX306490

VERSION AX306490.1 GI:17645710

KEYWORDS

SOURCE Cucumis sativus (cucumber)

ORGANISM Cucumis sativus

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids I; Cucurbitales; Cucurbitaceae; Cucumis.

REFERENCE 1

AUTHORS Berendes,F., Raat,H.G., Vogt,U. and Gouloudis,C.

TITLE Method for producing recombinant expansins

JOURNAL Patent: WO 0188163-A 1 22-NOV-2001;

Bayer Aktiengesellschaft (DE)

FEATURES

source location/Qualifiers

1..684 /organism="Cucumis sativus"

/mol_type="genomic DNA"

/db_xref="taxon:3659"

<1..684 /note="unnamed protein product"

CDS /codon_start=1

/protein_id="CAD19043.1"

/db_xref="GI:17645711"

/translation="DYGMQSGHATFYGGDASGTMGACGYGNLYSQGYGTNTVALS

BASE COUNT	163 a	179 c	164 g	178 t
ORIGIN	<p>TALPNNNGISGACGEMCTNPNKMCIPCTIIVTATNFCPPAFALPNNNGCNPLOH FDMASPAFLQIAQYRAGIVPVSFPRVCPMKKGGRFTTNGHSYNNVLITNVGAGADV HVSIVKISRITQMSMRNNGQNMOSNNYLNQGLSFVYTLSDGRTLLAYNNVNNMQP GQTEGCPQF"</p>			

Query Match	69.0%;	Score 684;	DB 6;	Length 684;
Best Local Similarity	100.0%;	Pred. No. 1.1e-176;		
Matches 684; Conservative	0;	Mismatches	0;	Indels 0;
				Gaps 0;

QY	223	GACTACGGGTGGCTGGCAAGCGGCGACGCACTTTTATGGGTGGTGAAGCATCTGGC	282
Db	1	GACTACGGGTGGCTGGCAAGCGGCGACGCCACTTTTATGGGTGGTGAAGCATCTGGC	60
QY	283	ACCATGGGTGAGACTTGTGGTATGGAAATTTATACGCCAAGGATATGGCAAGAACG	342
Db	61	ACCATGGGTGGAGCTTGTGGTATGGAAATTTATACGCCAAGGATATGGCAAGAACG	120
QY	343	GTGGCGCTGAGACACTGGGCTATTTAACAATGGAATTAAGTGTGGTCTTGCTTGGAAATG	402
Db	121	GTGGCGCTGAGACACTGGGCTATTTAACAATGGAATTAAGTGTGGTCTTGCTTGGAAATG	180
QY	403	ACTGTACAAACGACCCCTAAATGGTGCCTTCGGGAACTATTAGGGTCACTGCCAACAC	462
Db	181	ACTGTACAAACGACCCCTAAATGGTGCCTTCGGGAACTATTAGGGTCACTGCCAACAC	240
QY	463	TTTTGGCCCTCTAATCTTTGGTCTCCCTTAACAACAATGTGTGATGGTGCACCCCTCTCTC	522
Db	241	TTTTGGCCCTCTAATCTTTGGTCTCCCTTAACAACAATGTGTGATGGTGCACCCCTCTCTC	300
QY	523	CAACACTTCGACATGGCTGAGCGTGCCTTCCTCAATTCGCTCAATACCGAGCTGGTATC	582
Db	301	CAACACTTCGACATGGCTGAGCGTGCCTTCCTCAATTCGCTCAATACCGAGCTGGTATC	360
QY	583	GTCCCGCTCTCCTTTGTAAGGATCATGTATGAAGAAAGTGAGTGAAGTTTACAATC	642
Db	361	GTCCCGCTCTCCTTTGTAAGGATCATGTATGAAGAAAGTGAGTGAAGTTTACAATC	420
QY	643	AATGAGCCACTATPACTTCAACCTCGTTTGTATCAACAAACGTGGAGGGGACAGCGACATC	702
Db	421	AATGAGCCACTATPACTTCAACCTCGTTTGTATCAACAAACGTGGAGGGGACAGCGACATC	480
QY	703	CACCTGTGTGCATTAAGGGGTCTTGAACCTGGATGGCAATCATGTCTAGAAATTTGGGAC	762
Db	481	CACCTGTGTGCATTAAGGGGTCTTGAACCTGGATGGCAATCATGTCTAGAAATTTGGGAC	540
QY	763	CAAAACCTGGCAAAAGCAACATATCTCAATGGCCAAAGGCTTTCTTCAAGTCACTTT	822
Db	541	CAAAACCTGGCAAAAGCAACATATCTCAATGGCCAAAGGCTTTCTTCAAGTCACTTT	600
QY	823	AGTATGATGCGACACTCTCACTGCGCTATATCTGTTCCTTCAATTTGGCAATTTGGCCAA	882
Db	601	AGTATGATGCGACACTCTCACTGCGCTATATCTGTTCCTTCAATTTGGCAATTTGGCCAA	660
QY	883	ACCTATGAAGGCCCTCAATTTCTAA	906
Db	661	ACCTATGAAGGCCCTCAATTTCTAA	684

RESULT 3			
LOCUS	AR076514		
DEFINITION	AR076514	681 bp	DNA
ACCESSION	Sequence 1	from patent US 5959082.	linear
VERSION	AR076514		PAT 30-AUG-2000
KEYWORDS	AR076514.1	GI:10003260	
SOURCE	Unknown.		
ORGANISM	Unknown.		
REFERENCE	Unclassified.		
AUTHORS	1 (bases 1 to 681)		
	Coegrove,D.J., McQueen-Mason,S., Gultinan,M., Shcherban,T. and Shi,J.		

TITLE	Proteins catalyzing the extension of plant cell walls
JOURNAL	Patent: US 5959082-A 1 28-SEP-1999;
FEATURES	Location/Qualifiers
SOURCE	1 601

BASE COUNT	161 a	179 c	164 g	177 t
ORIGIN	/organism="unknown"			

Query Match	68.6%	Score 681	DB 6	Length 681
Best Local Similarity	100.0%	Pred. No.	7.5e-176	
Matches 681	Conservative 0	Mismatches 0	Indels 0	Gaps 0

QY	223	GACTACGGTGGCTGGGAGAGCGGCGACGCCACCTTTATGGTGGTGGACGCAATCGGC	282
Db	1	GACTACGGTGGCTGGGAGAGCGGCGACGCCACCTTTATGGTGGTGGACGCAATCGGC	60
QY	283	ACCATGGGTGGAGCTTGTGGGTATGGGAATTTATACGCCAAGGTATGGCAGACGACG	342
Db	61	ACCATGGGTGGAGCTTGTGGGTATGGGAATTTATACGCCAAGGTATGGCAGACGACG	120
QY	343	GTGGCGCTGAGCACTGCGGCTATTATTAACAATGGAATTAGTGTGGTGGCTTGCGAATG	402
Db	121	GTGGCGCTGAGCACTGCGGCTATTATTAACAATGGAATTAGTGTGTGGTGGCTTGCGAATG	180
QY	403	ACTTGTACAAAGCAGCCCTTAATGTGTGCTTCGGGAACTATTAGGTCACCTGCCAAC	462
Db	181	ACTTGTACAAAGCAGCCCTTAATGTGTGCTTCGGGAACTATTAGGTCACCTGCCAAC	240
QY	463	TTTTGGCCCTCACTTTTGCTCTCCCTTAACAACAATGGTGGATGGTGGCAACCCCTCTCTC	522
Db	241	TTTTGGCCCTCACTTTTGCTCTCCCTTAACAACAATGGTGGATGGTGGCAACCCCTCTCTC	300
QY	523	CAACACTTGCACATGCTGAGCCGTGCTTCCTTCAATCGCTCAATACCGAGCTGTATC	582
Db	301	CAACACTTGCACATGCTGAGCCGTGCTTCCTTCAATCGCTCAATACCGAGCTGTATC	360
QY	583	GTCCCGCTCTCTTTTGTGAGGGTACCATGTATGAAAGGTGGAGTGAATTTACAATC	642
Db	361	GTCCCGCTCTCTTTTGTGAGGGTACCATGTATGAAAGGTGGAGTGAATTTACAATC	420
QY	643	AATGGCACTCACTACTTCAACCTGCTTTTATGATCAACAACGTGGTGGCGCAGGCGACGTC	702
Db	421	AATGGCACTCACTACTTCAACCTGCTTTTATGATCAACAACGTGGTGGCGCAGGCGACGTC	480
QY	703	CACCTGTGTGCATTAAGGGGTCTCGAATGATGGCAATCCATGTCTAGAAATTGGGGC	762
Db	481	CACCTGTGTGCATTAAGGGGTCTCGAATGATGGCAATCCATGTCTAGAAATTGGGGC	540
QY	763	CAAAACTGGCAAGCAACAATCTATCTCAATAGGCAAGGCGCTTTCCTTCAAGTCACTCTT	822
Db	541	CAAAACTGGCAAGCAACAATCTATCTCAATAGGCAAGGCGCTTTCCTTCAAGTCACTCTT	600
QY	823	AGTGAATGTGCACTCTCACTGCGCTTAATCTGCTTCTTCAATTGGCAATTTGGCCAA	882
Db	601	AGTGAATGTGCACTCTCACTGCGCTTAATCTGCTTCTTCAATTGGCAATTTGGCCAA	660
QY	883	ACCTATGAAGGCCCTCAATTC 903	
Db	661	ACCTATGAAGGCCCTCAATTC 681	

RESULT 4	AR161478	681 bp	DNA	1linear	PAT 17-OCT-2001
LOCUS	AR161478				
DEFINITION	Sequence 1 from patent US 6255466.				
ACCESSION	AR161478				
VERSION	AR161478.1	GI:16227385			
KEYWORDS	.				
SOURCE	Unknown.				
ORGANISM	Unknown.				
REFERENCE	1 (bases 1 to 681)				
AUTHORS	Cosgrove,D.J., McQueen-Mason,S., Gulltman,M., Shcherban,T. and				

Shi, J.
 Title: Purified plant expansion proteins and DNA encoding same
 JOURNAL Patent: US 6255466-A 1 03-JUL-2001;
 FEATURES Location/Qualifiers
 source 1..681
 /organism="unknown"

BASE COUNT 161 a 179 c 164 g 177 t
 ORIGIN

Query Match 68.6%; Score 681; DB 6; Length 681;
 Best Local Similarity 100.0%; Pred. No. 7.5e-176;
 Matches 681; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

223 GACTACGGTGGCTGGAGAGCGGCGCCAGCCACCTTTATGGTGGTGGTGGTGGTGGC 282
 1 GACTACGGTGGCTGGAGAGCGGCGCCAGCCACCTTTATGGTGGTGGTGGTGGTGGC 60
 283 ACCATGGTGGAGCTTGGGTATGGGAATTTATACAGCCAAAGGATGGCAGAACAG 342
 61 ACCATGGTGGAGCTTGGGTATGGGAATTTATACAGCCAAAGGATGGCAGAACAG 120
 343 GTGGCGCTGAGCACTGCGCTATTTAACAATGATTAAGTTGGTGGTGGTGGTGGT 402
 121 GTGGCGCTGAGCACTGCGCTATTTAACAATGATTAAGTTGGTGGTGGTGGTGGT 180
 403 ACTTGTAACAAAGCAACCTTAATGGTGGCTTCGGGGAACATTAAGGTCACTGCAAC 462
 181 ACTTGTAACAAAGCAACCTTAATGGTGGCTTCGGGGAACATTAAGGTCACTGCAAC 240
 463 TTTTGCCCTCTCAACTTGTCTCTCCCTTAACAACAATGGTGGTGGTGGTGGTGGT 522
 241 TTTTGCCCTCTCAACTTGTCTCTCCCTTAACAACAATGGTGGTGGTGGTGGTGGT 300
 523 CAACACTTGACATGGCTGAGCGCTGCTTCAATGCTCAATACCGAGCTGGTATC 582
 301 CAACACTTGACATGGCTGAGCGCTGCTTCAATGCTCAATACCGAGCTGGTATC 360
 583 GTCCCGCTGCTCTTTCGTAGGGGTACCATGATGAAGAAGGTGGAGTTTACAATC 642
 361 GTCCCGCTGCTCTTTCGTAGGGGTACCATGATGAAGAAGGTGGAGTTTACAATC 420
 643 AATGGCACTCACTCACTCACTGCTTTCGTATGACAAAGTGGTGGCGAGCGACGTC 702
 421 AATGGCACTCACTCACTCACTGCTTTCGTATGACAAAGTGGTGGCGAGCGACGTC 480
 703 CACTCTGTGTGATTAAGGGGTCTGCACTGATGATGCAATCCATGCTTAAGAAATGGG 762
 481 CACTCTGTGTGATTAAGGGGTCTGCACTGATGATGCAATCCATGCTTAAGAAATGGG 540
 763 CAACACTTGCAAGCAACAATATGCAATGGCGAAGGCTTCCCTTGAAGTCACTTT 822
 541 CAACACTTGCAAGCAACAATATGCAATGGCGAAGGCTTCCCTTGAAGTCACTTT 600
 823 AGTGAATGGTGGCACTCTCACTGCTTAATCTGCTTCCCAATTTGGCAATTGGCCAA 882
 601 AGTGAATGGTGGCACTCTCACTGCTTAATCTGCTTCCCAATTTGGCAATTGGCCAA 660
 883 ACCATGAAGGCGCTCAATTC 903
 661 ACCATGAAGGCGCTCAATTC 681

RESULT 5
 AX306492 681 bp DNA linear PART 11-DEC-2001
 LOCUS AX306492 Sequence 3 from Patent WO0188163.
 DEFINITION AX306492
 ACCESSION AX306492
 VERSION AX306492.1 GI:17645712
 KEYWORDS
 SOURCE Cucumis sativus (cucumber);
 ORGANISM Cucumis sativus
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

rossids; eurosids I; Cucurbitales; Cucurbitaceae; Cucumis.
 1 Berendes, F., Rast, H. G., Vogt, U. and Gouloudis, C.
 TITLE Method for producing recombinant expansins
 JOURNAL Patent: WO 0188163-A 3 22-NOV-2001;
 FEATURES Location/Qualifiers
 source 1..681
 /organism="Cucumis sativus"
 /mol_type="genomic DNA"
 /db_xref="taxon:3659"
 <1..>678
 /note="unnamed protein product"

CDS

BASE COUNT 161 a 178 c 164 g 178 t
 ORIGIN

Query Match 68.2%; Score 676.2; DB 6; Length 681;
 Best Local Similarity 99.6%; Pred. No. 1.6e-174;
 Matches 678; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

223 GACTACGGTGGCTGGAGAGCGGCGCCAGCCACCTTTATGGTGGTGGTGGTGGC 282
 1 GACTACGGTGGCTGGAGAGCGGCGCCAGCCACCTTTATGGTGGTGGTGGTGGC 60
 283 ACCATGGTGGAGCTTGGGTATGGGAATTTATACAGCCAAAGGATGGCAGAACAG 342
 61 ACCATGGTGGAGCTTGGGTATGGGAATTTATACAGCCAAAGGATGGCAGAACAG 120
 343 GTGGCGCTGAGCACTGCGCTATTTAACAATGATTAAGTTGGTGGTGGTGGTGGT 402
 121 GTGGCGCTGAGCACTGCGCTATTTAACAATGATTAAGTTGGTGGTGGTGGTGGT 180
 403 ACTTGTAACAAAGCAACCTTAATGGTGGCTTCGGGGAACATTAAGGTCACTGCAAC 462
 181 ACTTGTAACAAAGCAACCTTAATGGTGGCTTCGGGGAACATTAAGGTCACTGCAAC 240
 463 TTTTGCCCTCTCAACTTGTCTCTCCCTTAACAACAATGGTGGTGGTGGTGGTGGT 522
 241 TTTTGCCCTCTCAACTTGTCTCTCCCTTAACAACAATGGTGGTGGTGGTGGTGGT 300
 523 CAACACTTGACATGGCTGAGCGCTGCTTCAATGCTCAATACCGAGCTGGTATC 582
 301 CAACACTTGACATGGCTGAGCGCTGCTTCAATGCTCAATACCGAGCTGGTATC 360
 583 GTCCCGCTGCTCTTTCGTAGGGGTACCATGATGAAGAAGGTGGAGTTTACAATC 642
 361 GTCCCGCTGCTCTTTCGTAGGGGTACCATGATGAAGAAGGTGGAGTTTACAATC 420
 643 AATGGCACTCACTCACTCACTGCTTTCGTATGACAAAGTGGTGGCGAGCGACGTC 702
 421 AATGGCACTCACTCACTCACTGCTTTCGTATGACAAAGTGGTGGCGAGCGACGTC 480
 703 CACTCTGTGTGATTAAGGGGTCTGCACTGATGATGCAATCCATGCTTAAGAAATGGG 762
 481 CACTCTGTGTGATTAAGGGGTCTGCACTGATGATGCAATCCATGCTTAAGAAATGGG 540
 763 CAACACTTGCAAGCAACAATATGCAATGGCGAAGGCTTCCCTTGAAGTCACTTT 822
 541 CAACACTTGCAAGCAACAATATGCAATGGCGAAGGCTTCCCTTGAAGTCACTTT 600
 823 AGTGAATGGTGGCACTCTCACTGCTTAATCTGCTTCCCAATTTGGCAATTGGCCAA 882
 601 AGTGAATGGTGGCACTCTCACTGCTTAATCTGCTTCCCAATTTGGCAATTGGCCAA 660
 883 ACCATGAAGGCGCTCAATTC 903


```

Db      661 ACCATGAGGCCCTCAATTC 681
|||||
RESULT 6
PAU93167      1109 bp  mRNA  linear  PLN 01-SEP-1998
LOCUS        Prunus armeniaca expansin (PA-Exp1) mRNA, complete cds.
DEFINITION
ACCESSION   U93167
VERSION     U93167.1  GI:3510537
KEYWORDS
SOURCE
ORGANISM    Prunus armeniaca (apricot)
            Prunus armeniaca
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            rosids; eurosids I; Rosales; Rosaceae; Amygdaloideae; Prunus.
REFERENCE
AUTHORS      Mbeguie-A-Mbeguie,D., Gomez,R.-M. and Filb-Lycaon,B.
TITLE        Molecular cloning and nucleotide sequence of expansin 1 (PA-Exp1)
            from apricot fruit
JOURNAL
REFERENCE    2 (bases 1 to 1109)
AUTHORS      Mbeguie-A-Mbeguie,D., Gomez,R.-M. and Filb-Lycaon,B.
TITLE        Direct Submission
JOURNAL      Submitted (12-MAR-1997) Station de Technologie des Produits
            Vegetaux, INRA, Site AGROPARC, Avignon 84914 Cedex 9, France
REFERENCE    3 (bases 1 to 1109)
AUTHORS      Mbeguie-A-Mbeguie,D., Gomez,R.-M. and Filb-Lycaon,B.
TITLE        Direct Submission
JOURNAL      Submitted (12-DEC-1997) Station de Technologie des Produits
            Vegetaux, INRA, Site AGROPARC, Avignon 84914 Cedex 9, France
REMARK
FEATURES
SOURCE
            1..1109
            /organism="Prunus armeniaca"
            /mol_type="mRNA"
            /strain="Bergeon"
            /db_xref="taxon:36596"
            /clone="pAPRI45"
            /tissue_type="mesocarp plus exocarp"
            /dev_stage="ripe fruit"
            1..1109
            /gene="PA-Exp1"
            74..838
            /gene="PA-Exp1"
            /codon_start=1
            /product="expansin"
            /protein_id="AAC33529.1"
            /db_xref="GI:3510538"
            /translation="MAPQALSLAPLALSLVFNLIHGAFADYGMGAHATPYGGD
            ASGTMGAGCGNLVSGYGTNTALSTLFPNNGSGCYEMRCNNDDPWCPSGSI
            VTATNCPNRFASNDNGKCNPLQHPDLAEAPFQIADIRAGIYVTFRRYPCMK
            GGIKFTINSHSYNLVLTINVGAGDVHSVISIGSRGQPMKRNQNNYNYING
            QSIKFTVTSIDGTGTSYNVAPNMOFGQTFSGGP"
BASE COUNT  301 a      254 c      242 g      312 t
ORIGIN
Query Match 45.7%; Score 453; DB 8; Length 1109;
Best Local Similarity 74.7%; Pred. No. 3,4e-113;
Matches 582; Conservative 0; Mismatches 195; Indels 2; Gaps 1;

```

```

QY      329 ATGCACGAACACGGTGGCGCTGAGCAGTCGGCTATTAAACAAATGATTAAGTTGCTG 388
Db      261 ATGGAACCAACACCTGACAGCTTTTAAGCACAGCCTTGTTAACAAATGGCTTAGCTGCT 320
QY      389 CTTCCTTCGAATGACTTGTACAAAGACCCCTTAATGATGCTCTCCGGAACTATTAGGG 448
Db      321 CTGTATTATGAATGAATGACATGACAAATGACCCCTGATGATGTCCTCTCGAAGCATCTTG 380
QY      449 TCATGCGACCAACTTTTGGCCCTCTCAACTTGTGCTGCCCTAACCAACAAATGGATGATG 508
Db      381 TTACTGCCACAAACTTTTGGCCCTCTCAACTTGTGCTGCCCTAACCAACAAATGGATGATG 440
QY      509 GCAACCTCTCTCTCAACACTTGACATGAGCTGAGCTGCTTCAATGCTCAAT 568
Db      441 GCATCTCTCCCTCCAGCACTTTGATTGCTAGAGCTGCTTCTTCAATGGCCCAAT 500
QY      569 ACCGAGCTGATGATGTCCTCCCTGCTCTCTTGTGATGGGTACCATGATGAAGAAAGTGGAG 628
Db      501 ACCGCGCTGGAGATTGGCTCTGTTACCTTCAGAAAGAGTGCCCTGTATGAGAAAGGAGGAA 560
QY      629 TGAGTTTCAATCAATGAGCACTCACTCACTCACTCACTCACTCACTCACTCACTCACTCACT 688
Db      561 TCAGATTCCACATCAATGAGCACTCACTCACTCACTCACTCACTCACTCACTCACTCACTCACT 620
QY      689 GCGCAGCGCAGCTCACTCTGTGTCATTAAGGGGTCTCGAATGATGAGCAATCCATGT 748
Db      621 GTGCAGGAGACGTCCTCACTAGTTTCAATCAAGGGGTCTCGAATGATGAGCAATCCATGT 680
QY      749 CTAGAAATTGGGGCCAAACCTGSCAAAGCAACAACTATGCAATGCGCAAGCCCTTCTCT 808
Db      681 CAAGAAACTGGGGGCAAACTGSCAAGCAACAACTATGCAATGCGCAAGCCCTTCTCTCT 740
QY      809 TTCAAGTCACTCTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 868
Db      741 TCAAGTCACTCTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 800
QY      869 GGCATTTGGCCAAACCTTGAAGGCCCTCAATTTCAACCATATGAGCCACACTGCTA 927
Db      801 GCGAGTTTGGTCAAGCTTCTCTGAGGGGTCAATTTTAGATTAATTCACACTAGATTATTA 859

```

RESULT 7
 AF049354 1177 bp mRNA linear PLN 16-DEC-1998
 LOCUS Nicotiana tabacum alpha-expansin precursor (Nt-EXPS) mRNA, partial
 DEFINITION cds.
 ACCESSION AF049354
 VERSION AF049354.1 GI:4027898
 KEYWORDS
 SOURCE
 ORGANISM Nicotiana tabacum (common tobacco)
 Nicotiana tabacum
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 Asteridae; lamiales; Solanales; Solanaceae; Nicotiana.
 1 (bases 1 to 1177)
 Link,B.M. and Cosgrove,D.J.
 Acid-growth response and alpha-expansins in suspension cultures of
 bright yellow 2 tobacco
 Journal Plant Physiol. 118 (3), 907-916 (1998)
 MEDLINE 9808735
 PUBMED
 REFERENCE 2 (bases 1 to 1177)
 AUTHORS Link,B.M. and Cosgrove,D.J.
 TITLE Direct Submission
 JOURNAL Submitted (20-FEB-1998) Biology, Pennsylvania State University, 208
 Mueller Laboratory, University Park, PA 16802, USA
 FEATURES
 source
 1..1177
 /organism="Nicotiana tabacum"
 /mol_type="mRNA"
 /cultivar="BY2"
 /db_xref="taxon:4097"
 /note="suspension culture"

[illegible]

Df		689	GCAACATGCTGCACCAGCAATTGGCAATTTGGCCAACTTTGAAGGGGCTCATTTT	748
Oy		905	AA 906	
Df		749	AA 750	
RESULT 8				
LOCUS		AB093029		
DEFINITION		Pyrus communis PCExp2 mRNA for expansin, complete cds.		
ACCESSION		AB093029		
VERSION		AB093029.1	GI:29467500	
KEYWORDS				
ORGANISM		Pyrus communis (pear)		
SOURCE		Eukaryote; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;		
		Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;		
		rosids; eurosoid I; Rosales; Rosaceae; Maloideae; Pyrus.		
REFERENCE		1		
AUTHORS		Hiwasa,K., Rose,J.K., Nakano,R., Inaba,A. and Kubo,Y.		
TITLE		Differential expression of seven alpha-expansin genes during growth		
JOURNAL		and ripening of pear fruit		
REFERENCE		Unpublished		
AUTHORS		2 (bases 1 to 1153)		
TITLE		Hiwasa,K., Kubo,Y., Nakano,R. and Inaba,A.		
JOURNAL		Direct Submission		
		Submitted (08-OCT-2002) Kyoto Hiwasa, Okayama University, Graduate		
		School of Natural Science and Technology, Tsushima-naka 1-1-1,		
		Okayama, Okayama 700-8530, Japan		
		(E-mail:k-hiwasa@cc.okayama-u.ac.jp, Tel:81-86-251-8338,		
		Fax:81-86-251-8338)		
FEATURES		Location/Qualifiers		
source		1..1153		
		/organism="Pyrus communis"		
		/mol_type="mRNA"		
		/cultivar="La France"		
		/db_xref="taxon:23211"		
		/tissue_type="softening fruit"		
		/dev_stage="ripening fruit"		
		/country="Japan"		
gene		1..1153		
		/gene="PCExp2"		
CDS		59..820		
		/gene="PCExp2"		
		/codon_start=1		
		/product="expansin"		
		/protein_id="BAC67189.1"		
		/db_xref="GI:29467501"		
		/translation="MAFTSHSTIALFVNLICLQGTGDYDYGMEGHATFYGGDA		
		SGTMCGACGYGLYSOGYGNTPALSTALFNPNLSGSCYEMCGSDPKMCLPGSLIV		
		TAINFCGPENPAONDNGMCNPLOHDLAEPAFLKIAOYRAGIPIPSFRVSCVKKG		
		GIEPTINGHSYFNLVIITNVGAGDYHVSISKSKIMQLSNMGWNSNYLNQG		
		SLSFQVYTISDGRILTVANNVAFGMWQFGQTREGQP"		
		59..133		
sigs_peptide		/gene="PCExp2"		
		/evidence=not experimental		
BASE COUNT		309 a 258 c 281 g 305 t		
ORIGIN				
Query Match		44.9%; Score 445.2; DB 8; Length 1153;		
Best Local Similarity		77.8%; Pred. No. 4,7e-111;		
Matches 537/, Conservative		0; Mismatches 153; Indels 0; Gaps 0;		
Oy		229	GGTGCGTCGAGACGCCGACACCACTTTTAATGAGCGTGTGACGATCTGGACCATG	288
Df		143	GGTGGAATGGAGGGCGGCATGCCACTTTTATGAGTGGTGTATGCTCTGGACATG	202
Oy		289	GGTGACCTGTTGGGTATGGAAATTTATACAGCCAAAGGATATGACGAAACACGATGCGC	348
Df		203	GGAGTGCTTGTTGTGATATGGAACTTGTACAGCCAAAGGATACGAAACCACTGCACGA	262

Oy		349	CTGAGCACTGGGCATTTTAAACAATGGATTAGTTGTGGTCGTGCTTGGAATAACATCTTG	408
Db		263	CTGAGCAGACTCTCTTTCAAACAATGGCTTAGCTCGGGCTCTTGCTATGATGAATTAAGT	322
Oy		409	ACAAACGACCCTAATATGGTGCCTTCCGGAAACTATTATGAGGTCACTGCCAACCTTTTGC	468
Db		323	GGCAGTAGACCCCAATATGGTGCCTCCCGGACAGCATCATGTACACGGCACCAATCTTGC	382
Oy		469	CCTCTTAACTTTGTCTCTCCCTTAAACAACAATGGTGGATGGTGCACCCCTCTCTCCACAC	528
Db		383	CCTCCCAACTTTGGCGAGGCCAAGACACATGGTGTGTGTCAACCCCTCTCTCCAGCAC	442
Oy		529	TTCGACATGGCTGAGCTGCCTCTCTTCAAAATCGCTCAATACCGAGCTGATGCTCCC	588
Db		443	TTTGATTTGGCTGAGCTGCTCTTCTTGAAAAATGGCCAATACAGAGCTGGAAATGTCCCC	502
Oy		589	GTCCTCTTTCTGTAAGGTACATGTATGAAAGAAAGGTGAGTGAGGTTTACATCATATGCG	648
Db		503	ATCTCTCTTCAAAAGGGTTTCGTGTGTGAAGAAGGAGGAATATGAGTTTCAATCAACCGGC	562
Oy		649	CACCTATCTCTCAACCTCGTTTTTGATCAACAACGTCGGTGGCGGACGAGCTCACTCT	708
Db		563	CACCTTATCTTCAACTTGGTTTGTATGATCAAGAACGTGAGAGACAGAGAGCTCACTCT	622
Oy		709	GTCGTGATTAAGGGGTCTCGAATCTGATGCGAATCATGTCTAAGAAATGGGGCCAAAC	768
Db		623	GTGTGATCAAAAGGTTCCAAAGACAGGGGTGGCAACCCCTGTCAAGAAATGGGGCCAGAC	682
Oy		769	TGGCAAGCAACAACCTATCTCAATGAGCCAAAGCCCTTCTTCAAGTCACTCTTAGAT	828
Db		683	TGGCAGAGCAACTCTTACTCTAACGGCCAGAGCTCTCTCTTCAGGTACACACGAC	742
Oy		829	GGTGGCACTCTCACTGCTTATATCTCGTTCCTTCATATGGCAATTTGGCCAAACCTAT	888
Db		743	GGCAAACTCTCACGGCCAAACATGTTGCGCGGGAACTGGCAGTTTGGCAAAACATTT	802
Oy		889	GAAGGCCCTCAATTCTTAACCATATCAGCC	918
Db		803	GAGGCGACTCAATTCTGAGACTCTCTCCGGC	832
RESULT 9				
AB093028				
LOCUS		1243 bp	mRNA	linear
DEFINITION			Pyrus communis Pckxpl mRNA for expansin, complete cds.	PLN 02-APR-2003
ACCESSION		AB093028		
VERSION		AB093028.1		GI:29467498
KEYWORDS				
SOURCE				
ORGANISM			Pyrus communis (pear)	
			Pyrus communis	
			Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;	
			Spermatophytes; Magnoliophyta; eudicotyledons; core eudicots;	
			Rosids; eurosoids I; Rosales; Rosaceae; Maloideae; Pyrus.	
REFERENCE				
AUTHORS			Hiwasa,K., Rose,J.K., Nakano,R., Inaba,A. and Kubo,Y.	
TITLE			Differential expression of seven alpha-expansin genes during growth	
JOURNAL			and ripening of pear fruit	
REFERENCE			Unpublished	
AUTHORS			2 (bases 1 to 1243)	
JOURNAL			Direct Submission	
TITLE			Submitted (08-OCT-2002) Kyoto Hiwasa, Okayama University, Graduate	
JOURNAL			School of Natural Science and Technology; Tsushima-naka 1-1-1,	
			Okayama, Okayama 700-8530, Japan	
			(E-mail:k-hiwasa@cc.okayama-u.ac.jp, Tel:81-86-251-8338,	
			Fax:81-86-251-8338)	
FEATURES				
source			Location/Qualifiers	
			1..1243	

[illegible]

FEATURES	source
gene	1. .1109 /organism="Prunus cerasus" /mol_type="mRNA" /db_xref="taxon:140311" /tissue_type="ripening fruit" /note="sour cherry" 1. .1109 /gene="EXP2" 75. .839 /gene="EXP2"
CDS	
RESULT 11	
LOCUS AF350937	1109 bp mRNA linear PLN 01-MAY-2007
DEFINITION Prunus cerasus expansin (EXP2) mRNA, complete cds.	
ACCESSION AF350937	
VERSION AF350937.1	GI:13898650
KEYWORDS	
SOURCE	
ORGANISM	Prunus cerasus Prunus cerasus Eukaryote; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids I; Rosales; Rosaceae; Amygdaloideae; Prunus. 1 (bases 1 to 1109) Yoo,S.-D., Gao,Z., Cantini,C., Loeschner,W. and van Nocker,S. Coordinated expression of genes encoding expansins and other cell wall-modifying enzymes is associated with pectin-related changes in the cell wall during ripening of cherry (P. cerasus) fruit Unpublished 2 (bases 1 to 1109) Yoo,S.-D. and van Nocker,S. Direct Submission Submitted (19-FEB-2001) Department of Horticulture, Michigan State University, 392A Plant and Soil Science Building, East Lansing, MI 48824, USA
JOURNAL	
REFERENCE	
AUTHORS	
TITLE	
JOURNAL	

```

/codon_start=1
/product="expansin"
/protein_id="AAK48846.1"
/db_xref="gi:13898651"
/transeq_label="MAP04LSTAPLALSLVFNHILHGAAPADYCGMECAHATPYGGED
ASGMGACACGICGNYISOSYGTNTALSLALFNNGSLSCSCYEMKCNNDPRKCRGSLIT
VLAITNFCPEPFAQNSDNGMCNPPLOHFDLIEPFLSLAQRAIVLPTFPRVFCMKR
GGSLFTNGHSYFNILVLTITNKGAGDVHSAVSIKSRRTGQPMSPHNMGNQMSNTYLNKG
QSLSFQVTTSDGRVITNNVNAAPGAMQVFCQRTSSGQF"

```

Query Match	44.6%	Score 442	DB 8	Length 1109
Best Local Similarity	70.6%	Pred. No. 3.6e-110		
Matches	604	Conservative	0	Mismatches 250; Indels 2; Gaps 1;
Qy	74	CTTCCCCCTCTCTCTTCTAAACCCACAAAACCCCACTTCTTCAACAACTATT	133	
Db	5	CCCTCCCTCGATAAACCAAAAGCTCTCTCTCTTCTTCTCTATTAAGAAATC	64	
Qy	134	TCAATATTAACCCATTCTATAGGCTTTTCTTACTACCTTCTCTCTCTTCTTC	193	
Db	65	ATATCAAAAAATGGCACCTCAGGATATCTTTAGCTCTCTAGCCCTCTCTGTATCT	124	
Qy	194	TTCCCTTCTTCTTGTCTT--CACCTGCGACTAGAGGAGGCGGAGAGGCGCACGC	251	
Db	125	CTTCAATCTTACCTTCAAGGTGCTTTTGTGATTAATAGTATGAGGAGCGCTCAGC	184	
Qy	252	CACCTTTATAGTATGATGATGACGATCTGGACCATGGATGGAGCTTGTGGATAGGA	311	
Db	185	CACCTTTTATAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATG	244	
Qy	312	TTTATACAGCCAGGATATGGACGAAACGAGTGGCGCTGAGCACTGCGCTATTAA	371	
Db	245	CTTGTACAGCCAGGATATGGACGAAACGAGTGGCGCTGAGCACTGCGCTATTAA	304	
Qy	372	TGATTTAAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG	431	
Db	305	TGCTTGAAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG	364	
Qy	432	TCCGGAACCTTATAGGCTCACTGACCAACCTTTTGGCTCTTACTTGTCTCCCTAA	491	
Db	365	TCTTGAAGCTCACTTGTATCTCTCAAACTTTTGGCTCTTACTTGTCTCCCTAA	424	
Qy	492	CAACAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG	551	
Db	425	CGAATATGCGGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG	484	
Qy	552	CCTTCAATGCTCAATATCGAGCTGATGATGATGATGATGATGATGATGATGATGATG	611	
Db	485	CTTCAATATGCTCAATATCGAGCTGATGATGATGATGATGATGATGATGATGATGATG	544	
Qy	612	TATGAAGAAAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG	671	
Db	545	TATGAAGAAAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG	604	
Qy	672	GATCAACAACTGCGTGGCGGAGCGAGCTCACTCTGTGTGATTAAGGGGTCTCAAC	731	
Db	605	GATCAACAACTGCGTGGCGGAGCGAGCTCACTCTGTGTGATTAAGGGGTCTCAAC	664	
Qy	732	TGATGCGAATCATGCTAGAAAAATGGGGCCAAAATGCGAAGCAACATATTCTCAA	791	
Db	665	AGGCTGCGAATCATGCTAGAAAAATGGGGCCAAAATGCGAAGCAACATATTCTCAA	724	
Qy	792	TGCGCAAGGCTTCTCTTCAAGTCACTCTTAAGTATGATGATGATGATGATGATGATG	851	
Db	725	TGCGCAAGGCTTCTCTTCAAGTCACTCTTAAGTATGATGATGATGATGATGATGATG	784	
Qy	852	TCTGCTTCTTCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG	911	
Db	785	CGTGGCCCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG	844	
Qy	912	ATCAGCCACTGCTTA	927	

[illegible]

QY 480 TGGCTCCCTAACAATGGATGATGGAACCTCTCTCCAACTGCAACTGCACTGGC 539
 DB 419 TCTCACTGTCACGAAATGAGGCGGCGGTCGCAATCTCTCTCCAACTGCACTGGC 478
 QY 540 TGAAGCTGCTTCTTCAATGCTCAATACGAGCTGGTATCGTCCGCTCTCTTTCG 599
 DB 479 CGAGCTGCTTCTTCAATGCTCAATACGAGCTGGTATCGTCCGCTCTTTCG 538
 QY 600 TGAAGCTGCTTCTTCAATGCTCAATACGAGCTGGTATCGTCCGCTCTTTCG 659
 DB 539 TGAAGCTGCTTCTTCAATGCTCAATACGAGCTGGTATCGTCCGCTCTTTCG 598
 QY 660 TGAAGCTGCTTCTTCAATGCTCAATACGAGCTGGTATCGTCCGCTCTTTCG 719
 DB 599 TGAAGCTGCTTCTTCAATGCTCAATACGAGCTGGTATCGTCCGCTCTTTCG 658
 QY 720 TGAAGCTGCTTCTTCAATGCTCAATACGAGCTGGTATCGTCCGCTCTTTCG 779
 DB 659 TGAAGCTGCTTCTTCAATGCTCAATACGAGCTGGTATCGTCCGCTCTTTCG 718
 QY 780 TGAAGCTGCTTCTTCAATGCTCAATACGAGCTGGTATCGTCCGCTCTTTCG 839
 DB 719 TGAAGCTGCTTCTTCAATGCTCAATACGAGCTGGTATCGTCCGCTCTTTCG 778
 QY 840 TGAAGCTGCTTCTTCAATGCTCAATACGAGCTGGTATCGTCCGCTCTTTCG 899
 DB 779 TGAAGCTGCTTCTTCAATGCTCAATACGAGCTGGTATCGTCCGCTCTTTCG 838
 QY 900 TGAAGCTGCTTCTTCAATGCTCAATACGAGCTGGTATCGTCCGCTCTTTCG 927
 DB 839 TGAAGCTGCTTCTTCAATGCTCAATACGAGCTGGTATCGTCCGCTCTTTCG 866

RESULT 13
 CAR291817 1035 bp mRNA linear PLN 19-DEC-2000
 LOCUS Cicer arietinum mRNA for expansin, clone CanExp-2.
 DEFINITION AJ291817 GI:11932091
 ACCESSION
 VERSION
 KEYWORDS
 SOURCE Cicer arietinum (chickpea)
 ORGANISM Cicer arietinum
 Bacteria; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Ciceraceae; Cicer.
 REFERENCE 1
 AUTHORS Dopic, B., Sanchez, M. A. and Labrador, E.
 TITLE An second expansin is expressed in chickpea epicotyls
 JOURNAL Unpublished
 REFERENCE 2 (bases 1 to 1035)
 AUTHORS Labrador, E.
 TITLE Direct Submission
 JOURNAL Submitted (15-DEC-2000) Labrador E., Dpto. Fisiologia Vegetal, Univ. Salamanca, Campus Miguel de Unamuno. Pza. Doctores de la Reina s/n, E-37007, SPAIN
 FEATURES
 source
 1.1035
 Location/Qualifiers
 /organism="Cicer arietinum"
 /mol_type="mRNA"
 /cultivar="Castellana"
 /db_xref="taxon:3827"
 /clone="CanExp-2"
 /issue_type="etioloated epicotyls"
 /clone_lib="CAN-5"
 /dev_stage="5 days old seedling"
 /country="Spain"
 /codon_start=1
 /product="expansin"
 /protein_id="CAC19184.1"
 /db_xref="GI:11932092"
 /translation="MAQKRLMAHQERSIVLKGLIFPFMMNMOSALADYGMGNAHAT

CDS

RESULT 14
 AY083166 1108 bp mRNA linear PLN 10-APR-2002
 LOCUS Malus x domestica expansin 1 (Exp1) mRNA, complete cds.
 DEFINITION AY083166
 ACCESSION AY083166
 VERSION
 KEYWORDS
 SOURCE Malus x domestica (apple tree)
 ORGANISM Malus x domestica
 Bacteria; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosids; eurosids I; Rosales; Rosaceae; Maloideae; Malus.
 REFERENCE 1 (bases 1 to 1108)

BASE COUNT 312 a 168 c 213 g 342 t
 ORIGIN
 FYGGDASGTMGGACGAGCNILYSOGVGTNTAALSTALPNNGLSCGSCEYMRCDNDPRMC
 KPGSITVATNFCPPNPSPLANNNGMCPPLDHPMAPPLQIAEYAGIYPSVFR
 VPKMGKGIREFITNHSYFNLVTVNAGVSHSVTKGSTRGNQSHSRMGQWQMS
 NSYNGGIPSLSPVITSDRITMSLVNVAASNMOFGOTFGQAGP"

Query Match 44.2%; Score 438.8; DB 8; Length 1035;
 Best Local Similarity 77.2%; Pred. No. 2.7e-109;
 Matches 533; Conservative 0; Mismatches 157; Indels 0; Gaps 0;

QY 218 TGGCTGACAGAGGCTGGGACGAGCGGACGCCACCTTTATGATGGTGGTGGCAT 277
 DB 124 TGGCTGATATGATGGTGGGAGGCTCTCATGCCACTTTCTATGATGGGATGCTT 183
 QY 278 CTGGACCAATGGGATGGGATGGGATGGGATTTATACGCCAAGGATATGACAGA 337
 DB 184 CTGGACCAATGGGATGGGATGGGATGGGATTTATACGCCAAGGATATGACAGA 243
 QY 338 ACAGGCTGGGCTGGGACCTGGCTATTTAACAATGATTAAGTTGGTGGTCTTTCG 397
 DB 244 ACAGGCTGGGCTGGGACCTGGCTATTTAACAATGATTAAGTTGGTGGTCTTTCG 303
 QY 398 AATGACTTGTACAAACGACCCCTAATGATGGGCTTCGGGAACTATTAGGTCACCTGCA 457
 DB 304 AATGACTTGTACAAACGACCCCTAATGATGGGCTTCGGGAACTATTAGGTCACCTGCA 363
 QY 458 CCACTTTTGGCCCTCTTAATTTGCTCTCTTCAACAACAATGATGGTGGTGGTGGT 517
 DB 364 CCACTTTTGGCCCTCTTAATTTGCTCTCTTCAACAACAATGATGGTGGTGGTGGT 423
 QY 518 CTCTCAACACTTGCACATGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 577
 DB 424 CTCTCAACACTTGCACATGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 483
 QY 578 GTATGTCGCCGCTCTCTCTTGTAGGATGATGATGATGATGATGATGATGATGATGAT 637
 DB 484 GTATGTCGCCGCTCTCTCTTGTAGGATGATGATGATGATGATGATGATGATGATGAT 543
 QY 638 CAATCAATGGCCACTCATCTTCAACCTGTTTGTATCAACAACGTCGGTGGGACGCG 697
 DB 544 CAATCAATGGCCACTCATCTTCAACCTGTTTGTATCAACAACGTCGGTGGGACGCG 603
 QY 698 AGTCCACTCTTGTGATTAAGGCTCTCCAACTGATGATGATGATGATGATGATGATGAT 757
 DB 604 AGTCCACTCTTGTGATTAAGGCTCTCCAACTGATGATGATGATGATGATGATGATGAT 663
 QY 758 GGGGCAAAAATGGGCAAAAGCAACAATCTCAATGATGATGATGATGATGATGATGATGAT 817
 DB 664 GGGGCAAAAATGGGCAAAAGCAACAATCTCAATGATGATGATGATGATGATGATGATGAT 723
 QY 818 CTCTAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 877
 DB 724 CCACAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 783
 QY 878 GCCAATCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 907
 DB 784 GTCAATCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT

AUTHORS Trivedi, P. K. and Solomos, T.
TITLE Characterization of expansin cDNA from apple
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 1108)
AUTHORS Trivedi, P. K. and Solomos, T.
TITLE Direct Submission
JOURNAL Submitted (08-MAR-2002) Department of Natural

BASE COUNT	317 a	250 c	243 g	297 t	1 others
ORIGIN					

Accession	Sequence	Position
D6	660 TGGGTCAAAACCTGGCAGAGCACTCATTACTCAATGGCCAGCCCTCTCTTCCAAATGTC	719
QY	817 ACTCTTAGTGATGATGTCGCACCTCTCACTGCCTATAATCTGGTTCCTTCCAAATGGCAATT	876
D6	720 ACCACAGATGACGGTAGAACCCTGACAGAGCTAACAACTGGCTCTCTGTATATGGCAGTTT	779
QY	877 GGCCTAAACCTATGAAAGGCCCTCAATTCTTAACCATATAGCCACACT	923
D6	780 GGGCAGACATTCTCAGGGGGGCAATTTTAAATTAATTCACCTAGACT	826

RESULT	15
LOCUS	AY079206
DEFINITION	AY079206 1262 bp mRNA linear PLN 15-APR-2003 Mirabilis jalapa cell wall protein Exp4 precursor, mRNA, complete cds.
ACCESSION	AY079206
VERSION	AY079206.1 GI:28624705
KEYWORDS	
SOURCE	Mirabilis jalapa (garden four-o'clock)
ORGANISM	Mirabilis jalapa

```

*
sig_peptide 76.147

```

Db 250 CAGGGTATGAGACANATACAGAGCATTAAGTACAGCATTTTATACATGATTTAAGT 309
Qy 382 TGTGTGCTTGTCTCGAATGACTGTACAAAGACCTTAATGTGCTCCGGGAACT 441
Db 310 TGTGGATGCTGTGCTAAGAAATGAAATGATGATCCAAATGTGTAGACTGTAGT 369
Qy 442 ATTAGGGTCACTGCCACCACTTTTGGCCTCCTAATTGCTCTCCCTAACAAATGCT 501
Db 370 ATAGTGTGACTGCAACCAATTTTGTGTCCACCTAATTAATGCTTAATTAACAATGCT 429
Qy 502 GGATGAGTGAACCTCTCTCCACACTGACATGCTGAGCTGCTCCCTCAATC 561
Db 430 GGATGAGTGAATCTCTCTCTCAACACTTGAATGCTCAACCTGCTTCTTAACAAT 489
Qy 562 GCTCAATACCGAGCTGTATGCTCCCGTCTCTTGTAGGGTACCATGTATGAAGAA 621
Db 490 GCTCAATACCGTGTGTATGCTCCCATTTCTCCGAAGGGTACCTGTGCAAGAAA 549
Qy 622 GGTGAGTGAAGTTTACAAATCAATGAGCCACTCAATCACTGCTGTTTGTATCAGAAC 681
Db 550 GCGGGAATTAAGATTCAACCGTCAACGACACTCAATCACTGCTTGTGTACGAAC 609
Qy 682 GTGCGTGGCGAGGCGAGCTCACTGTGTGATTAAGGGGTCTGAACTGATGGCAA 741
Db 610 GTGCGCGAGCGGTGATGTCCATGCAAGTGTGATCAAGGGTTCAAAAACGGGTGGCAA 669
Qy 742 TCCATGTCTAGAATTTGGGCGCAAACTGGCAAAAGCAACAATCTCAATGGCCAAAGC 801
Db 670 GCAATGTCAAGGAATTTGGGCGCAAAATTTGGCAGAGCAATTTCTATGTAATGGCCAAAGT 729
Qy 802 CTTTCTTTCAAGTCACTTGTAGTGTGTGCACTCTCACTGCTTATATCTGTTCT 861
Db 730 TTGTCTTTCAAGTCACTGTAAGTGTGAGAGACTGTCACTAGTAAATATTTGCTCT 789
Qy 862 TCCAATTTGCAATTTGGCCAAACCTATGAAGGCCCTCAATTTCAACCAT 912
Db 790 GCTAATTTGCAATTTGGCAAACTTATGTGGGTCTCAATTTCAAAACATA 840

Search completed: December 18, 2003, 21:57:22
Job time : 3655 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: December 18, 2003, 17:45:13 ; Search time 41 Seconds
(without alignments)
967.845 Million cell updates/sec

Title: US-09-383-579C-10

Perfect score: 1394
Sequence: 1 MAFSYSPFSLFLPFFVF.....AYNLVPSNMQFGQYEGPQF 250

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :
1: A_Geneseq_19Jun03:*
2: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1980.DAT:*
3: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1981.DAT:*
4: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1982.DAT:*
5: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1983.DAT:*
6: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1984.DAT:*
7: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1985.DAT:*
8: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1986.DAT:*
9: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1987.DAT:*
10: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1988.DAT:*
11: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1989.DAT:*
12: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1990.DAT:*
13: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1991.DAT:*
14: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1992.DAT:*
15: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1993.DAT:*
16: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1994.DAT:*
17: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1995.DAT:*
18: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1996.DAT:*
19: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1997.DAT:*
20: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1998.DAT:*
21: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1999.DAT:*
22: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2000.DAT:*
23: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2001.DAT:*
24: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2002.DAT:*
25: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2003.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1275	91.5	227	17	AA94527
2	1275	91.5	227	23	AA94527
3	1269	91.0	226	23	AA94527
4	1131	81.1	223	23	AB898474
5	1085	77.8	253	21	AA635443
6	1085	77.8	253	21	AA635443
7	1041	74.7	241	21	AA606546
8	1041	74.7	241	21	AA651633
9	1041	74.7	241	21	AA651647

10	1041	74.7	249	21	AA606545	Arabidopsis thalia
11	1041	74.7	249	21	AA651632	Arabidopsis thalia
12	1041	74.7	249	21	AA651646	Arabidopsis thalia
13	1041	74.7	259	21	AA606544	Arabidopsis thalia
14	1041	74.7	259	21	AA651631	Arabidopsis thalia
15	1041	74.7	280	21	AA651645	Arabidopsis thalia
16	1030	73.9	228	23	AA680771	N. tabacum expansi
17	1026.5	73.6	281	21	AA643341	Arabidopsis thalia
18	1026	73.6	228	17	AA694528	Rice expansin. Or
19	1024.5	73.5	282	21	AA623850	Arabidopsis thalia
20	1024	73.5	251	21	AA623852	Arabidopsis thalia
21	1024	73.5	251	21	AA643343	Arabidopsis thalia
22	1024	73.5	253	21	AA623851	Arabidopsis thalia
23	1024	73.5	253	21	AA643342	Arabidopsis thalia
24	1002.5	71.9	227	17	AA694532	Arabidopsis expans
25	999	71.7	250	22	AA600414	Tomato seed expans
26	993	71.2	257	21	AA636445	Arabidopsis thalia
27	970.5	69.6	207	21	AA625444	Arabidopsis thalia
28	970.5	69.6	207	21	AA646484	Arabidopsis thalia
29	970	69.6	241	21	AA605453	Arabidopsis thalia
30	970	69.6	249	21	AA605452	Arabidopsis thalia
31	970	69.6	255	21	AA605451	Arabidopsis thalia
32	965	69.2	242	21	AA636570	Arabidopsis thalia
33	965	69.2	249	21	AA636569	Arabidopsis thalia
34	965	69.2	255	21	AA636568	Arabidopsis thalia
35	962	69.0	225	17	AA694531	Arabidopsis expans
36	944	67.7	262	21	AA629931	Arabidopsis thalia
37	944	67.7	273	21	AA629930	Arabidopsis thalia
38	939	67.4	255	21	AA630325	Arabidopsis thalia
39	939	67.4	257	21	AA630324	Arabidopsis thalia
40	938.5	67.3	258	23	AA620570	Pear expansin 1 (B
41	934	67.0	250	21	AA609622	Arabidopsis thalia
42	934	67.0	280	21	AA609620	Arabidopsis thalia
43	934	67.0	280	21	AA609620	Arabidopsis thalia
44	928	66.6	263	22	AA600412	Tomato seed expans
45	895	64.2	210	21	AA636446	Arabidopsis thalia

ALIGNMENTS

RESULT 1	AA94527	standard; protein; 227 AA.
ID	AA94527	
AC	AA94527	
XX		
DT	25-MAR-2003 (updated)	
DT	08-JUL-1996 (first entry)	
XX		
DE	Cucurbit expansin-29.	
XX		
KW	Expansin-29; plant cell wall; cellulose; paper recycling; de-linking; polysaccharide; cucumber.	
XX		
OS	Cucurbit sativus var. Burpee Pickler.	
XX		
PN	AA9540262-A.	
PD	04-APR-1996.	
XX		
PF	06-DEC-1995; 95AU-0040262.	
XX		
PR	12-MAY-1993; 93US-0060944.	
PR	12-MAY-1995; 95US-0440517.	
XX	12-MAY-1994; 94AU-0068320.	
PA	(PENN-) PENN STATE RES FOUNO.	
XX		
PT	Cosgrove DJ, McQueen-Mason S;	
XX		
DR	WPI; 1996-201150/21.	
DR	N-PSDB; AAT13320.	

XX Expansin proteins which alter the mechanical strength of
PT poly:saccharide(s) - useful in paper mfr. and recycling
XX
PS Claim 7; Page 30; 60pp; English.
XX
CC Cucurbit expansin-29 (AAR94527) is a member of a novel class of
CC proteins that catalyze the extension of plant cell walls and the
CC weakening of the hydrogen bonds in pure cellulose. It can be obtd.
CC by expression of an isolated cDNA clone (see AAT1320) in bacterial or
CC other host cells. Expansin proteins have also been identified in cat
CC coleoptiles, in Arabidopsis (see AAR94530-32) and in rice (AAR94528-29),
CC and appear to be broadly distributed throughout the plant kingdom.
CC Expansins can be used e.g. in the mfr., de-linking and recycling of
CC paper, in the textile industry, to aid delignification processes, to
CC alter gel mechanical strength, etc.
CC (Updated on 25-MAR-2003 to correct PR field.)
CC
CC (Updated on 25-MAR-2003 to correct PR field.)
SQ Sequence 227 AA;
Query Match 91.5%; Score 1275; DB 17; Length 227;
Best Local Similarity 100.0%; Pred. No. 3,1e-118;
Matches 227; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 24 DYGGWQSGHATFYGGDASGTWGAAGYGNLYSGYGTNTVALSTALFNNGLSCGACPEM 83
DB 1 DYGGWQSGHATFYGGDASGTWGAAGYGNLYSGYGTNTVALSTALFNNGLSCGACPEM 60
QY 84 TCTNDPKMCLPGTIRVTATNFCPPNFALPNNNGWCNPLOHPDMAEPALQIAOYRAGI 143
DB 61 TCTNDPKMCLPGTIRVTATNFCPPNFALPNNNGWCNPLOHPDMAEPALQIAOYRAGI 120
QY 144 VVFSFRVPCMKKGGVRFITNGHSYFNLYLITNVGAGADVHSVSIKSGRTGQMSRMWG 203
DB 121 VVFSFRVPCMKKGGVRFITNGHSYFNLYLITNVGAGADVHSVSIKSGRTGQMSRMWG 180
QY 204 QNWQSNNTYLNQGLSFQVTLSDGRTLTAYNLVPSNMWQGYEGPOF 250
DB 181 QNWQSNNTYLNQGLSFQVTLSDGRTLTAYNLVPSNMWQGYEGPOF 227
RESULT 2
AAG80768
ID AAG80768 standard; Protein; 227 AA.
XX
AC AAG80768;
XX
DT 19-APR-2002 (first entry)
XX
DE C. sativus SI expansin homologue fragment.
XX
KW Expansin; SI; cellulose-based textile; cotton; paper recycling;
KM paper pulp; plant tissue; papermaking; cucumber.
XX
OS Cucumis sativus.
XX
XX DE10032630-A1.
XX
PD 22-NOV-2001.
XX
PF 05-JUL-2000; 2000DE-1032630.
XX
PR 16-MAY-2000; 2000DE-1023561.
XX
PA (FARB) BAYER AG.
XX
PI Berendes F, Rast HG, Vogt U, Gouloudis C,
XX
DR WPI; 2002-155755/21.
XX
DR N-PSDB; ABA97161.
XX
PT Vector encoding an expansin, useful in treatment of cellulosic

PT materials for paper recycling, providing large-scale production -
XX
XX Example 1; Page 11-14; 22pp; German.
PS
XX
CC This invention describes a novel vector (A) comprising (i) nucleic acid
CC (i) encoding an expansin (ii) and (ii) coupled sequences that allow
CC expression of (i) in microorganisms. The recombinant expansins described
CC in the invention are used in preparation, treatment and finishing of
CC cellulose-based textiles (e.g. cotton) or in recycling of paper or for
CC preparation of pulp from plant tissue, as a substitute for corrosive
CC chemicals currently used in papermaking. Recombinant methods make
CC possible large scale production of expansins possible. This sequence
CC represents the Cucumis sativus (cucumber) SI expansin homologue fragment
CC described in the invention.
XX
SQ Sequence 227 AA;
Query Match 91.5%; Score 1275; DB 23; Length 227;
Best Local Similarity 100.0%; Pred. No. 3,1e-118;
Matches 227; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 24 DYGGWQSGHATFYGGDASGTWGAAGYGNLYSGYGTNTVALSTALFNNGLSCGACPEM 83
DB 1 DYGGWQSGHATFYGGDASGTWGAAGYGNLYSGYGTNTVALSTALFNNGLSCGACPEM 60
QY 84 TCTNDPKMCLPGTIRVTATNFCPPNFALPNNNGWCNPLOHPDMAEPALQIAOYRAGI 143
DB 61 TCTNDPKMCLPGTIRVTATNFCPPNFALPNNNGWCNPLOHPDMAEPALQIAOYRAGI 120
QY 144 VVFSFRVPCMKKGGVRFITNGHSYFNLYLITNVGAGADVHSVSIKSGRTGQMSRMWG 203
DB 121 VVFSFRVPCMKKGGVRFITNGHSYFNLYLITNVGAGADVHSVSIKSGRTGQMSRMWG 180
QY 204 QNWQSNNTYLNQGLSFQVTLSDGRTLTAYNLVPSNMWQGYEGPOF 250
DB 181 QNWQSNNTYLNQGLSFQVTLSDGRTLTAYNLVPSNMWQGYEGPOF 227
RESULT 3
AAG80769
ID AAG80769 standard; Protein; 226 AA.
XX
AC AAG80769;
XX
DT 19-APR-2002 (first entry)
XX
DE C. sativus expansin csexp1a fragment.
XX
KW Expansin; cellulose-based textile; cotton; paper recycling; csexp1a;
KM paper pulp; plant tissue; papermaking; cucumber.
XX
OS Cucumis sativus.
XX
XX DE10032630-A1.
XX
PD 22-NOV-2001.
XX
PF 05-JUL-2000; 2000DE-1032630.
XX
PR 16-MAY-2000; 2000DE-1023561.
XX
PA (FARB) BAYER AG.
XX
PI Berendes F, Rast HG, Vogt U, Gouloudis C,
XX
DR WPI; 2002-155755/21.
XX
DR N-PSDB; ABA97162.
XX
PT Vector encoding an expansin, useful in treatment of cellulosic
XX
PS Example 1; Page 14-16; 22pp; German.

CC This invention describes a novel vector (A) comprising (i) nucleic acid
 CC (1) encoding an expansin (II) and (ii) coupled sequences that allow
 CC expression of (i) in microorganisms. The recombinant expansins described
 CC in the invention are used in preparation, treatment and finishing of
 CC cellulose-based textiles (e.g. cotton) or in recycling of paper or for
 CC preparation of pulp from plant tissue, as a substitute for corrosive
 CC chemicals currently used in papermaking. Recombinant methods make
 CC possible large scale production of expansins possible. This sequence
 CC represents the *Cucumis sativus* (cucumber) expansin, csepla, fragment
 CC described in the invention.

XX Sequence 226 AA;

Query Match 91.0%; Score 1269; DB 23; Length 226;
 Best Local Similarity 100.0%; Pred. No. 1.2e-117;
 Matches 226; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 24 DYGMOSGHATFYGGDASGTMGACGYGNLYSGYGTNTVALSTALFNNGLSCGACFEM 83

DB 1 DYGMOSGHATFYGGDASGTMGACGYGNLYSGYGTNTVALSTALFNNGLSCGACFEM 60

QY 84 TCTNDPKWCLPGTIRVATNFCPPNFALPNNNGCMCPLOHFDMAEPALQIAQYRAGI 143

DB 61 TCTNDPKWCLPGTIRVATNFCPPNFALPNNNGCMCPLOHFDMAEPALQIAQYRAGI 120

QY 144 VPSFRRVPCMKKGVRTINGHSYFNLVLTNVGAGDVHSVSIKSRGTQMSMRNG 203

DB 121 VPSFRRVPCMKKGVRTINGHSYFNLVLTNVGAGDVHSVSIKSRGTQMSMRNG 180

QY 204 QNMOSNNYLNQGLSFQVTLSDGRTLTAYNLVPSNMFGQTYEGPQ 249

DB 181 QNMOSNNYLNQGLSFQVTLSDGRTLTAYNLVPSNMFGQTYEGPQ 226

RESULT 4

ID ABB98474 standard; Protein; 223 AA.

XX ABB98474;

DT 01-NOV-2002 (first entry)

XX Plant expansin consensus sequence.

XX Longibrachiatum; filamentous fungus; swollenin; cotton fibre swelling;
 KM cellulose; cellulosic substrate; animal food; biomass; glucose;
 KM paper manufacture; laundry detergent; plant; expansin.

XX Unidentified.

XX US2002086350-A1.

XX 04-JUL-2002.

XX 09-JUL-1998; 98US-0112498.

XX 11-JUL-1997; 97US-0893766.

XX (SWAN/) SWANSON B A.

XX (WARD/) WARD M.

XX (PENT/) PENTTILA M.

XX (JAAK/) JAAKKO P.

XX (SALO/) SALOHEIMO M.

XX Swanson BA, Ward M, Penttila M, Jaakko P, Saloheimo M;

XX WPI; 2002-642241/69.

XX Novel swollenin protein isolated from fungus or bacteria, has
 PT applications in cleaning textiles (laundry detergents and pre-wash
 PT compositions), modifying textiles (depilling, color restoration,
 PT anti-greying)

PS Example 1; Fig 2; 20pp; English.

XX The present invention relates to swollenin from *Trichoderma reesei*
 CC (longibrachiatum, a filamentous fungus). Swollenins facilitate weakening
 CC of filter paper and the swelling of cotton fibres without having
 CC cellulolytic activity i.e., catalytic activity involving the breakage of
 CC individual cellulose strands into smaller monomer (glucose) or oligomers
 CC (polysaccharides). Swollenin and its coding sequence are useful in
 CC methods for altering the properties of cellulosic substrate. Preferably
 CC the methods are useful for altering the nutritional properties of animal
 CC feed, altering the properties of fabric or yarn comprising cellulosic
 CC fibres, altering properties of cellulosic biomass during its reduction to
 CC glucose, altering properties of wood pulp or its derivatives during paper
 CC manufacture, and altering properties of cellulosic corn husk fibre during
 CC its reduction to glucose. The swollenin coding sequence has utility in
 CC many applications for which cellulase is currently used, for example,
 CC cleaning textiles (laundry detergents and pre-wash compositions),
 CC modifying textiles (depilling, colour restoration, anti-greying), and
 CC improvement of the nutritive value of animal feeds. Since the swollenin
 CC coding sequence is expressed by a fungus, it can be produced in large
 CC quantities. The present sequence is a consensus sequence for plant
 CC expansin, which was used in a sequence alignment with a partial swollenin
 CC protein sequence. It was found that there was a 21.7% identity between
 CC the sequences.

XX Sequence 223 AA;

Query Match 81.1%; Score 1131; DB 23; Length 223;
 Best Local Similarity 88.4%; Pred. No. 5.9e-104;
 Matches 199; Conservative 16; Mismatches 8; Indels 2; Gaps 2;

QY 26 GGMOSHAATFYGGDASGTMGACGYGNLYSGYGTNTVALSTALFNNGLSCGACFEMTC 85

DB 1 GGMOSHAATFYGGDASGTMGACGYGNLYSGYGTNTVALSTALFNNGLSCGACFELTC 60

QY 86 TNDPKWCLPGTIRVATNFCPPNFALPNNNGCMCPLOHFDMAEPALQIAQYRAGI 145

DB 61 DNDPKWCLPGTIRVATNFCPPNFALPNNNGCMCPLOHFDMAEPALQIAQYRAGI 120

QY 146 VPSFRRVPCMKKGVRTINGHSYFNLVLTNVGAGDVHSVSIKSRGTQMSMRNGON 205

DB 121 VPSFRRVPCMKKGVRTINGHSYFNLVLTNVGAGDVHSVSIKSRGTQMSMRNGON 180

QY 206 WOSNNYLNQGLSFQVTLSDGRTLTAYNLVPSNMFGQTYEGPQ 250

DB 181 WOSNNYLNQGLSFQVTLSDGRTVTS-NVAPNMFGQTYEGPQ 223

RESULT 5

ID AAG25443 standard; Protein; 253 AA.

XX AAG25443;

DT 17-OCT-2000 (first entry)

XX Arabidopsis thaliana protein fragment SEQ ID NO: 29510.

XX Protein identification; signal transduction pathway; metabolic pathway;
 KM hybridisation assay; genetic mapping; gene expression control; promoter;
 KM termination sequence.

XX Arabidopsis thaliana.

XX EP1033405-A2.

XX 06-SEP-2000.

XX 25-FEB-2000; 2000EP-0301439.

XX 25-FEB-1999; 99US-0121825.

XX 05-MAR-1999; 99US-0123180.

XX 09-MAR-1999; 99US-0123548.

PR 23-MAR-1999; 99US-0125788.
PR 25-MAR-1999; 99US-0126264.
PR 29-MAR-1999; 99US-0126785.
PR 01-APR-1999; 99US-0127462.
PR 06-APR-1999; 99US-0128234.
PR 08-APR-1999; 99US-0128714.
PR 16-APR-1999; 99US-0129845.
PR 19-APR-1999; 99US-0130077.
PR 21-APR-1999; 99US-0130449.
PR 23-APR-1999; 99US-0130510.
PR 28-APR-1999; 99US-0131449.
PR 30-APR-1999; 99US-0132048.
PR 30-APR-1999; 99US-0132407.
PR 04-MAY-1999; 99US-0132484.
PR 05-MAY-1999; 99US-0132485.
PR 06-MAY-1999; 99US-0132486.
PR 07-MAY-1999; 99US-0132863.
PR 11-MAY-1999; 99US-0134256.
PR 14-MAY-1999; 99US-0134218.
PR 14-MAY-1999; 99US-0134219.
PR 14-MAY-1999; 99US-0134221.
PR 14-MAY-1999; 99US-0134370.
PR 18-MAY-1999; 99US-0134768.
PR 19-MAY-1999; 99US-0134941.
PR 20-MAY-1999; 99US-0135124.
PR 21-MAY-1999; 99US-0135353.
PR 24-MAY-1999; 99US-0135629.
PR 25-MAY-1999; 99US-0136021.
PR 27-MAY-1999; 99US-0136392.
PR 28-MAY-1999; 99US-0136782.
PR 01-JUN-1999; 99US-0137222.
PR 03-JUN-1999; 99US-0137528.
PR 04-JUN-1999; 99US-0137502.
PR 07-JUN-1999; 99US-0137724.
PR 08-JUN-1999; 99US-0138094.
PR 10-JUN-1999; 99US-0138540.
PR 10-JUN-1999; 99US-0138847.
PR 14-JUN-1999; 99US-0139119.
PR 16-JUN-1999; 99US-0139452.
PR 17-JUN-1999; 99US-0139453.
PR 18-JUN-1999; 99US-0139454.
PR 18-JUN-1999; 99US-0139455.
PR 18-JUN-1999; 99US-0139456.
PR 18-JUN-1999; 99US-0139457.
PR 18-JUN-1999; 99US-0139458.
PR 18-JUN-1999; 99US-0139459.
PR 18-JUN-1999; 99US-0139460.
PR 18-JUN-1999; 99US-0139461.
PR 18-JUN-1999; 99US-0139462.
PR 18-JUN-1999; 99US-0139463.
PR 18-JUN-1999; 99US-0139750.
PR 18-JUN-1999; 99US-0139763.
PR 21-JUN-1999; 99US-0139817.
PR 22-JUN-1999; 99US-0139899.
PR 23-JUN-1999; 99US-0140353.
PR 23-JUN-1999; 99US-0140354.
PR 24-JUN-1999; 99US-0140695.
PR 28-JUN-1999; 99US-0140823.
PR 29-JUN-1999; 99US-0140991.
PR 30-JUN-1999; 99US-0141287.
PR 01-JUL-1999; 99US-0141287.
PR 01-JUL-1999; 99US-0142154.
PR 02-JUL-1999; 99US-0142055.
PR 06-JUL-1999; 99US-0142390.
PR 08-JUL-1999; 99US-0142803.
PR 09-JUL-1999; 99US-0142920.
PR 12-JUL-1999; 99US-0142977.
PR 13-JUL-1999; 99US-0143542.
PR 14-JUL-1999; 99US-0143624.
PR 15-JUL-1999; 99US-0144005.

PR 16-JUL-1999; 99US-0144085.
PR 16-JUL-1999; 99US-0144086.
PR 19-JUL-1999; 99US-0144325.
PR 19-JUL-1999; 99US-0144331.
PR 19-JUL-1999; 99US-0144332.
PR 19-JUL-1999; 99US-0144333.
PR 19-JUL-1999; 99US-0144334.
PR 19-JUL-1999; 99US-0144335.
PR 20-JUL-1999; 99US-0144352.
PR 20-JUL-1999; 99US-0144632.
PR 20-JUL-1999; 99US-0144884.
PR 21-JUL-1999; 99US-0144814.
PR 21-JUL-1999; 99US-0145086.
PR 21-JUL-1999; 99US-0145088.
PR 22-JUL-1999; 99US-0145085.
PR 22-JUL-1999; 99US-0145087.
PR 22-JUL-1999; 99US-0145089.
PR 22-JUL-1999; 99US-0145192.
PR 23-JUL-1999; 99US-0145145.
PR 23-JUL-1999; 99US-0145218.
PR 23-JUL-1999; 99US-0145224.
PR 26-JUL-1999; 99US-0145276.
PR 27-JUL-1999; 99US-0145913.
PR 27-JUL-1999; 99US-0145918.
PR 27-JUL-1999; 99US-0145919.
PR 28-JUL-1999; 99US-0145951.
PR 02-AUG-1999; 99US-0146386.
PR 02-AUG-1999; 99US-0146388.
PR 03-AUG-1999; 99US-0146389.
PR 03-AUG-1999; 99US-0147038.
PR 04-AUG-1999; 99US-0147204.
PR 04-AUG-1999; 99US-0147302.
PR 05-AUG-1999; 99US-0147192.
PR 05-AUG-1999; 99US-0147260.
PR 06-AUG-1999; 99US-0147303.
PR 06-AUG-1999; 99US-0147416.
PR 09-AUG-1999; 99US-0147493.
PR 09-AUG-1999; 99US-0147935.
PR 10-AUG-1999; 99US-0148171.
PR 11-AUG-1999; 99US-0148319.
PR 12-AUG-1999; 99US-0148341.
PR 13-AUG-1999; 99US-0148565.
PR 13-AUG-1999; 99US-0148684.
PR 16-AUG-1999; 99US-0149368.
PR 17-AUG-1999; 99US-0149175.
PR 18-AUG-1999; 99US-0149426.
PR 20-AUG-1999; 99US-0149722.
PR 20-AUG-1999; 99US-0149723.
PR 20-AUG-1999; 99US-0149929.
PR 23-AUG-1999; 99US-0149902.
PR 23-AUG-1999; 99US-0149902.
PR 23-AUG-1999; 99US-0149930.
PR 25-AUG-1999; 99US-0150566.
PR 26-AUG-1999; 99US-0150884.
PR 27-AUG-1999; 99US-0151065.
PR 27-AUG-1999; 99US-0151066.
PR 27-AUG-1999; 99US-0151080.
PR 30-AUG-1999; 99US-0151303.
PR 31-AUG-1999; 99US-0151438.
PR 01-SEP-1999; 99US-0151930.
PR 07-SEP-1999; 99US-0152363.
PR 10-SEP-1999; 99US-0153070.
PR 13-SEP-1999; 99US-0153758.
PR 15-SEP-1999; 99US-0154018.
PR 16-SEP-1999; 99US-0154039.
PR 20-SEP-1999; 99US-0154179.
PR 22-SEP-1999; 99US-0155139.
PR 23-SEP-1999; 99US-0155486.
PR 24-SEP-1999; 99US-0155659.
PR 28-SEP-1999; 99US-0156458.
PR 29-SEP-1999; 99US-0156596.
PR 04-OCT-1999; 99US-0157117.
PR 05-OCT-1999; 99US-0157753.
PR 06-OCT-1999; 99US-0157865.

PR 07-OCT-1999; 99US-0158029.
PR 08-OCT-1999; 99US-0158232.
PR 12-OCT-1999; 99US-0158369.
PR 13-OCT-1999; 99US-0159293.
PR 13-OCT-1999; 99US-0159294.
PR 13-OCT-1999; 99US-0159295.
PR 14-OCT-1999; 99US-0159329.
PR 14-OCT-1999; 99US-0159330.
PR 14-OCT-1999; 99US-0159331.
PR 14-OCT-1999; 99US-0159637.
PR 14-OCT-1999; 99US-0159638.
PR 18-OCT-1999; 99US-0159564.
PR 21-OCT-1999; 99US-0160741.
PR 21-OCT-1999; 99US-0160767.
PR 21-OCT-1999; 99US-0160768.
PR 21-OCT-1999; 99US-0160770.
PR 21-OCT-1999; 99US-0160814.
PR 21-OCT-1999; 99US-0160815.
PR 22-OCT-1999; 99US-0160980.
PR 22-OCT-1999; 99US-0160981.
PR 22-OCT-1999; 99US-0160989.
PR 25-OCT-1999; 99US-0161404.
PR 25-OCT-1999; 99US-0161405.
PR 25-OCT-1999; 99US-0161406.
PR 26-OCT-1999; 99US-0161359.
PR 26-OCT-1999; 99US-0161360.
PR 26-OCT-1999; 99US-0161361.
PR 28-OCT-1999; 99US-0161920.
PR 28-OCT-1999; 99US-0161922.
PR 28-OCT-1999; 99US-0161993.
PR 29-OCT-1999; 99US-0162142.

Query Match 77.8%; Score 1085; DB 21; Length 253;
Best Local Similarity 77.9%; Pred. No. 2.6e-99;

Matches 194; Conservative 22; Mismatches 31; Indels 2; Gaps 2;

QY 4 SYSPFSLFLPFFV-FTFADYGMQSGHATFYGGDASGTMGACGNYLSQGYGTN 62
D 5 SYLKYSTISLIVLFLGTHGDGCGHATFYGGDASGTMGACGNYLSQGYGTN 64
D 63 TVALSTALFNNGISCGACFEMTCTNDPKCLPGTIRVTATNFCPPNPNNGGWCNPP 122
D 65 TVALSTALFNNGJLTGACYEMKCNDDPRWCLGSTITVTATNFCPPNPNGLSNDNGWCNPP 124
QY 123 LQHFDAEPFLIAOYRAGIVPSFRVRCKKGGVRFTHSHSYFNLVLTNNVGAGD 182
D 125 LQHFDAEPFLIAOYRAGIVPSFRVRCKKGGVRFTHSHSYFNLVLTNNVGAGD 184
QY 183 VHSVSIGKSRRT-GMOSKSRMGMOSNNYLNQGLSFQVTLSDGRTLTAYNLVPSNMQF 241
D 185 VHAVSIGKSKTQSMQMSRMGMOSNNYLNQGLSFQVTLSDGRTLTAYNLVPSNMQF 244
QY 242 GQTYEGPOF 250
D 245 GQTYEGPOF 253

RESULT 6
AAG46483
ID AAG46483 standard; Protein; 253 AA.

AC AAG46483;

DT 18-OCT-2000 (first entry)

DE Arabidopsis thaliana protein fragment SEQ ID NO: 58485.

KM Protein identification: signal transduction pathway; metabolic pathway;
hybridisation assay; genetic mapping; gene expression control; promoter;
termination sequence.

OS Arabidopsis thaliana.

XX

PN EPI033405-A2.
XX
4PD 06-SEP-2000.
XX
PF 25-FEB-2000; 2000EP-0301439.
XX
PR 25-FEB-1999; 99US-0121825.
PR 05-MAR-1999; 99US-0123180.
PR 09-MAR-1999; 99US-0123548.
PR 22-MAR-1999; 99US-0125788.
PR 25-MAR-1999; 99US-0126264.
PR 29-MAR-1999; 99US-0126785.
PR 01-APR-1999; 99US-0127462.
PR 06-APR-1999; 99US-0128234.
PR 08-APR-1999; 99US-0128714.
PR 16-APR-1999; 99US-0129845.
PR 19-APR-1999; 99US-0130077.
PR 21-APR-1999; 99US-0130449.
PR 23-APR-1999; 99US-0130510.
PR 28-APR-1999; 99US-0130891.
PR 30-APR-1999; 99US-0132048.
PR 30-APR-1999; 99US-0132407.
PR 04-MAY-1999; 99US-0132484.
PR 05-MAY-1999; 99US-0132485.
PR 06-MAY-1999; 99US-0132486.
PR 07-MAY-1999; 99US-0132487.
PR 11-MAY-1999; 99US-0132863.
PR 11-MAY-1999; 99US-0134256.
PR 14-MAY-1999; 99US-0134218.
PR 14-MAY-1999; 99US-0134219.
PR 14-MAY-1999; 99US-0134321.
PR 14-MAY-1999; 99US-0134370.
PR 18-MAY-1999; 99US-0134768.
PR 19-MAY-1999; 99US-0134941.
PR 20-MAY-1999; 99US-0135124.
PR 21-MAY-1999; 99US-0135353.
PR 24-MAY-1999; 99US-0135629.
PR 25-MAY-1999; 99US-0136021.
PR 27-MAY-1999; 99US-0136392.
PR 28-MAY-1999; 99US-0136782.
PR 01-JUN-1999; 99US-0137222.
PR 03-JUN-1999; 99US-0137528.
PR 04-JUN-1999; 99US-0137528.
PR 07-JUN-1999; 99US-0137724.
PR 08-JUN-1999; 99US-0138094.
PR 10-JUN-1999; 99US-0138540.
PR 10-JUN-1999; 99US-0138847.
PR 14-JUN-1999; 99US-0139119.
PR 16-JUN-1999; 99US-0139452.
PR 16-JUN-1999; 99US-0139453.
PR 17-JUN-1999; 99US-0139492.
PR 18-JUN-1999; 99US-0139454.
PR 18-JUN-1999; 99US-0139455.
PR 18-JUN-1999; 99US-0139456.
PR 18-JUN-1999; 99US-0139457.
PR 18-JUN-1999; 99US-0139458.
PR 18-JUN-1999; 99US-0139459.
PR 18-JUN-1999; 99US-0139460.
PR 18-JUN-1999; 99US-0139461.
PR 18-JUN-1999; 99US-0139462.
PR 18-JUN-1999; 99US-0139463.
PR 18-JUN-1999; 99US-0139750.
PR 18-JUN-1999; 99US-0139763.
PR 21-JUN-1999; 99US-0139817.
PR 22-JUN-1999; 99US-0139869.
PR 23-JUN-1999; 99US-0140353.
PR 23-JUN-1999; 99US-0140354.
PR 24-JUN-1999; 99US-0140695.
PR 28-JUN-1999; 99US-0140823.
PR 29-JUN-1999; 99US-0140991.
PR 30-JUN-1999; 99US-0141287.
PR 01-JUL-1999; 99US-0141842.

XX Arabidopsis thaliana protein fragment SEQ ID NO: 3357.
DE
XX Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.
XX Arabidopsis thaliana.
OS
PN EPI033405-A2.
XX
PD 06-SEP-2000.
XX
PF 25-FEB-2000; 2000EP-0301439.
XX
PR 25-FEB-1999; 99US-0121825.
PR 05-MAR-1999; 99US-0123160.
PR 09-MAR-1999; 99US-0123548.
PR 23-MAR-1999; 99US-0125788.
PR 25-MAR-1999; 99US-0126264.
PR 29-MAR-1999; 99US-0126785.
PR 01-APR-1999; 99US-0127462.
PR 06-APR-1999; 99US-0128234.
PR 08-APR-1999; 99US-0128714.
PR 16-APR-1999; 99US-0129845.
PR 19-APR-1999; 99US-0130077.
PR 21-APR-1999; 99US-0130449.
PR 23-APR-1999; 99US-0130510.
PR 28-APR-1999; 99US-0130891.
PR 30-APR-1999; 99US-0131449.
PR 30-APR-1999; 99US-0132407.
PR 04-MAY-1999; 99US-0132484.
PR 05-MAY-1999; 99US-0132485.
PR 06-MAY-1999; 99US-0132486.
PR 06-MAY-1999; 99US-0132487.
PR 07-MAY-1999; 99US-0132863.
PR 11-MAY-1999; 99US-0134256.
PR 14-MAY-1999; 99US-0134218.
PR 14-MAY-1999; 99US-0134221.
PR 14-MAY-1999; 99US-0134221.
PR 14-MAY-1999; 99US-0134370.
PR 18-MAY-1999; 99US-0134768.
PR 19-MAY-1999; 99US-0134941.
PR 20-MAY-1999; 99US-0135124.
PR 21-MAY-1999; 99US-0135353.
PR 24-MAY-1999; 99US-0135629.
PR 25-MAY-1999; 99US-0136021.
PR 27-MAY-1999; 99US-0136392.
PR 28-MAY-1999; 99US-0136782.
PR 01-JUN-1999; 99US-0137232.
PR 03-JUN-1999; 99US-0137528.
PR 04-JUN-1999; 99US-0137528.
PR 07-JUN-1999; 99US-0137724.
PR 08-JUN-1999; 99US-0138094.
PR 10-JUN-1999; 99US-0138540.
PR 10-JUN-1999; 99US-0138847.
PR 14-JUN-1999; 99US-0139119.
PR 16-JUN-1999; 99US-0139452.
PR 16-JUN-1999; 99US-0139453.
PR 17-JUN-1999; 99US-0139453.
PR 18-JUN-1999; 99US-0139454.
PR 18-JUN-1999; 99US-0139455.
PR 18-JUN-1999; 99US-0139456.
PR 18-JUN-1999; 99US-0139457.
PR 18-JUN-1999; 99US-0139458.
PR 18-JUN-1999; 99US-0139459.
PR 18-JUN-1999; 99US-0139460.
PR 18-JUN-1999; 99US-0139461.
PR 18-JUN-1999; 99US-0139462.
PR 18-JUN-1999; 99US-0139463.
PR 18-JUN-1999; 99US-0139750.
PR 18-JUN-1999; 99US-0139763.

PR 21-JUN-1999; 99US-0139817.
PR 22-JUN-1999; 99US-0139899.
PR 23-JUN-1999; 99US-0140353.
PR 23-JUN-1999; 99US-0140354.
PR 24-JUN-1999; 99US-0140685.
PR 28-JUN-1999; 99US-0140823.
PR 29-JUN-1999; 99US-0140991.
PR 30-JUN-1999; 99US-0141287.
PR 01-JUL-1999; 99US-0141842.
PR 01-JUL-1999; 99US-0142154.
PR 02-JUL-1999; 99US-0142055.
PR 06-JUL-1999; 99US-0142390.
PR 08-JUL-1999; 99US-0142803.
PR 09-JUL-1999; 99US-0142920.
PR 12-JUL-1999; 99US-0142977.
PR 13-JUL-1999; 99US-0143542.
PR 14-JUL-1999; 99US-0143624.
PR 15-JUL-1999; 99US-0144005.
PR 16-JUL-1999; 99US-0144085.
PR 16-JUL-1999; 99US-0144086.
PR 19-JUL-1999; 99US-0144325.
PR 19-JUL-1999; 99US-0144331.
PR 19-JUL-1999; 99US-0144332.
PR 19-JUL-1999; 99US-0144333.
PR 19-JUL-1999; 99US-0144334.
PR 20-JUL-1999; 99US-0144335.
PR 20-JUL-1999; 99US-0144352.
PR 20-JUL-1999; 99US-0144632.
PR 20-JUL-1999; 99US-0144884.
PR 21-JUL-1999; 99US-0144814.
PR 21-JUL-1999; 99US-0145086.
PR 21-JUL-1999; 99US-0145088.
PR 22-JUL-1999; 99US-0145085.
PR 22-JUL-1999; 99US-0145087.
PR 22-JUL-1999; 99US-0145089.
PR 22-JUL-1999; 99US-0145192.
PR 23-JUL-1999; 99US-0145145.
PR 23-JUL-1999; 99US-0145218.
PR 23-JUL-1999; 99US-0145218.
PR 26-JUL-1999; 99US-0145276.
PR 27-JUL-1999; 99US-0145913.
PR 27-JUL-1999; 99US-0145918.
PR 27-JUL-1999; 99US-0145919.
PR 28-JUL-1999; 99US-0145951.
PR 02-AUG-1999; 99US-0146386.
PR 02-AUG-1999; 99US-0146388.
PR 02-AUG-1999; 99US-0146389.
PR 03-AUG-1999; 99US-0147038.
PR 04-AUG-1999; 99US-0147204.
PR 04-AUG-1999; 99US-0147302.
PR 05-AUG-1999; 99US-0147302.
PR 05-AUG-1999; 99US-0147260.
PR 06-AUG-1999; 99US-0147303.
PR 06-AUG-1999; 99US-0147303.
PR 09-AUG-1999; 99US-0147416.
PR 09-AUG-1999; 99US-0147493.
PR 09-AUG-1999; 99US-0147935.
PR 10-AUG-1999; 99US-0148171.
PR 11-AUG-1999; 99US-0148319.
PR 12-AUG-1999; 99US-0148341.
PR 13-AUG-1999; 99US-0148685.
PR 16-AUG-1999; 99US-0148684.
PR 17-AUG-1999; 99US-0149368.
PR 18-AUG-1999; 99US-0149175.
PR 18-AUG-1999; 99US-0149126.
PR 20-AUG-1999; 99US-0149722.
PR 20-AUG-1999; 99US-0149723.
PR 20-AUG-1999; 99US-0149929.
PR 23-AUG-1999; 99US-0149902.
PR 23-AUG-1999; 99US-0149930.
PR 26-AUG-1999; 99US-0150566.
PR 26-AUG-1999; 99US-0150884.
PR 27-AUG-1999; 99US-0151065.
PR 27-AUG-1999; 99US-0151066.

```
PR 27-AUG-1999: 99US-0151080.
PR 30-AUG-1999: 99US-0151303.
PR 31-AUG-1999: 99US-0151318.
PR 01-SEP-1999: 99US-0151330.
PR 07-SEP-1999: 99US-0152363.
PR 10-SEP-1999: 99US-0153070.
PR 13-SEP-1999: 99US-0153758.
PR 15-SEP-1999: 99US-0154018.
PR 16-SEP-1999: 99US-0154039.
PR 20-SEP-1999: 99US-0154779.
PR 22-SEP-1999: 99US-0155139.
PR 23-SEP-1999: 99US-0155486.
PR 24-SEP-1999: 99US-0155659.
PR 28-SEP-1999: 99US-0156458.
PR 29-SEP-1999: 99US-0156596.
PR 04-OCT-1999: 99US-0157117.
PR 05-OCT-1999: 99US-0157753.
PR 06-OCT-1999: 99US-0157865.
PR 07-OCT-1999: 99US-0158029.
PR 08-OCT-1999: 99US-0158232.
PR 12-OCT-1999: 99US-0158369.
PR 13-OCT-1999: 99US-0159293.
PR 13-OCT-1999: 99US-0159294.
PR 13-OCT-1999: 99US-0159295.
PR 14-OCT-1999: 99US-0159329.
PR 14-OCT-1999: 99US-0159330.
PR 14-OCT-1999: 99US-0159331.
PR 14-OCT-1999: 99US-0159331.
PR 14-OCT-1999: 99US-0159637.
PR 14-OCT-1999: 99US-0159638.
PR 18-OCT-1999: 99US-0159584.
PR 21-OCT-1999: 99US-0160741.
PR 21-OCT-1999: 99US-0160767.
PR 21-OCT-1999: 99US-0160768.
PR 21-OCT-1999: 99US-0160770.
PR 21-OCT-1999: 99US-0160814.
PR 21-OCT-1999: 99US-0160815.
PR 22-OCT-1999: 99US-0160980.
PR 22-OCT-1999: 99US-0160981.
PR 22-OCT-1999: 99US-0160989.
PR 25-OCT-1999: 99US-0161404.
PR 25-OCT-1999: 99US-0161405.
PR 25-OCT-1999: 99US-0161406.
PR 26-OCT-1999: 99US-0161359.
PR 26-OCT-1999: 99US-0161360.
PR 26-OCT-1999: 99US-0161361.
PR 28-OCT-1999: 99US-0161920.
PR 28-OCT-1999: 99US-0161922.
PR 28-OCT-1999: 99US-0161993.
PR 29-OCT-1999: 99US-0162142.
```

Query Match 74.7%; Score 1041; DB 21; Length 241;
Best Local Similarity 79.6%; Pred. No. 5,6e-95;
Matches 179; Conservative 23; Mismatches 23; Indels 0; Gaps 0;

```
QY 26 GGMQSHAFYGGGDSGTWGCAGCGNLYSGCYGNTYALSTALFNNGLSCGACPEMTC 85
DB 16 GGMNNAHAFYGGGDSGTWGCAGCGNLYSGCYGNTYALSTALFNNGLSCGACPEMTC 75
QY 86 TNDPKACLPGTIRVTATNFCPPFALPNNNGCMCPLOHFDMAEPFLQIAQYRGIYV 145
DB 76 ENDGKMKCLPGSIVTATNFCPPFALPNNNGCMCPLOHFDMAEPFLQIAQYRGIYV 135
QY 146 VSFRRVPCMKKGAVRTINGSHSYFNLVLTITNVGAGDVHVSITKSGRTGMSMRNMGON 205
DB 136 VSYRRVPCRRRGIRRTINGSHSYFNLVLTITNVGAGDVHSAIKGSRVTQAMSRMGON 195
QY 206 KMSNNYLNQGLSFQTLSDGRTLTXNVLVPSWMOGQGYEGRQF 250
DB 196 WQSNYSYLNQGLSFQTLSDGRTLTXNVLVPSWMOGQGYEGRQF 240
```

RESULT 8
AAGS1633

```
ID AAGS1633 standard; Protein; 241 AA.
XX AAGS1633;
AC 18-OCT-2000 (first entry)
XX
DT
XX
DE Arabidopsis thaliana protein fragment SEQ ID NO: 65551.
XX
KW Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.
XX
OS Arabidopsis thaliana.
XX
PN EP1033405-A2.
XX
PD 06-SEP-2000.
XX
PF 25-FEB-2000; 2000EP-0301439.
XX
PR 25-FEB-1999: 99US-0121825.
PR 05-MAR-1999: 99US-0123180.
PR 09-MAR-1999: 99US-0123548.
PR 23-MAR-1999: 99US-0125788.
PR 25-MAR-1999: 99US-0126264.
PR 29-MAR-1999: 99US-0126785.
PR 01-APR-1999: 99US-0127462.
PR 06-APR-1999: 99US-0128234.
PR 08-APR-1999: 99US-0128714.
PR 16-APR-1999: 99US-0129845.
PR 19-APR-1999: 99US-0130077.
PR 21-APR-1999: 99US-0130449.
PR 23-APR-1999: 99US-0130510.
PR 28-APR-1999: 99US-0131491.
PR 30-APR-1999: 99US-0132048.
PR 30-APR-1999: 99US-0132407.
PR 04-MAY-1999: 99US-0132484.
PR 05-MAY-1999: 99US-0132485.
PR 06-MAY-1999: 99US-0132486.
PR 07-MAY-1999: 99US-0132487.
PR 11-MAY-1999: 99US-0134256.
PR 14-MAY-1999: 99US-0134218.
PR 14-MAY-1999: 99US-0134219.
PR 14-MAY-1999: 99US-0134221.
PR 14-MAY-1999: 99US-0134370.
PR 18-MAY-1999: 99US-0134768.
PR 19-MAY-1999: 99US-0134941.
PR 20-MAY-1999: 99US-0135124.
PR 21-MAY-1999: 99US-0135353.
PR 24-MAY-1999: 99US-0135629.
PR 25-MAY-1999: 99US-0136021.
PR 27-MAY-1999: 99US-0136392.
PR 28-MAY-1999: 99US-0136782.
PR 01-JUN-1999: 99US-0137222.
PR 03-JUN-1999: 99US-0137528.
PR 04-JUN-1999: 99US-0137502.
PR 07-JUN-1999: 99US-0137724.
PR 08-JUN-1999: 99US-0138094.
PR 10-JUN-1999: 99US-0138540.
PR 10-JUN-1999: 99US-0138847.
PR 14-JUN-1999: 99US-0139119.
PR 16-JUN-1999: 99US-0139452.
PR 17-JUN-1999: 99US-0139453.
PR 18-JUN-1999: 99US-0139454.
PR 18-JUN-1999: 99US-0139455.
PR 18-JUN-1999: 99US-0139456.
PR 18-JUN-1999: 99US-0139457.
PR 18-JUN-1999: 99US-0139458.
PR 18-JUN-1999: 99US-0139459.
PR 18-JUN-1999: 99US-0139460.
```



```
PR 18-JUN-1999; 99US-0139461.
PR 18-JUN-1999; 99US-0139462.
PR 18-JUN-1999; 99US-0139463.
PR 18-JUN-1999; 99US-0139750.
PR 18-JUN-1999; 99US-0139753.
PR 21-JUN-1999; 99US-0139817.
PR 22-JUN-1999; 99US-0139899.
PR 23-JUN-1999; 99US-0140353.
PR 23-JUN-1999; 99US-0140354.
PR 24-JUN-1999; 99US-0140695.
PR 28-JUN-1999; 99US-0140823.
PR 29-JUN-1999; 99US-0140991.
PR 30-JUN-1999; 99US-0141287.
PR 01-JUL-1999; 99US-0142154.
PR 01-JUL-1999; 99US-0142182.
PR 02-JUL-1999; 99US-0142055.
PR 06-JUL-1999; 99US-0142390.
PR 08-JUL-1999; 99US-0142803.
PR 09-JUL-1999; 99US-0142920.
PR 12-JUL-1999; 99US-0142977.
PR 13-JUL-1999; 99US-0143542.
PR 14-JUL-1999; 99US-0143624.
PR 15-JUL-1999; 99US-0144005.
PR 16-JUL-1999; 99US-0144085.
PR 16-JUL-1999; 99US-0144086.
PR 19-JUL-1999; 99US-0144325.
PR 19-JUL-1999; 99US-0144331.
PR 19-JUL-1999; 99US-0144332.
PR 19-JUL-1999; 99US-0144333.
PR 19-JUL-1999; 99US-0144334.
PR 19-JUL-1999; 99US-0144335.
PR 20-JUL-1999; 99US-0144352.
PR 20-JUL-1999; 99US-0144884.
PR 21-JUL-1999; 99US-0144814.
PR 21-JUL-1999; 99US-0145086.
PR 21-JUL-1999; 99US-0145088.
PR 22-JUL-1999; 99US-0145085.
PR 22-JUL-1999; 99US-0145087.
PR 22-JUL-1999; 99US-0145089.
PR 22-JUL-1999; 99US-0145182.
PR 23-JUL-1999; 99US-0145185.
PR 23-JUL-1999; 99US-0145224.
PR 23-JUL-1999; 99US-0145224.
PR 26-JUL-1999; 99US-0145276.
PR 27-JUL-1999; 99US-0145913.
PR 27-JUL-1999; 99US-0145918.
PR 27-JUL-1999; 99US-0145919.
PR 28-JUL-1999; 99US-0145951.
PR 02-AUG-1999; 99US-0146386.
PR 02-AUG-1999; 99US-0146388.
PR 02-AUG-1999; 99US-0146389.
PR 03-AUG-1999; 99US-0147204.
PR 04-AUG-1999; 99US-0147205.
PR 04-AUG-1999; 99US-0147208.
PR 04-AUG-1999; 99US-0147302.
PR 05-AUG-1999; 99US-0147319.
PR 05-AUG-1999; 99US-0147320.
PR 06-AUG-1999; 99US-0147323.
PR 06-AUG-1999; 99US-0147303.
PR 06-AUG-1999; 99US-0147416.
PR 09-AUG-1999; 99US-0147493.
PR 09-AUG-1999; 99US-0147935.
PR 10-AUG-1999; 99US-0148171.
PR 11-AUG-1999; 99US-0148319.
PR 12-AUG-1999; 99US-0148341.
PR 13-AUG-1999; 99US-0148565.
PR 13-AUG-1999; 99US-0148684.
PR 16-AUG-1999; 99US-0149368.
PR 17-AUG-1999; 99US-0149175.
PR 18-AUG-1999; 99US-0149426.
PR 20-AUG-1999; 99US-0149722.
PR 20-AUG-1999; 99US-0149723.
PR 20-AUG-1999; 99US-0149929.
PR 23-AUG-1999; 99US-0149902.

PR 23-AUG-1999; 99US-0149930.
PR 25-AUG-1999; 99US-0150566.
PR 26-AUG-1999; 99US-0150884.
PR 27-AUG-1999; 99US-0151065.
PR 27-AUG-1999; 99US-0151066.
PR 27-AUG-1999; 99US-0151080.
PR 30-AUG-1999; 99US-0151303.
PR 31-AUG-1999; 99US-0151308.
PR 01-SEP-1999; 99US-0151930.
PR 07-SEP-1999; 99US-0152363.
PR 10-SEP-1999; 99US-0153070.
PR 13-SEP-1999; 99US-0153758.
PR 15-SEP-1999; 99US-0154018.
PR 16-SEP-1999; 99US-0154039.
PR 20-SEP-1999; 99US-0154779.
PR 22-SEP-1999; 99US-0155139.
PR 23-SEP-1999; 99US-0155486.
PR 24-SEP-1999; 99US-0155659.
PR 28-SEP-1999; 99US-0156458.
PR 29-SEP-1999; 99US-0156596.
PR 04-OCT-1999; 99US-0157117.
PR 05-OCT-1999; 99US-0157753.
PR 06-OCT-1999; 99US-0157865.
PR 07-OCT-1999; 99US-0158029.
PR 08-OCT-1999; 99US-0158232.
PR 12-OCT-1999; 99US-0158369.
PR 13-OCT-1999; 99US-0159293.
PR 13-OCT-1999; 99US-0159294.
PR 13-OCT-1999; 99US-0159295.
PR 14-OCT-1999; 99US-0159329.
PR 14-OCT-1999; 99US-0159330.
PR 14-OCT-1999; 99US-0159331.
PR 14-OCT-1999; 99US-0159637.
PR 14-OCT-1999; 99US-0159638.
PR 18-OCT-1999; 99US-0159584.
PR 21-OCT-1999; 99US-0160741.
PR 21-OCT-1999; 99US-0160767.
PR 21-OCT-1999; 99US-0160768.
PR 21-OCT-1999; 99US-0160770.
PR 21-OCT-1999; 99US-0160778.
PR 21-OCT-1999; 99US-0160814.
PR 21-OCT-1999; 99US-0160815.
PR 22-OCT-1999; 99US-0160980.
PR 22-OCT-1999; 99US-0160981.
PR 22-OCT-1999; 99US-0160989.
PR 25-OCT-1999; 99US-0161404.
PR 25-OCT-1999; 99US-0161405.
PR 25-OCT-1999; 99US-0161406.
PR 25-OCT-1999; 99US-0161407.
PR 26-OCT-1999; 99US-0161359.
PR 26-OCT-1999; 99US-0161360.
PR 26-OCT-1999; 99US-0161361.
PR 26-OCT-1999; 99US-0161361.
PR 28-OCT-1999; 99US-0161820.
PR 28-OCT-1999; 99US-0161922.
PR 28-OCT-1999; 99US-0161993.
PR 29-OCT-1999; 99US-0162142.

Query Match 74.7%; Score 1041; DB 21; Length 241;
Best Local Similarity 79.6%; Pred. No. 5.6e-95;
Matches 179; Conservative 23; Mismatches 23; Indels 0; Gaps 0;

Qy 26 GCMQSGHATFYGGDASGTGACGYGNLYSQGYGTNTVALSTALFNNGISGACFEPMC 85
Db 16 GGMNNAHATFYGGDASGTGACGYGNLYSQGYGTNTVALSTALFNNGISGACFEIRC 75
Qy 86 TNDPKWCLPRTIRVATNTFCPPNFALPNNNGCMNPLQHFDMABPAFLQIAQYRAGIYP 145
Db 76 ENDGKWCLPGSIYVATNTFCPPNFALPNNNGCMNPLQHFDMABPAFLQIAQYRAGIYP 135
Qy 146 VSFRRVPCMKKGAVRTINGHSYFNVLITNVGAGADVSVSTKGSRTGQSMRMGON 205
Db 136 VSTRVPCRRRGIRRTINGHSYFNVLITNVGAGADVSAALKGSRTVQAMSRMGON 195
Qy 206 MOSNNYINGGLSFQVTLSDGRTLTAYNLVPSNMQFCQTYEGPOF 250
Db 206 MOSNNYINGGLSFQVTLSDGRTLTAYNLVPSNMQFCQTYEGPOF 250
```

Db	196	WQSN5YINGQALSPKVTTSDBQRTVSTNAPAGNSYQGTAGQF	240
RESULT 9			
ID	AAG51647	standard; Protein: 241 AA.	
XX			
AC	AAG51647;		
XX			
DT	18-OCT-2000	(first entry)	
XX			
DE	Arabidopsis thaliana protein fragment SEQ ID NO: 65570.		
XX			
KW	Protein identification; signal transduction pathway; metabolic pathway;		
XX	hybridisation assay; genetic mapping; gene expression control; promoter		
XX	termination sequence.		
OS	Arabidopsis thaliana.		
XX			
FN	EP1033405-A2.		
XX			
PD	06-SEP-2000.		
XX			
PF	25-FEB-2000; 2000EP-0301439.		
XX			
PR	25-FEB-1999;	99US-0121825.	
PR	05-MAR-1999;	99US-0123180.	
PR	09-MAR-1999;	99US-0123548.	
PR	23-MAR-1999;	99US-0125788.	
PR	25-MAR-1999;	99US-0126264.	
PR	29-MAR-1999;	99US-0126785.	
PR	01-APR-1999;	99US-0127462.	
PR	06-APR-1999;	99US-0128234.	
PR	08-APR-1999;	99US-0128714.	
PR	16-APR-1999;	99US-0129845.	
PR	19-APR-1999;	99US-0130077.	
PR	21-APR-1999;	99US-0130449.	
PR	23-APR-1999;	99US-0130510.	
PR	23-APR-1999;	99US-0130891.	
PR	28-APR-1999;	99US-0131449.	
PR	30-APR-1999;	99US-0132048.	
PR	30-APR-1999;	99US-0132407.	
PR	04-MAY-1999;	99US-0132484.	
PR	05-MAY-1999;	99US-0132485.	
PR	06-MAY-1999;	99US-0132486.	
PR	06-MAY-1999;	99US-0132487.	
PR	07-MAY-1999;	99US-0132487.	
PR	11-MAY-1999;	99US-0132863.	
PR	11-MAY-1999;	99US-0134256.	
PR	14-MAY-1999;	99US-0134218.	
PR	14-MAY-1999;	99US-0134219.	
PR	14-MAY-1999;	99US-0134221.	
PR	14-MAY-1999;	99US-0134370.	
PR	18-MAY-1999;	99US-0134768.	
PR	19-MAY-1999;	99US-0134941.	
PR	20-MAY-1999;	99US-0135124.	
PR	21-MAY-1999;	99US-0135353.	
PR	24-MAY-1999;	99US-0135629.	
PR	25-MAY-1999;	99US-0136021.	
PR	27-MAY-1999;	99US-0136382.	
PR	28-MAY-1999;	99US-0136782.	
PR	01-JUN-1999;	99US-0137222.	
PR	03-JUN-1999;	99US-0137528.	
PR	04-JUN-1999;	99US-0137502.	
PR	07-JUN-1999;	99US-0137724.	
PR	08-JUN-1999;	99US-0138094.	
PR	10-JUN-1999;	99US-0138540.	
PR	10-JUN-1999;	99US-0138847.	
PR	14-JUN-1999;	99US-0139119.	
PR	16-JUN-1999;	99US-0139452.	
PR	17-JUN-1999;	99US-0139453.	
PR	17-JUN-1999;	99US-0139492.	
PR	18-JUN-1999;	99US-0139454.	
PR	18-JUN-1999;	99US-0139455.	

```
PR 18-AUG-1999; 99US-0149426.
PR 20-AUG-1999; 99US-0149722.
PR 20-AUG-1999; 99US-0149723.
PR 20-AUG-1999; 99US-0149929.
PR 22-AUG-1999; 99US-0149920.
PR 23-AUG-1999; 99US-0149930.
PR 25-AUG-1999; 99US-0150566.
PR 26-AUG-1999; 99US-0150884.
PR 27-AUG-1999; 99US-0151065.
PR 27-AUG-1999; 99US-0151066.
PR 27-AUG-1999; 99US-0151080.
PR 30-AUG-1999; 99US-0151303.
PR 31-AUG-1999; 99US-0151438.
PR 01-SEP-1999; 99US-0151930.
PR 07-SEP-1999; 99US-0152363.
PR 10-SEP-1999; 99US-0153070.
PR 13-SEP-1999; 99US-0153758.
PR 15-SEP-1999; 99US-0154018.
PR 16-SEP-1999; 99US-0154039.
PR 20-SEP-1999; 99US-0154779.
PR 22-SEP-1999; 99US-0155139.
PR 23-SEP-1999; 99US-0155486.
PR 24-SEP-1999; 99US-0155659.
PR 28-SEP-1999; 99US-0156458.
PR 29-SEP-1999; 99US-0156596.
PR 04-OCT-1999; 99US-0157117.
PR 05-OCT-1999; 99US-0157753.
PR 06-OCT-1999; 99US-0157865.
PR 07-OCT-1999; 99US-0158029.
PR 08-OCT-1999; 99US-0158232.
PR 12-OCT-1999; 99US-0158369.
PR 13-OCT-1999; 99US-0159293.
PR 13-OCT-1999; 99US-0159295.
PR 14-OCT-1999; 99US-0159329.
PR 14-OCT-1999; 99US-0159330.
PR 14-OCT-1999; 99US-0159331.
PR 14-OCT-1999; 99US-0159637.
PR 14-OCT-1999; 99US-0159638.
PR 16-OCT-1999; 99US-0159584.
PR 21-OCT-1999; 99US-0160741.
PR 21-OCT-1999; 99US-0160767.
PR 21-OCT-1999; 99US-0160778.
PR 21-OCT-1999; 99US-0160770.
PR 21-OCT-1999; 99US-0160815.
PR 21-OCT-1999; 99US-0160815.
PR 22-OCT-1999; 99US-0160980.
PR 22-OCT-1999; 99US-0160981.
PR 22-OCT-1999; 99US-0160989.
PR 25-OCT-1999; 99US-0161404.
PR 25-OCT-1999; 99US-0161405.
PR 25-OCT-1999; 99US-0161406.
PR 26-OCT-1999; 99US-0161359.
PR 26-OCT-1999; 99US-0161360.
PR 26-OCT-1999; 99US-0161361.
PR 28-OCT-1999; 99US-0161920.
PR 28-OCT-1999; 99US-0161992.
PR 28-OCT-1999; 99US-0161993.
PR 29-OCT-1999; 99US-0162142.

Query Match 74.7%; Score 1041; DB 21; Length 241;
Best Local Similarity 79.6%; Pred. No. 5,6e-95;
Matches 179; Conservative 23; Mismatches 23; Indels 0; Gaps 0;
```

```
DB 136 VSYRVPCCRRGCGIRFTINGHSYFNVLITVVGAGDVHSAIKGSRVWQAMSRWNGON 195
QY 206 WOSNNTLNGOGLSFOYTLSDGRFTLVNLPVSNWQGOPTYESPOF 250
DB 196 WOSNNTLNGOGLSFOYTLSDGRFTLVNLPVSNWQGOPTYESPOF 240

RESULT 10
ID AAG06545 standard; Protein; 249 AA.
AC AAG06545;
XX 17-OCT-2000 (first entry)
DE Arabidopsis thaliana protein fragment SEQ ID NO: 3356.
XX Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.
XX Arabidopsis thaliana.
XX EP1033405-A2.
XX PD 06-SEP-2000.
XX PF 25-FEB-2000; 2000EP-0301439.
XX 25-FEB-1999; 99US-0121825.
PR 05-MAR-1999; 99US-0123180.
PR 09-MAR-1999; 99US-0123548.
PR 22-MAR-1999; 99US-0125788.
PR 25-MAR-1999; 99US-0126264.
PR 29-MAR-1999; 99US-0126785.
PR 01-APR-1999; 99US-0127462.
PR 06-APR-1999; 99US-0128234.
PR 08-APR-1999; 99US-0128714.
PR 16-APR-1999; 99US-0129845.
PR 19-APR-1999; 99US-0130077.
PR 21-APR-1999; 99US-0130449.
PR 23-APR-1999; 99US-0130510.
PR 28-APR-1999; 99US-0130891.
PR 30-APR-1999; 99US-0131449.
PR 30-APR-1999; 99US-0132048.
PR 04-MAY-1999; 99US-0132407.
PR 05-MAY-1999; 99US-0132485.
PR 06-MAY-1999; 99US-0132486.
PR 07-MAY-1999; 99US-0132487.
PR 11-MAY-1999; 99US-0134256.
PR 14-MAY-1999; 99US-0134219.
PR 14-MAY-1999; 99US-0134221.
PR 14-MAY-1999; 99US-0134370.
PR 18-MAY-1999; 99US-0134768.
PR 19-MAY-1999; 99US-0134941.
PR 20-MAY-1999; 99US-0135124.
PR 21-MAY-1999; 99US-0135353.
PR 24-MAY-1999; 99US-0135629.
PR 25-MAY-1999; 99US-0136021.
PR 27-MAY-1999; 99US-0136392.
PR 28-MAY-1999; 99US-0136782.
PR 03-JUN-1999; 99US-0137222.
PR 04-JUN-1999; 99US-0137528.
PR 07-JUN-1999; 99US-0137724.
PR 08-JUN-1999; 99US-0138094.
PR 10-JUN-1999; 99US-0138540.
PR 14-JUN-1999; 99US-0138847.
PR 14-JUN-1999; 99US-0139119.
```

PR	16-JUN-1999;	9905-0139452;
PR	16-JUN-1999;	9905-0139453;
PR	17-JUN-1999;	9905-0139492;
PR	18-JUN-1999;	9905-0139454;
PR	18-JUN-1999;	9905-0139455;
PR	18-JUN-1999;	9905-0139456;
PR	18-JUN-1999;	9905-0138457;
PR	18-JUN-1999;	9905-0138458;
PR	18-JUN-1999;	9905-0139459;
PR	18-JUN-1999;	9905-0139460;
PR	18-JUN-1999;	9905-0139461;
PR	23-JUN-1999;	9905-0140353;
PR	23-JUN-1999;	9905-0140354;
PR	24-JUN-1999;	9905-0140695;
PR	28-JUN-1999;	9905-0140823;
PR	29-JUN-1999;	9905-0140991;
PR	30-JUN-1999;	9905-0141287;
PR	01-JUL-1999;	9905-0141842;
PR	01-JUL-1999;	9905-0142154;
PR	02-JUL-1999;	9905-0142055;
PR	06-JUL-1999;	9905-0142390;
PR	08-JUL-1999;	9905-0142803;
PR	09-JUL-1999;	9905-0142920;
PR	12-JUL-1999;	9905-0142977;
PR	13-JUL-1999;	9905-0143542;
PR	14-JUL-1999;	9905-0143624;
PR	15-JUL-1999;	9905-0144005;
PR	16-JUL-1999;	9905-0144085;
PR	16-JUL-1999;	9905-0144325;
PR	19-JUL-1999;	9905-0144326;
PR	19-JUL-1999;	9905-0144331;
PR	19-JUL-1999;	9905-0144332;
PR	19-JUL-1999;	9905-0144333;
PR	21-JUL-1999;	9905-0144814;
PR	21-JUL-1999;	9905-0145086;
PR	21-JUL-1999;	9905-0145085;
PR	22-JUL-1999;	9905-0145087;
PR	22-JUL-1999;	9905-0145089;
PR	22-JUL-1999;	9905-0145192;
PR	23-JUL-1999;	9905-0145145;
PR	23-JUL-1999;	9905-0145218;
PR	23-JUL-1999;	9905-0145224;
PR	26-JUL-1999;	9905-0145276;
PR	27-JUL-1999;	9905-0145913;
PR	27-JUL-1999;	9905-0145918;
PR	27-JUL-1999;	9905-0145919;
PR	28-JUL-1999;	9905-0145951;
PR	02-AUG-1999;	9905-0145386;
PR	02-AUG-1999;	9905-0145388;
PR	03-AUG-1999;	9905-0145389;
PR	03-AUG-1999;	9905-0147038;
PR	04-AUG-1999;	9905-0147204;
PR	04-AUG-1999;	9905-0147302;
PR	05-AUG-1999;	9905-0147192;
PR	05-AUG-1999;	9905-0147260;
PR	06-AUG-1999;	9905-0147303;
PR	06-AUG-1999;	9905-0147416;
PR	09-AUG-1999;	9905-0147493;
PR	09-AUG-1999;	9905-0147935;
PR	10-AUG-1999;	9905-0148171;
PR	11-AUG-1999;	9905-0148319;

PR	12-ANG-1999;	99US-0148364;
PR	13-ANG-1999;	99US-0148365;
PR	13-ANG-1999;	99US-0148684;
PR	16-ANG-1999;	99US-0149175;
PR	17-ANG-1999;	99US-0149168;
PR	18-ANG-1999;	99US-0149426;
PR	20-ANG-1999;	99US-0149722;
PR	20-ANG-1999;	99US-0149723;
PR	20-ANG-1999;	99US-0149902;
PR	23-ANG-1999;	99US-0149902;
PR	23-ANG-1999;	99US-0149930;
PR	25-ANG-1999;	99US-0150566;
PR	26-ANG-1999;	99US-0150884;
PR	27-ANG-1999;	99US-0151065;
PR	27-ANG-1999;	99US-0151066;
PR	27-ANG-1999;	99US-0151080;
PR	30-ANG-1999;	99US-0151303;
PR	31-ANG-1999;	99US-0151338;
PR	01-SEP-1999;	99US-0152363;
PR	07-SEP-1999;	99US-0152363;
PR	10-SEP-1999;	99US-0153070;
PR	13-SEP-1999;	99US-0153758;
PR	15-SEP-1999;	99US-0154018;
PR	16-SEP-1999;	99US-0154039;
PR	20-SEP-1999;	99US-0154479;
PR	22-SEP-1999;	99US-0155139;
PR	23-SEP-1999;	99US-0155486;
PR	24-SEP-1999;	99US-0155658;
PR	28-SEP-1999;	99US-0156458;
PR	29-SEP-1999;	99US-0156596;
PR	04-OCT-1999;	99US-0157117;
PR	05-OCT-1999;	99US-0157753;
PR	06-OCT-1999;	99US-0157865;
PR	07-OCT-1999;	99US-0158029;
PR	08-OCT-1999;	99US-0158232;
PR	12-OCT-1999;	99US-0158369;
PR	13-OCT-1999;	99US-0159283;
PR	13-OCT-1999;	99US-0159294;
PR	13-OCT-1999;	99US-0159329;
PR	14-OCT-1999;	99US-0159330;
PR	14-OCT-1999;	99US-0159637;
PR	14-OCT-1999;	99US-0159638;
PR	16-OCT-1999;	99US-0159584;
PR	21-OCT-1999;	99US-0160741;
PR	21-OCT-1999;	99US-0160767;
PR	21-OCT-1999;	99US-0160768;
PR	21-OCT-1999;	99US-0160770;
PR	21-OCT-1999;	99US-0160814;
PR	21-OCT-1999;	99US-0160815;
PR	22-OCT-1999;	99US-0160980;
PR	22-OCT-1999;	99US-0160981;
PR	22-OCT-1999;	99US-0160989;
PR	25-OCT-1999;	99US-0161404;
PR	25-OCT-1999;	99US-0161405;
PR	26-OCT-1999;	99US-0161406;
PR	26-OCT-1999;	99US-0161359;
PR	26-OCT-1999;	99US-0161360;
PR	26-OCT-1999;	99US-0161361;
PR	28-OCT-1999;	99US-0161392;
PR	28-OCT-1999;	99US-0161393;
PR	29-OCT-1999;	99US-0162142;
PR	29-OCT-1999;	99US-0162143;

Query Match	74.78;	Score 1041;	DB 21;	Length 249;
-------------	--------	-------------	--------	-------------

Best Local Similarity 79.6%; Pred. No. 5.9e-95;

```

Matches 179; Conservative 23; Mismatches 23; Indels 0; Gaps 0;

```

[illegible]

26 GGWQSGHATFYGGDASGTMGACGYNLYSQGYGTNTVALSTALFNNGLSGCAFCFEMTC 85

```

QY      26  GGMQSGHATPYGGGDASGTMGCACGYNLYSQGYGTNTVALSTALFNNGLSCGACFEEMTC  85
      ||| : ||||| ||||| ||||| ||||| : ||||| ||||| ||||| ||||| : ||| :
Db      24  GGMVNAHATPYGGGDASGTMGCACGYNLYSQGYGTSTALSTALFNNGLSCGSCPEIRIC  83

```

QY 86 TNDPKWCLPCTIRYATNFCPPNPNNGGWCNPPLOHFDMAEPALQIAYRAGIIVP 145
DB 84 ENNGKWCCLPESIVVTATNFCPPNPNALNNGGWCNPPLEHFDLQPVFORIAQYRAGIIVP 143
QY 146 VSPFRVPCMKRGVRFITNGHSYFNVLITVNGAGGVHSISIGSPTGQSMERNNGON 205
DB 144 VSTRVPCRRRGGRFIFITNGHSYFNVLITVNGAGGVHSISIGSPTGQSMERNNGON 203
QY 206 MOSNNYINGQGLSPQVTLSDGRLLTAVNLVPSNMQFGQTYEGPOF 250
DB 204 MQSNSYINGQALSPKVTTSDDRTIVSFNAPAGMSYQGTAFAGQF 248
RESULT 11
AAG51632
ID AAG51632 standard; Protein; 249 AA.
XX
AC AAG51632;
XX
DT 18-OCT-2000 (first entry)
XX
DE Arabidopsis thaliana protein fragment SEQ ID NO: 65550.*
XX
KW Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.
XX
OS Arabidopsis thaliana.
XX
PN EPI033405-A2.
XX
PD 06-SEP-2000.
XX
PF 25-FEB-2000; 2000EP-0301439.
XX
PR 25-FEB-1999; 99US-0121825.
PR 05-MAR-1999; 99US-0123180.
PR 09-MAR-1999; 99US-0123548.
PR 23-MAR-1999; 99US-0125788.
PR 25-MAR-1999; 99US-0126264.
PR 29-MAR-1999; 99US-0126785.
PR 01-APR-1999; 99US-0127462.
PR 06-APR-1999; 99US-0128234.
PR 08-APR-1999; 99US-0128714.
PR 16-APR-1999; 99US-0129845.
PR 19-APR-1999; 99US-0130077.
PR 21-APR-1999; 99US-0130449.
PR 23-APR-1999; 99US-0130510.
PR 28-APR-1999; 99US-0131449.
PR 30-APR-1999; 99US-0132048.
PR 30-APR-1999; 99US-0132407.
PR 04-MAY-1999; 99US-0132484.
PR 05-MAY-1999; 99US-0132485.
PR 06-MAY-1999; 99US-0132486.
PR 07-MAY-1999; 99US-0132487.
PR 11-MAY-1999; 99US-0132863.
PR 14-MAY-1999; 99US-0134218.
PR 14-MAY-1999; 99US-0134219.
PR 14-MAY-1999; 99US-0134221.
PR 18-MAY-1999; 99US-0134370.
PR 18-MAY-1999; 99US-0134768.
PR 19-MAY-1999; 99US-0134941.
PR 20-MAY-1999; 99US-0135124.
PR 21-MAY-1999; 99US-0135353.
PR 24-MAY-1999; 99US-0135629.
PR 25-MAY-1999; 99US-0136021.
PR 27-MAY-1999; 99US-0136382.
PR 28-MAY-1999; 99US-0136782.
PR 01-JUN-1999; 99US-0137222.
PR 03-JUN-1999; 99US-0137528.
PR 04-JUN-1999; 99US-0137502.

PR 07-JUN-1999; 99US-0137724.
PR 08-JUN-1999; 99US-0138094.
PR 10-JUN-1999; 99US-0138540.
PR 10-JUN-1999; 99US-0138847.
PR 14-JUN-1999; 99US-0139119.
PR 16-JUN-1999; 99US-0139452.
PR 16-JUN-1999; 99US-0139453.
PR 17-JUN-1999; 99US-0139492.
PR 18-JUN-1999; 99US-0139454.
PR 18-JUN-1999; 99US-0139455.
PR 18-JUN-1999; 99US-0139456.
PR 18-JUN-1999; 99US-0139457.
PR 18-JUN-1999; 99US-0139458.
PR 18-JUN-1999; 99US-0139459.
PR 18-JUN-1999; 99US-0139460.
PR 18-JUN-1999; 99US-0139461.
PR 18-JUN-1999; 99US-0139462.
PR 18-JUN-1999; 99US-0139463.
PR 18-JUN-1999; 99US-0139750.
PR 18-JUN-1999; 99US-0139763.
PR 21-JUN-1999; 99US-0139817.
PR 22-JUN-1999; 99US-0139899.
PR 23-JUN-1999; 99US-0140353.
PR 23-JUN-1999; 99US-0140354.
PR 24-JUN-1999; 99US-0140685.
PR 28-JUN-1999; 99US-0140823.
PR 29-JUN-1999; 99US-0140991.
PR 30-JUN-1999; 99US-0141287.
PR 01-JUL-1999; 99US-0141842.
PR 01-JUL-1999; 99US-0142154.
PR 02-JUL-1999; 99US-0142055.
PR 06-JUL-1999; 99US-0142390.
PR 08-JUL-1999; 99US-0142803.
PR 09-JUL-1999; 99US-0142820.
PR 12-JUL-1999; 99US-0142977.
PR 13-JUL-1999; 99US-0143542.
PR 14-JUL-1999; 99US-0143624.
PR 15-JUL-1999; 99US-0144005.
PR 16-JUL-1999; 99US-0144085.
PR 16-JUL-1999; 99US-0144086.
PR 19-JUL-1999; 99US-0144325.
PR 19-JUL-1999; 99US-0144331.
PR 19-JUL-1999; 99US-0144332.
PR 19-JUL-1999; 99US-0144333.
PR 19-JUL-1999; 99US-0144334.
PR 19-JUL-1999; 99US-0144335.
PR 20-JUL-1999; 99US-0144332.
PR 20-JUL-1999; 99US-0144632.
PR 21-JUL-1999; 99US-0144814.
PR 21-JUL-1999; 99US-0145086.
PR 21-JUL-1999; 99US-0145088.
PR 22-JUL-1999; 99US-0145085.
PR 22-JUL-1999; 99US-0145087.
PR 22-JUL-1999; 99US-0145089.
PR 22-JUL-1999; 99US-0145192.
PR 23-JUL-1999; 99US-0145145.
PR 23-JUL-1999; 99US-0145218.
PR 23-JUL-1999; 99US-0145224.
PR 26-JUL-1999; 99US-0145276.
PR 27-JUL-1999; 99US-0145913.
PR 27-JUL-1999; 99US-0145918.
PR 27-JUL-1999; 99US-0145919.
PR 28-JUL-1999; 99US-0145951.
PR 28-JUL-1999; 99US-0146386.
PR 02-AUG-1999; 99US-0146388.
PR 02-AUG-1999; 99US-0146389.
PR 03-AUG-1999; 99US-0147038.
PR 04-AUG-1999; 99US-0147204.
PR 04-AUG-1999; 99US-0147302.
PR 05-AUG-1999; 99US-0147192.
PR 05-AUG-1999; 99US-0147260.
PR 06-AUG-1999; 99US-0147303.

PR 27-MAY-1999; 99US-0136392.
 PR 28-MAY-1999; 99US-0136782.
 PR 01-JUN-1999; 99US-0137222.
 PR 03-JUN-1999; 99US-0137528.
 PR 04-JUN-1999; 99US-0137502.
 PR 07-JUN-1999; 99US-0137724.
 PR 08-JUN-1999; 99US-0138094.
 PR 10-JUN-1999; 99US-0138540.
 PR 14-JUN-1999; 99US-0138847.
 PR 16-JUN-1999; 99US-0139119.
 PR 16-JUN-1999; 99US-0139452.
 PR 17-JUN-1999; 99US-0139433.
 PR 18-JUN-1999; 99US-0139454.
 PR 18-JUN-1999; 99US-0139455.
 PR 18-JUN-1999; 99US-0139456.
 PR 18-JUN-1999; 99US-0139457.
 PR 18-JUN-1999; 99US-0139457.
 PR 18-JUN-1999; 99US-0139459.
 PR 18-JUN-1999; 99US-0139460.
 PR 18-JUN-1999; 99US-0139461.
 PR 18-JUN-1999; 99US-0139462.
 PR 18-JUN-1999; 99US-0139463.
 PR 18-JUN-1999; 99US-0139750.
 PR 21-JUN-1999; 99US-0139763.
 PR 22-JUN-1999; 99US-0139817.
 PR 23-JUN-1999; 99US-0140353.
 PR 23-JUN-1999; 99US-0140354.
 PR 24-JUN-1999; 99US-0140695.
 PR 28-JUN-1999; 99US-0140683.
 PR 29-JUN-1999; 99US-0140691.
 PR 30-JUN-1999; 99US-0141287.
 PR 01-JUL-1999; 99US-0141842.
 PR 01-JUL-1999; 99US-0142154.
 PR 02-JUL-1999; 99US-0142055.
 PR 06-JUL-1999; 99US-0142390.
 PR 08-JUL-1999; 99US-0142803.
 PR 09-JUL-1999; 99US-0142920.
 PR 12-JUL-1999; 99US-0142977.
 PR 13-JUL-1999; 99US-0143542.
 PR 14-JUL-1999; 99US-0143624.
 PR 15-JUL-1999; 99US-0144005.
 PR 16-JUL-1999; 99US-0144085.
 PR 16-JUL-1999; 99US-0144325.
 PR 19-JUL-1999; 99US-0144331.
 PR 19-JUL-1999; 99US-0144332.
 PR 19-JUL-1999; 99US-0144333.
 PR 19-JUL-1999; 99US-0144334.
 PR 19-JUL-1999; 99US-0144334.
 PR 19-JUL-1999; 99US-0144335.
 PR 20-JUL-1999; 99US-0144352.
 PR 20-JUL-1999; 99US-0144632.
 PR 20-JUL-1999; 99US-0144844.
 PR 21-JUL-1999; 99US-0144814.
 PR 21-JUL-1999; 99US-0145086.
 PR 21-JUL-1999; 99US-0145088.
 PR 22-JUL-1999; 99US-0145085.
 PR 22-JUL-1999; 99US-0145087.
 PR 22-JUL-1999; 99US-0145089.
 PR 22-JUL-1999; 99US-0145192.
 PR 23-JUL-1999; 99US-0145145.
 PR 23-JUL-1999; 99US-0145218.
 PR 23-JUL-1999; 99US-0145224.
 PR 26-JUL-1999; 99US-0145276.
 PR 27-JUL-1999; 99US-0145913.
 PR 27-JUL-1999; 99US-0145918.
 PR 27-JUL-1999; 99US-0145919.
 PR 28-JUL-1999; 99US-0145951.
 PR 02-AUG-1999; 99US-0146386.
 PR 02-AUG-1999; 99US-0146388.
 PR 02-AUG-1999; 99US-0146389.
 PR 03-AUG-1999; 99US-0147038.

PR 04-AUG-1999; 99US-0147204.
 PR 04-AUG-1999; 99US-0147302.
 PR 05-AUG-1999; 99US-0147192.
 PR 05-AUG-1999; 99US-0147260.
 PR 06-AUG-1999; 99US-0147303.
 PR 06-AUG-1999; 99US-0147416.
 PR 09-AUG-1999; 99US-0147493.
 PR 09-AUG-1999; 99US-0147935.
 PR 10-AUG-1999; 99US-0148171.
 PR 11-AUG-1999; 99US-0148319.
 PR 12-AUG-1999; 99US-0148341.
 PR 13-AUG-1999; 99US-0148565.
 PR 13-AUG-1999; 99US-0148684.
 PR 16-AUG-1999; 99US-0149368.
 PR 17-AUG-1999; 99US-0149175.
 PR 18-AUG-1999; 99US-0149426.
 PR 20-AUG-1999; 99US-0149722.
 PR 20-AUG-1999; 99US-0149723.
 PR 20-AUG-1999; 99US-0149929.
 PR 23-AUG-1999; 99US-0149902.
 PR 23-AUG-1999; 99US-0149930.
 PR 25-AUG-1999; 99US-0150566.
 PR 26-AUG-1999; 99US-0150884.
 PR 27-AUG-1999; 99US-0151065.
 PR 27-AUG-1999; 99US-0151066.
 PR 27-AUG-1999; 99US-0151080.
 PR 30-AUG-1999; 99US-0151303.
 PR 31-AUG-1999; 99US-0151438.
 PR 01-SEP-1999; 99US-0151930.
 PR 07-SEP-1999; 99US-0152363.
 PR 10-SEP-1999; 99US-0153070.
 PR 13-SEP-1999; 99US-0153758.
 PR 15-SEP-1999; 99US-0154018.
 PR 16-SEP-1999; 99US-0154039.
 PR 20-SEP-1999; 99US-0154779.
 PR 22-SEP-1999; 99US-0155139.
 PR 23-SEP-1999; 99US-0155139.
 PR 24-SEP-1999; 99US-0155486.
 PR 28-SEP-1999; 99US-0155659.
 PR 29-SEP-1999; 99US-0156458.
 PR 29-SEP-1999; 99US-0156596.
 PR 04-OCT-1999; 99US-0157117.
 PR 05-OCT-1999; 99US-0157153.
 PR 06-OCT-1999; 99US-0157865.
 PR 07-OCT-1999; 99US-0158029.
 PR 08-OCT-1999; 99US-0158232.
 PR 12-OCT-1999; 99US-0158369.
 PR 13-OCT-1999; 99US-0159293.
 PR 13-OCT-1999; 99US-0159294.
 PR 13-OCT-1999; 99US-0159295.
 PR 14-OCT-1999; 99US-0159330.
 PR 14-OCT-1999; 99US-0159331.
 PR 14-OCT-1999; 99US-0159331.
 PR 14-OCT-1999; 99US-0159637.
 PR 14-OCT-1999; 99US-0159638.
 PR 18-OCT-1999; 99US-0159638.
 PR 21-OCT-1999; 99US-0160741.
 PR 21-OCT-1999; 99US-0160767.
 PR 21-OCT-1999; 99US-0160768.
 PR 21-OCT-1999; 99US-0160770.
 PR 21-OCT-1999; 99US-0160814.
 PR 21-OCT-1999; 99US-0160815.
 PR 22-OCT-1999; 99US-0160980.
 PR 22-OCT-1999; 99US-0160981.
 PR 22-OCT-1999; 99US-0160989.
 PR 25-OCT-1999; 99US-0161405.
 PR 25-OCT-1999; 99US-0161405.
 PR 25-OCT-1999; 99US-0161406.
 PR 26-OCT-1999; 99US-0161359.
 PR 26-OCT-1999; 99US-0161360.
 PR 26-OCT-1999; 99US-0161361.
 PR 28-OCT-1999; 99US-0161920.
 PR 28-OCT-1999; 99US-0161992.
 PR 28-OCT-1999; 99US-0161993.

PR 29-OCT-1999; 99US-0162142.
Query Match 74.7%; Score 1041; DB 21; Length 249;
Best Local Similarity 79.6%; Pred. No. 5,9e-95;
Matches 179; Conservative 23; Mismatches 23; Indels 0; Gaps 0;
QY 26 GGGGCGHATFFYGGGASGAGCGGNNYSQGYGNTATATATLFPNNLSGACAFEMTC 85
DB 24 GGMNAHAATFFYGGGASGAGCGGNNYSQGYGNTATATLFPNNLSGACAFEMTC 83
QY 86 TNDPMKCLPGTIRVATNFCPPNFALPNNNGCMCPPLQHPDABEAPLQIAQYAGIYP 145
DB 84 ENDGKMCPLGSIIVTATNTNCPNNMALANNNGCMCPLEHPDLAQVFPQRIAQYAGIYP 143
QY 146 VSFRRVPCMKKGGVARTINGHSYFNLVLTITNVGAGDVHSVSIKSGRTGQSMRNWGN 205
DB 144 VSYRRVPCRRRGISIFHTINGHSYFNLVLTITNVGAGDVHSAIKSGRTVWQAMSRWGN 203
QY 206 WQNNVYINGGGLSPQVTLSDGRTITAYNLVPSNMQCGQYEGPOF 250
DB 204 WQNNVYINGGGLSPQVTLSDGRTITAYNLVPSNMQCGQYEGPOF 248
RESULT 13
ID AAG06544 standard; Protein; 259 AA.
XX AAG06544;
AC AAG06544;
XX 17-OCT-2000 (first entry)
DT 17-OCT-2000 (first entry)
XX Arabidopsis thaliana protein fragment SEQ ID NO: 3355.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 3355.
XX Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
XX termination sequence.
XX Arabidopsis thaliana.
OS Arabidopsis thaliana.
XX EP1033405-A2.
XX 06-SEP-2000.
PD 06-SEP-2000.
XX 25-FEB-2000; 2000EP-0301439.
PF 25-FEB-1999; 99US-0121825.
XX 25-FEB-1999; 99US-0123180.
PR 05-MAR-1999; 99US-0123548.
PR 09-MAR-1999; 99US-0125788.
PR 23-MAR-1999; 99US-0126264.
PR 25-MAR-1999; 99US-0126785.
PR 29-MAR-1999; 99US-0126785.
PR 01-APR-1999; 99US-0128234.
PR 06-APR-1999; 99US-0128234.
PR 08-APR-1999; 99US-0128234.
PR 16-APR-1999; 99US-0129845.
PR 19-APR-1999; 99US-0130077.
PR 21-APR-1999; 99US-0130449.
PR 23-APR-1999; 99US-0130510.
PR 23-APR-1999; 99US-0130891.
PR 28-APR-1999; 99US-0131449.
PR 30-APR-1999; 99US-0132048.
PR 30-APR-1999; 99US-0132407.
PR 04-MAY-1999; 99US-0132484.
PR 05-MAY-1999; 99US-0132485.
PR 06-MAY-1999; 99US-0132486.
PR 06-MAY-1999; 99US-0132487.
PR 07-MAY-1999; 99US-0132863.
PR 11-MAY-1999; 99US-0134256.
PR 14-MAY-1999; 99US-0134218.
PR 14-MAY-1999; 99US-0134219.
PR 14-MAY-1999; 99US-0134221.
PR 14-MAY-1999; 99US-0134370.
PR 18-MAY-1999; 99US-0134768.

PR 19-MAY-1999; 99US-0134941.
PR 20-MAY-1999; 99US-0135124.
PR 21-MAY-1999; 99US-0135353.
PR 24-MAY-1999; 99US-0135629.
PR 25-MAY-1999; 99US-0136021.
PR 27-MAY-1999; 99US-0136392.
PR 28-MAY-1999; 99US-0136782.
PR 01-JUN-1999; 99US-0137222.
PR 03-JUN-1999; 99US-0137528.
PR 04-JUN-1999; 99US-0137502.
PR 07-JUN-1999; 99US-0137724.
PR 08-JUN-1999; 99US-0138094.
PR 10-JUN-1999; 99US-0138540.
PR 14-JUN-1999; 99US-0138847.
PR 16-JUN-1999; 99US-0139119.
PR 16-JUN-1999; 99US-0139452.
PR 16-JUN-1999; 99US-0139453.
PR 17-JUN-1999; 99US-0139492.
PR 18-JUN-1999; 99US-0139454.
PR 18-JUN-1999; 99US-0139455.
PR 18-JUN-1999; 99US-0139456.
PR 18-JUN-1999; 99US-0139457.
PR 18-JUN-1999; 99US-0139458.
PR 18-JUN-1999; 99US-0139459.
PR 18-JUN-1999; 99US-0139460.
PR 18-JUN-1999; 99US-0139461.
PR 18-JUN-1999; 99US-0139462.
PR 18-JUN-1999; 99US-0139463.
PR 18-JUN-1999; 99US-0139750.
PR 18-JUN-1999; 99US-0139763.
PR 21-JUN-1999; 99US-0139817.
PR 22-JUN-1999; 99US-0139899.
PR 23-JUN-1999; 99US-0140353.
PR 23-JUN-1999; 99US-0140354.
PR 24-JUN-1999; 99US-0140695.
PR 28-JUN-1999; 99US-0140823.
PR 29-JUN-1999; 99US-0140991.
PR 30-JUN-1999; 99US-0141287.
PR 01-JUL-1999; 99US-0141842.
PR 01-JUL-1999; 99US-0142154.
PR 02-JUL-1999; 99US-0142055.
PR 06-JUL-1999; 99US-0142390.
PR 08-JUL-1999; 99US-0142803.
PR 09-JUL-1999; 99US-0142920.
PR 12-JUL-1999; 99US-0142977.
PR 13-JUL-1999; 99US-0143542.
PR 14-JUL-1999; 99US-0143624.
PR 15-JUL-1999; 99US-0144005.
PR 16-JUL-1999; 99US-0144085.
PR 16-JUL-1999; 99US-0144086.
PR 19-JUL-1999; 99US-0144325.
PR 19-JUL-1999; 99US-0144331.
PR 19-JUL-1999; 99US-0144332.
PR 19-JUL-1999; 99US-0144333.
PR 19-JUL-1999; 99US-0144334.
PR 19-JUL-1999; 99US-0144335.
PR 20-JUL-1999; 99US-0144352.
PR 20-JUL-1999; 99US-0144632.
PR 20-JUL-1999; 99US-0144884.
PR 21-JUL-1999; 99US-0144814.
PR 21-JUL-1999; 99US-0145086.
PR 21-JUL-1999; 99US-0145088.
PR 22-JUL-1999; 99US-0145085.
PR 22-JUL-1999; 99US-0145087.
PR 22-JUL-1999; 99US-0145089.
PR 22-JUL-1999; 99US-0145192.
PR 23-JUL-1999; 99US-0145145.
PR 23-JUL-1999; 99US-0145218.
PR 23-JUL-1999; 99US-0145224.
PR 26-JUL-1999; 99US-0145276.
PR 27-JUL-1999; 99US-0145913.
PR 27-JUL-1999; 99US-0145918.
PR 27-JUL-1999; 99US-0145919.

	PR	26-OCT-1999;	99US-0161360.
	PR	26-OCT-1999;	99US-0161361.
	PR	28-OCT-1999;	99US-0161920.
	PR	28-OCT-1999;	99US-0161992.
	PR	28-OCT-1999;	99US-0161993.
	PR	29-OCT-1999;	99US-0162142.
	Query Match		
	Beet Local Similarity 79.7%; Score 1041; DB 21; Length 259;		
	Matches 179; Conservative 23; Mismatches 23; Indels 0; Gaps 0		
QY	26	GGMOSGATPFYGGDASGTWAGACGYGNLYSQGYGTMTVLSTLFPNNGSCGCPEMTCC	85
Dd	34	GGMINAHATFYGGDASGTWAGACGYGNLYSQGYGTMTVLSTLFPNNGSCGCPEIRTC	93
QY	86	TNDPMCLPRTIRATNFCEPNFALPDNNGMCNPLOHFDMAEPALOIAQYRAGIVP	145
Dd	94	ENDGRKCLPGSIVVTATNFCEPNNALANNNGMKNPFLHFDAQPFGRIAQYRAIIVP	155
QY	146	VSPRRVPCMKKGVRFTTNGHSYNLVLTITVVGAGDVHSVSIKGSRTGMQSMRNMGON	205
Dd	154	VSYRRVPCCRRCRGIRFTTNGHSYNLVLTITVVGAGDVHSAIKGSRTVMQMSRMNMGON	213
QY	206	WQSNNTYLNGGLSFQVTLSDSRITATNLVPSNMQFCQTEGPVF	250
Dd	214	WQSNNTYLNGGLSFQVTLSDSRITATNLVPSNMQFCQTEGPVF	258
RESULT 14			
ID	AAG51631	standard; Protein; 259 AA.	
XX	AAG51631;		
DT	18-OCT-2000	(first entry)	
DE	Arabidopsis thaliana protein fragment SEQ ID NO: 65549.		
KX	Protein identification; signal transduction pathway; metabolic pathway;		
KW	hybridisation assay; genetic mapping; gene expression control; promoter;		
KX	termination sequence.		
OS	Arabidopsis thaliana.		
PX	EPI033405-A2.		
PD	06-SEP-2000.		
XX			
PF	25-FEB-2000;	2000EP-0301439.	
XX			
PR	25-FEB-1999;	99US-0121825.	
PR	05-MAR-1999;	99US-0123180.	
PR	09-MAR-1999;	99US-0123548.	
PR	23-MAR-1999;	99US-0125788.	
PR	25-MAR-1999;	99US-0126264.	
PR	29-MAR-1999;	99US-0126785.	
PR	01-APR-1999;	99US-0127462.	
PR	06-APR-1999;	99US-0128234.	
PR	08-APR-1999;	99US-0128714.	
PR	16-APR-1999;	99US-0129845.	
PR	19-APR-1999;	99US-0130077.	
PR	21-APR-1999;	99US-0130449.	
PR	23-APR-1999;	99US-0130510.	
PR	23-APR-1999;	99US-0130891.	
PR	28-APR-1999;	99US-0131449.	
PR	30-APR-1999;	99US-0132048.	
PR	04-MAY-1999;	99US-0132407.	
PR	05-MAY-1999;	99US-0132484.	
PR	06-MAY-1999;	99US-0132485.	
PR	06-MAY-1999;	99US-0132486.	
PR	06-MAY-1999;	99US-0132487.	
PR	07-MAY-1999;	99US-0132863.	
PR	11-MAY-1999;	99US-0134256.	

PR 14-MAY-1999; 99US-0134218.
PR 14-MAY-1999; 99US-0134219.
PR 14-MAY-1999; 99US-0134221.
PR 14-MAY-1999; 99US-0134370.
PR 18-MAY-1999; 99US-0134768.
PR 19-MAY-1999; 99US-0134941.
PR 20-MAY-1999; 99US-0135124.
PR 21-MAY-1999; 99US-0135353.
PR 24-MAY-1999; 99US-0135629.
PR 25-MAY-1999; 99US-0136021.
PR 27-MAY-1999; 99US-0136392.
PR 28-MAY-1999; 99US-0136782.
PR 01-JUN-1999; 99US-0137222.
PR 03-JUN-1999; 99US-0137528.
PR 04-JUN-1999; 99US-0137502.
PR 07-JUN-1999; 99US-0137724.
PR 08-JUN-1999; 99US-0138094.
PR 10-JUN-1999; 99US-0138540.
PR 10-JUN-1999; 99US-0138847.
PR 14-JUN-1999; 99US-0139319.
PR 16-JUN-1999; 99US-0139452.
PR 16-JUN-1999; 99US-0139453.
PR 17-JUN-1999; 99US-0139492.
PR 18-JUN-1999; 99US-0139454.
PR 18-JUN-1999; 99US-0139455.
PR 18-JUN-1999; 99US-0139456.
PR 18-JUN-1999; 99US-0139457.
PR 18-JUN-1999; 99US-0139458.
PR 18-JUN-1999; 99US-0139459.
PR 18-JUN-1999; 99US-0139460.
PR 18-JUN-1999; 99US-0139461.
PR 18-JUN-1999; 99US-0139462.
PR 18-JUN-1999; 99US-0139463.
PR 18-JUN-1999; 99US-0139750.
PR 18-JUN-1999; 99US-0139763.
PR 21-JUN-1999; 99US-0139817.
PR 22-JUN-1999; 99US-0139819.
PR 23-JUN-1999; 99US-0140353.
PR 23-JUN-1999; 99US-0140354.
PR 24-JUN-1999; 99US-0140695.
PR 28-JUN-1999; 99US-0140893.
PR 29-JUN-1999; 99US-0140921.
PR 30-JUN-1999; 99US-0141287.
PR 01-JUL-1999; 99US-0141842.
PR 01-JUL-1999; 99US-0142154.
PR 02-JUL-1999; 99US-0142055.
PR 06-JUL-1999; 99US-0142390.
PR 08-JUL-1999; 99US-0142803.
PR 09-JUL-1999; 99US-0142820.
PR 12-JUL-1999; 99US-0142877.
PR 13-JUL-1999; 99US-0143542.
PR 14-JUL-1999; 99US-0143624.
PR 15-JUL-1999; 99US-0144005.
PR 16-JUL-1999; 99US-0144085.
PR 16-JUL-1999; 99US-0144086.
PR 19-JUL-1999; 99US-0144325.
PR 19-JUL-1999; 99US-0144331.
PR 19-JUL-1999; 99US-0144332.
PR 19-JUL-1999; 99US-0144333.
PR 19-JUL-1999; 99US-0144334.
PR 19-JUL-1999; 99US-0144335.
PR 20-JUL-1999; 99US-0144352.
PR 20-JUL-1999; 99US-0144632.
PR 20-JUL-1999; 99US-0144684.
PR 21-JUL-1999; 99US-0144814.
PR 21-JUL-1999; 99US-0145086.
PR 21-JUL-1999; 99US-0145088.
PR 22-JUL-1999; 99US-0145085.
PR 22-JUL-1999; 99US-0145087.
PR 22-JUL-1999; 99US-0145089.
PR 22-JUL-1999; 99US-0145192.
PR 23-JUL-1999; 99US-0145145.
PR 23-JUL-1999; 99US-0145218.

PR 23-JUL-1999; 99US-0145224.
PR 26-JUL-1999; 99US-0145276.
PR 27-JUL-1999; 99US-0145918.
PR 27-JUL-1999; 99US-0145919.
PR 28-JUL-1999; 99US-0145951.
PR 02-AUG-1999; 99US-0146386.
PR 02-AUG-1999; 99US-0146388.
PR 02-AUG-1999; 99US-0146389.
PR 03-AUG-1999; 99US-0147038.
PR 04-AUG-1999; 99US-0147204.
PR 04-AUG-1999; 99US-0147302.
PR 05-AUG-1999; 99US-0147192.
PR 05-AUG-1999; 99US-0147260.
PR 06-AUG-1999; 99US-0147303.
PR 06-AUG-1999; 99US-0147304.
PR 09-AUG-1999; 99US-0147493.
PR 09-AUG-1999; 99US-0147935.
PR 10-AUG-1999; 99US-0148171.
PR 11-AUG-1999; 99US-0148319.
PR 12-AUG-1999; 99US-0148341.
PR 13-AUG-1999; 99US-0148565.
PR 13-AUG-1999; 99US-0148684.
PR 16-AUG-1999; 99US-0149368.
PR 17-AUG-1999; 99US-0149175.
PR 18-AUG-1999; 99US-0149426.
PR 20-AUG-1999; 99US-0149722.
PR 20-AUG-1999; 99US-0149723.
PR 20-AUG-1999; 99US-0149929.
PR 23-AUG-1999; 99US-0149902.
PR 23-AUG-1999; 99US-0149930.
PR 25-AUG-1999; 99US-0150566.
PR 26-AUG-1999; 99US-0150884.
PR 27-AUG-1999; 99US-0151065.
PR 27-AUG-1999; 99US-0151080.
PR 30-AUG-1999; 99US-0151303.
PR 31-AUG-1999; 99US-0151438.
PR 01-SEP-1999; 99US-0151930.
PR 07-SEP-1999; 99US-0152363.
PR 10-SEP-1999; 99US-0153070.
PR 13-SEP-1999; 99US-0153758.
PR 15-SEP-1999; 99US-0154018.
PR 16-SEP-1999; 99US-0154039.
PR 20-SEP-1999; 99US-0154779.
PR 22-SEP-1999; 99US-0155139.
PR 23-SEP-1999; 99US-0155486.
PR 24-SEP-1999; 99US-0155659.
PR 28-SEP-1999; 99US-0156458.
PR 29-SEP-1999; 99US-0156596.
PR 04-OCT-1999; 99US-0157117.
PR 05-OCT-1999; 99US-0157753.
PR 06-OCT-1999; 99US-0157865.
PR 07-OCT-1999; 99US-0158029.
PR 08-OCT-1999; 99US-0158232.
PR 12-OCT-1999; 99US-0158369.
PR 13-OCT-1999; 99US-0158293.
PR 13-OCT-1999; 99US-0159294.
PR 13-OCT-1999; 99US-0159295.
PR 14-OCT-1999; 99US-0159329.
PR 14-OCT-1999; 99US-0159330.
PR 14-OCT-1999; 99US-0159331.
PR 14-OCT-1999; 99US-0159637.
PR 14-OCT-1999; 99US-0159638.
PR 18-OCT-1999; 99US-0159584.
PR 21-OCT-1999; 99US-0160741.
PR 21-OCT-1999; 99US-0160767.
PR 21-OCT-1999; 99US-0160768.
PR 21-OCT-1999; 99US-0160770.
PR 21-OCT-1999; 99US-0160814.
PR 21-OCT-1999; 99US-0160815.
PR 22-OCT-1999; 99US-0160980.
PR 22-OCT-1999; 99US-0160981.

PR 22-OCT-1999; 99US-0160989.
PR 25-OCT-1999; 99US-0161404.
PR 25-OCT-1999; 99US-0161405.
PR 25-OCT-1999; 99US-0161406.
PR 25-OCT-1999; 99US-0161359.
PR 26-OCT-1999; 99US-0161359.
PR 26-OCT-1999; 99US-0161360.
PR 26-OCT-1999; 99US-0161361.
PR 28-OCT-1999; 99US-0161920.
PR 28-OCT-1999; 99US-0161992.
PR 28-OCT-1999; 99US-0161993.
PR 29-OCT-1999; 99US-0162142.

Query Match 74.7%; Score 1041; DB 21; Length 259;
Best Local Similarity 79.6%; Pred. No. 6,2e-95;
Matches 179; Conservative 23; Mismatches 23; Indels 0; Gaps 0;

QY 26 GGNMGGATFTYGGDAGTGWGAGCGNLYSGYGTNTALSTLFFNNGLSCGCFEMTC 85
DB 34 GGMINAHATFYGGDAGTGWGAGCGNLYSGYGTNTALSTLFFNNGLSCGCFEIRC 93

QY 86 TNDPKMCLPGTIRYATATNFCPPNFPALPNNNGMCPNPILOHDMAPFLQIAOYRAGIYP 145
DB 94 ENDKMKCLPGSIVTATNFCPPNFPALPNNNGMCPNPILOHDMAPFLQIAOYRAGIYP 153

QY 146 VSPFRVPCMKKGVRFITNGHSYFNLYLITVVGAGDVHSVIXKSRGTGMQSMRRNGON 205
DB 154 VSYRVRPCRRRGIRFITNGHSYFNLYLITVVGAGDVHSVIXKSRGTGMQSMRRNGON 213

QY 206 WQSNNTYNGCGLSRQVLTSDRITLTAFLVPSNMQFCQTYEGPDP 250
DB 214 WQSNNTYNGCGLSRQVLTSDRITLTAFLVPSNMQFCQTYEGPDP 258

RESULT 15

AAG51645
ID AAG51645 standard; Protein; 280 AA.

AC AAG51645;

XX 18-OCT-2000 (first entry)

DE Arabidopsis thaliana protein fragment SEQ ID NO: 65568.

XX Protein identification; signal transduction pathway; metabolic pathway;
KM hybridisation assay; genetic mapping; gene expression control; promoter;
KM termination sequence.

XX Arabidopsis thaliana.

OS EP1033405-A2.

PN EP1033405-A2.

XX 06-SEP-2000.

PD 25-FEB-2000; 2000EP-0301439.

XX 25-FEB-1999; 99US-0121825.

PR 05-MAR-1999; 99US-0123180.

PR 09-MAR-1999; 99US-0123548.

PR 23-MAR-1999; 99US-0125768.

PR 25-MAR-1999; 99US-0126264.

PR 01-APR-1999; 99US-0127462.

PR 06-APR-1999; 99US-0128234.

PR 08-APR-1999; 99US-0128714.

PR 16-APR-1999; 99US-0129845.

PR 19-APR-1999; 99US-0130077.

PR 21-APR-1999; 99US-0130449.

PR 23-APR-1999; 99US-0130510.

PR 28-APR-1999; 99US-0130891.

PR 30-APR-1999; 99US-0132048.

PR 30-APR-1999; 99US-0132407.

PR 04-MAY-1999; 99US-0132484.

PR 05-MAY-1999; 99US-0132485.

PR 06-MAY-1999; 99US-0132486.

PR 06-MAY-1999; 99US-0132487.

PR 07-MAY-1999; 99US-0132863.

PR 11-MAY-1999; 99US-0134256.

PR 14-MAY-1999; 99US-0134218.

PR 14-MAY-1999; 99US-0134219.

PR 14-MAY-1999; 99US-0134370.

PR 18-MAY-1999; 99US-0134376.

PR 19-MAY-1999; 99US-0134941.

PR 20-MAY-1999; 99US-0135124.

PR 21-MAY-1999; 99US-0135353.

PR 24-MAY-1999; 99US-0135629.

PR 25-MAY-1999; 99US-0136021.

PR 27-MAY-1999; 99US-0136382.

PR 28-MAY-1999; 99US-0136782.

PR 01-JUN-1999; 99US-0137222.

PR 03-JUN-1999; 99US-0137528.

PR 04-JUN-1999; 99US-0137502.

PR 07-JUN-1999; 99US-0137724.

PR 08-JUN-1999; 99US-0138094.

PR 10-JUN-1999; 99US-0138540.

PR 10-JUN-1999; 99US-0138847.

PR 14-JUN-1999; 99US-0139119.

PR 16-JUN-1999; 99US-0139452.

PR 17-JUN-1999; 99US-0139482.

PR 18-JUN-1999; 99US-0139454.

PR 18-JUN-1999; 99US-0139455.

PR 18-JUN-1999; 99US-0139456.

PR 18-JUN-1999; 99US-0139457.

PR 18-JUN-1999; 99US-0139458.

PR 18-JUN-1999; 99US-0139459.

PR 18-JUN-1999; 99US-0139460.

PR 18-JUN-1999; 99US-0139461.

PR 18-JUN-1999; 99US-0139462.

PR 18-JUN-1999; 99US-0139463.

PR 18-JUN-1999; 99US-0139464.

PR 18-JUN-1999; 99US-0139465.

PR 23-JUN-1999; 99US-0140353.

PR 24-JUN-1999; 99US-0140354.

PR 28-JUN-1999; 99US-0140823.

PR 29-JUN-1999; 99US-0140991.

PR 30-JUN-1999; 99US-0141287.

PR 01-JUL-1999; 99US-0141842.

PR 02-JUL-1999; 99US-0142055.

PR 06-JUL-1999; 99US-0142390.

PR 08-JUL-1999; 99US-0142803.

PR 09-JUL-1999; 99US-0142920.

PR 12-JUL-1999; 99US-0142977.

PR 13-JUL-1999; 99US-0143542.

PR 14-JUL-1999; 99US-0143564.

PR 15-JUL-1999; 99US-0144005.

PR 16-JUL-1999; 99US-0144085.

PR 16-JUL-1999; 99US-0144086.

PR 19-JUL-1999; 99US-0144325.

PR 19-JUL-1999; 99US-0144331.

PR 19-JUL-1999; 99US-0144332.

PR 19-JUL-1999; 99US-0144333.

PR 19-JUL-1999; 99US-0144334.

PR 20-JUL-1999; 99US-0144335.

PR 20-JUL-1999; 99US-0144352.

PR 20-JUL-1999; 99US-0144632.

PR 21-JUL-1999; 99US-0144884.

PR 21-JUL-1999; 99US-0144814.

PR 21-JUL-1999; 99US-0145086.

PR 21-JUL-1999; 99US-0145088.

PR 22-JUL-1999; 99US-0145085.

PR 21-OCT-1999; 99US-0160770.
PR 21-OCT-1999; 99US-0160814.
PR 21-OCT-1999; 99US-0160815.
PR 22-OCT-1999; 99US-0160980.
PR 22-OCT-1999; 99US-0160981.
PR 22-OCT-1999; 99US-0160989.
PR 25-OCT-1999; 99US-0161404.
PR 25-OCT-1999; 99US-0161405.
PR 25-OCT-1999; 99US-0161406.
PR 26-OCT-1999; 99US-0161359.
PR 26-OCT-1999; 99US-0161360.
PR 26-OCT-1999; 99US-0161361.
PR 28-OCT-1999; 99US-0161920.
PR 28-OCT-1999; 99US-0161992.
PR 28-OCT-1999; 99US-0161993.
PR 29-OCT-1999; 99US-0162142.

Query Match	74.7%	Score 1041;	DB 21;	Length 280;
Best Local Similarity	79.6%	Pred. No. 6.9e-95;		
Matches 179; Conservative	23;	Mismatches 23;	Indels 0;	Gaps 0

Qy	20	GGMOSHAIFYFGGGBASGTMGAGCGYGLYQOYGTINTVALSTLFPNNIGSCGCFEMTC	85
Db	55	GGINNAHATFFGGGDASGTMGAGCGYGLYQOYGTISTALSTLFPNNIGSCGCFEIRC	114
Qy	86	TNDPKACLTGTRVATATNFCPPNFAFPNNNGWCNPLQHFDEMAEPALQIAYRAGIVP	145
Db	115	ENDKKCKLPGSLVITATATNFCPPNNAANNNGWCNPLFHHDLAQVFGRIAQYRAGIVP	174
Qy	146	VSEFRVPCMKKGQVRFITNGHSYFNLVLTITVGAAGDVHSYISIKGSRTGMOSSRMNGON	205
Db	175	VSYRVRPCRRRGIRFITNGHSYFNLVLTITVGAAGDVHSAIIGSRTRTVQAMSRMNGON	234
Qy	206	WQSNMYLNGQLSPQVLTISDGRITLAVNLVPSNMQPGQYTGAPQF	250
Db	235	WQSNSTYLNQALSPKVTYSIDGRITVFAALPAGMSYGTTFAGGQF	279

Search completed: December 18, 2003, 17:48:25
Job time : 43 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Comugen Ltd.

OM protein - protein search, using sw model

Run on: December 18, 2003, 17:47:38 ; Search time 21 Seconds
(without alignments)
503.701 Million cell updates/sec

Title: US-09-383-579c-10
Perfect score: 1394
Sequence: 1 MAFSYSPFSLFLPFFVF.....AYNLVPSNMQFGQYEGPQF 250

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*
1: /cgn2_6/ptodata/1/1aa/5A COMB.pep:*
2: /cgn2_6/ptodata/1/1aa/5B COMB.pep:*
3: /cgn2_6/ptodata/1/1aa/6A COMB.pep:*
4: /cgn2_6/ptodata/1/1aa/6B COMB.pep:*
5: /cgn2_6/ptodata/1/1aa/PCTUS COMB.pep:*
6: /cgn2_6/ptodata/1/1aa/backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1275	91.5	227	4	US-09-112-498A-5
2	1265	90.7	227	3	US-09-092-160-7
3	1131	81.1	223	4	US-09-112-498A-3
4	1035	74.2	233	4	US-09-112-498A-11
5	1032	74.0	237	4	US-09-112-498A-7
6	1026	73.6	228	2	US-08-440-517A-2
7	1026	73.6	228	3	US-09-092-160-2
8	1022.5	73.4	222	4	US-09-112-498A-8
9	1011.5	72.6	226	2	US-08-440-517A-6
10	1011.5	72.6	226	3	US-09-092-160-6
11	962	69.0	225	2	US-08-440-517A-5
12	962	69.0	225	3	US-09-092-160-5
13	939	67.4	241	4	US-09-112-498A-10
14	937	67.2	238	4	US-09-112-498A-13
15	889.5	63.8	233	4	US-09-112-498A-9
16	884	63.4	234	4	US-09-112-498A-6
17	857.5	61.5	222	4	US-08-440-517A-3
18	857.5	61.5	222	3	US-09-092-160-3
19	841.5	60.4	225	4	US-09-362-642-2
20	839.5	60.2	225	2	US-08-845-539-2
21	825.5	59.2	233	4	US-09-112-498A-12
22	797	57.2	179	2	US-08-845-539-6
23	797	57.2	179	4	US-09-362-642-6
24	773.5	55.5	227	2	US-08-440-517A-4
25	773.5	55.5	227	3	US-09-092-160-4
26	732	52.5	167	2	US-08-845-539-4
27	732	52.5	167	4	US-09-362-642-4

28	248.5	17.8	261	1	US-07-971-096-2	Sequence 2, Appl
29	248.5	17.8	261	1	US-08-175-096-2	Sequence 2, Appl
30	239	17.1	263	4	US-09-811-672-10	Sequence 10, Appl
31	236	16.9	246	3	US-08-441-507-21	Sequence 21, Appl
32	236	16.9	246	4	US-07-969-875A-21	Sequence 21, Appl
33	234	16.8	272	3	US-08-441-507-15	Sequence 15, Appl
34	234	16.8	272	4	US-07-969-875A-15	Sequence 15, Appl
35	233	16.7	263	1	US-07-971-096-4	Sequence 4, Appl
36	233	16.7	263	3	US-08-175-096-4	Sequence 4, Appl
37	233	16.7	263	1	US-08-413-874-6	Sequence 6, Appl
38	233	16.7	263	3	US-08-434-818-6	Sequence 6, Appl
39	233	16.7	263	3	US-08-433-288-6	Sequence 6, Appl
40	233	16.7	263	3	US-08-174-739A-6	Sequence 6, Appl
41	233	16.7	263	4	US-08-434-256-6	Sequence 6, Appl
42	207	14.8	245	3	US-08-441-507-24	Sequence 24, Appl
43	207	14.8	197	3	US-07-969-875A-24	Sequence 24, Appl
44	173	12.4	197	4	US-08-441-507-5	Sequence 5, Appl
45	173	12.4	197	4	US-07-969-875A-5	Sequence 5, Appl

ALIGNMENTS

```
RESULT 1
US-09-112-498A-5
; Sequence 5, Application US/09112498A
; Patent No. 6458928
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: MICROBIAL SWOLLENTIN PROTEIN, DNA SEQUENCES
; TITLE OF INVENTION: ENCODING SUCH SWOLLENTINS AND METHOD OF PRODUCING SUCH
; NUMBER OF INVENTION: SWOLLENTINS
; NUMBER OF SEQUENCES: 31
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patent in Release #1.0, Version #1.25 (BPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/112,498A
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 98/14226
; FILING DATE:
; APPLICATION NUMBER: US 08/893,766
; FILING DATE: 11-JUL-1997
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 227 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; US-09-112-498A-5

Query Match          91.5%; Score 1275; DB 4; Length 227;
Best Local Similarity 100.0%; Pred. No. 8.7e-117;
Matches 227; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

QY	24	DYWGWSGHATFFGGDASGTWAGACGYNLVSQYGTIVTALSTALFNNGLSCGACFEW	83
DB	1	DYWGWSGHATFFGGDASGTWAGACGYNLVSQYGTIVTALSTALFNNGLSCGACFEW	60
QY	84	TCINDRKWCLPGIRITATNFCEPPNALPNNNGMCPPLQHPDMAEPALQIAQYRAGI	143
DB	61	TCINDRKWCLPGIRITATNFCEPPNALPNNNGMCPPLQHPDMAEPALQIAQYRAGI	120
QY	144	VPVSPFRVRCMKKGGVFTTNGHSYFNVLVLTIVTGAGDVHSISGSRGTGMSRMNG	203
DB	121	VPVSPFRVRCMKKGGVFTTNGHSYFNVLVLTIVTGAGDVHSISGSRGTGMSRMNG	180
QY	204	QNMWSNNYLNQGLSPQVTLSDGRTLTAYNLVPSNMQFGQYEGPQF	250
DB	181	QNMWSNNYLNQGLSPQVTLSDGRTLTAYNLVPSNMQFGQYEGPQF	227

RESULT 2

US-09-092-160-7

Sequence 7, Application US/09092160C

Patent No. 6255466

GENERAL INFORMATION:

APPLICANT: Cosgrove, Daniel J

APPLICANT: McQueen-Mason, Simon

APPLICANT: Gullitman, Mark J

APPLICANT: Shcherban, Tatyana

APPLICANT: Shi, Jun

TITLE OF INVENTION: PURIFIED EXPANSIN PROTEINS

FILE REFERENCE: 1194/IC1403

CURRENT APPLICATION NUMBER: US/09/092,160C

EARLIER FILING DATE: 1998-06-05

EARLIER APPLICATION NUMBER: 08/440,517

EARLIER FILING DATE: 1995-05-12

EARLIER APPLICATION NUMBER: 08/242,090

EARLIER FILING DATE: 1994-05-12

EARLIER APPLICATION NUMBER: 08/060,944

EARLIER FILING DATE: 1993-05-12

NUMBER OF SEQ ID NOS: 7

SOFTWARE: Patentin Ver. 2.1

SEQ ID NO 7

LENGTH: 227

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE: OTHER INFORMATION: Description of Artificial Sequence: cucumber

OTHER INFORMATION: expansin

US-09-092-160-7

Query Match 90.7%; Score 1265; DB 3; Length 227;

Best Local Similarity 99.1%; Pred. No. 8.3e-116;

Matches 225; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Db 24 DYGWQSHATFYGGDASGTMGACGYNLYSGYGTNTVALSTALFNNGLSCGACFEM 83

Db 1 DYGWQSHATFYGGDASGTMGACGYNLYSGYGTNTVALSTALFNNGLSCGACFEM 60

Db 84 TCTNPKMCLPGTIRVTATNFCPPNFALPNNNGWMCNPLQHFDMAPFLQIAQYRAGI 143

Db 61 TCTNPKMCLPGTIRVTATNFCPPNFALPNNNGWMCNPLQHFDMAPFLQIAQYRAGI 120

Db 144 VVSEFRVPCMKKGVRFTINGHSYFNLYLITNVGAGDVHSVSIKSRGTGQMSRMNG 203

Db 121 VVSEFRVPCMKKGVRFTINGHSYFNLYLITNVGAGDVHSVSIKSRGTGQMSRMNG 180

Db 204 QWQSNNTYINGQGLSFQVTLSDGRTLTAYNLVPSNMQFGQTYEGPOF 250

Db 181 QWQSNNTYINGQGLSFQVTLSDGRTLTAYNLVPSNMQFGQTYEGPOF 227

Db

RESULT 3

US-09-112-498A-3

Sequence 3, Application US/09112498A

Patent No. 6458928

GENERAL INFORMATION:

APPLICANT:

TITLE OF INVENTION: MICROBIAL SWOLLENIN PROTEIN, DNA SEQUENCES

TITLE OF INVENTION: ENCODING SUCH SWOLLENIN AND METHOD OF PRODUCING SUCH

NUMBER OF SEQUENCES: 31

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/112,498A

FILING DATE:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 98/14226

FILING DATE: US 08/893,766

FILING DATE: 11-JUL-1997

INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:

LENGTH: 223 amino acids

TYPE: amino acid

TOPOLOGY: unknown

MOLECULE TYPE: protein

US-09-112-498A-3

Query Match 81.1%; Score 1131; DB 4; Length 223;

Best Local Similarity 88.4%; Pred. No. 9.9e-103;

Matches 199; Conservative 16; Mismatches 8; Indels 2; Gaps 2;

Db 26 GGMQSHATFYGGDASGTMGACGYNLYSGYGTNTVALSTALFNNGLSCGACFEMTC 85

Db 1 GGMQSHATFYGGDASGTMGACGYNLYSGYGTNTVALSTALFNNGLSCGACFEMTC 60

Db 86 TNDPVMCLPGTIRVTATNFCPPNFALPNNNGWMCNPLQHFDMAPFLQIAQYRAGI 145

Db 61 DNDPVMCLPGTIRVTATNFCPPNFALPNNNGWMCNPLQHFDMAPFLQIAQYRAGI 120

Db 146 VVSEFRVPCMKKGVRFTINGHSYFNLYLITNVGAGDVHSVSIKSRGTGQMSRMNG 205

Db 121 VVSEFRVPCMKKGVRFTINGHSYFNLYLITNVGAGDVHSVSIKSRGTGQMSRMNG 180

Db

Db 206 WQSNNTYINGQGLSFQVTLSDGRTLTAYNLVPSNMQFGQTYEGPOF 250

Db 181 WQSNNTYINGQGLSFQVTLSDGRTLTAYNLVPSNMQFGQTYEGPOF 223

Db

RESULT 4

US-09-112-498A-11

Sequence 11, Application US/09112498A

Patent No. 6458928

GENERAL INFORMATION:

APPLICANT:

TITLE OF INVENTION: MICROBIAL SWOLLENIN PROTEIN, DNA SEQUENCES

TITLE OF INVENTION: ENCODING SUCH SWOLLENIN AND METHOD OF PRODUCING SUCH

NUMBER OF SEQUENCES: 31

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/112,498A

FILING DATE:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 98/14226

FILING DATE:

APPLICATION NUMBER: US 08/893,766

FILING DATE: 11-JUL-1997

INFORMATION FOR SEQ ID NO: 11:

SEQUENCE CHARACTERISTICS:

LENGTH: 233 amino acids

TYPE: amino acid

TOPOLOGY: unknown

MOLECULE TYPE: protein

US-09-112-498A-11

Query Match 74.2%; Score 1035; DB 4; Length 233;

Best Local Similarity 78.1%; Pred. No. 2.5e-93;

Matches 178; Conservative 23; Mismatches 27; Indels 0; Gaps 0;

Db 23 ADYGWQSHATFYGGDASGTMGACGYNLYSGYGTNTVALSTALFNNGLSCGACFEM 82

Db 6 ADYGWQSHATFYGGDASGTMGACGYNLYSGYGTNTVALSTALFNNGLSCGACFEM 65

Db

Db 83 MTCTNDPVMCLPGTIRVTATNFCPPNFALPNNNGWMCNPLQHFDMAPFLQIAQYRAGI 142

Db 66 LRCNDQWCLPGSVTATATNLCPPNYALPRDDGWCNPPRPHDMPALQIGVYRAG 125
Qy 143 IVPSPFRVCMKGGVFTINGHSYFNVLITVVGAGDVHSISGSRGMSRMN 202
Db 126 IVPSPFRVCMKGGVFTINGHSYFNVLITVVGAGDVHSISGSRGMSRMN 185
Qy 203 GQWQSNVYNGQSLSFQVTLSDGRTLTAYNLVPSNMQFGQTYEGPOF 250
Db 186 GQWQSNVYNGQSLSFQVTLSDGRTLTAYNLVPSNMQFGQTYEGPOF 233

RESULT 5
US-09-112-498A-7
Sequence 7, Application US/09112498A
Patent No. 6458928
GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: MICROBIAL SWOLLENIN PROTEIN, DNA SEQUENCES
TITLE OF INVENTION: ENCODING SUCH SWOLLENIN AND METHOD OF PRODUCING SUCH
TITLE OF INVENTION: SWOLLENIN
NUMBER OF SEQUENCES: 31
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/112,498A
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 98/14226
FILING DATE:
APPLICATION NUMBER: US 08/893,766
FILING DATE: 11-JUL-1997
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 237 amino acids
TYPE: amino acid
TOPOLOGY: unknown
US-09-112-498A-7

Query Match 74.0%; Score 1032; DB 4; Length 237;
Best local Similarity 79.0%; Pred. No. 5e-93;
Matches 177; Conservative 23; Mismatches 24; Indels 0; Gaps 0;

Qy 26 GQWQSNVYNGQSLSFQVTLSDGRTLTAYNLVPSNMQFGQTYEGPOF 85
Db 12 GQWQSNVYNGQSLSFQVTLSDGRTLTAYNLVPSNMQFGQTYEGPOF 71
Qy 86 TNDPKMCLPGTIRITATNFCPPNPNALPNNNGMCNPPLOHFDMAEPALQIAYRAGIYP 145
Db 72 QNDGKMWCLPGSIVTATNFCPPNPNALPNNNGMCNPPLOHFDMAEPALQIAYRAGIYP 131
Qy 146 VSPFRVCMKGGVFTINGHSYFNVLITVVGAGDVHSISGSRGMSRMN 205
Db 132 VSPFRVCMKGGVFTINGHSYFNVLITVVGAGDVHSISGSRGMSRMN 191
Qy 206 WQSNVYNGQSLSFQVTLSDGRTLTAYNLVPSNMQFGQTYEGPOF 249
Db 192 WQSNVYNGQSLSFQVTLSDGRTLTAYNLVPSNMQFGQTYEGPOF 235

RESULT 6
US-08-440-517A-2
Sequence 2, Application US/08440517A
Patent No. 5959082
GENERAL INFORMATION:
APPLICANT: COSGROVE, DANIEL J.;
APPLICANT: GUILTINAN, MARK;
APPLICANT: SCHERBAN, TATYANA;
APPLICANT: SHI, JUN
TITLE OF INVENTION: PURIFIED EXPANSIN PROTEINS

NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESS: INTELLECTUAL PROPERTY OFFICE, THE
ADDRESS: PENNSYLVANIA STATE UNIVERSITY
STREET: 113 TECHNOLOGY CENTER
CITY: UNIVERSITY PARK
STATE: PENNSYLVANIA
COUNTRY: UNITED STATES OF AMERICA
ZIP: 16802-7000
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: NEC 286
OPERATING SYSTEM: DOS
SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/440,517A
FILING DATE:
CLASSIFICATION: 530
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 228
TYPE: AMINO ACID
TOPOLOGY: UNKNOWN
US-08-440-517A-2

Query Match 73.6%; Score 1026; DB 2; Length 228;
Best local Similarity 79.3%; Pred. No. 1.8e-97;
Matches 176; Conservative 22; Mismatches 24; Indels 0; Gaps 0;

Qy 26 GQWQSNVYNGQSLSFQVTLSDGRTLTAYNLVPSNMQFGQTYEG 85
Db 3 GQWQSNVYNGQSLSFQVTLSDGRTLTAYNLVPSNMQFGQTYEG 62
Qy 86 TNDPKMCLPGTIRITATNFCPPNPNALPNNNGMCNPPLOHFDMAEPALQIAYRAGIYP 145
Db 63 QNDGKMWCLPGSIVTATNFCPPNPNALPNNNGMCNPPLOHFDMAEPALQIAYRAGIYP 122
Qy 146 VSPFRVCMKGGVFTINGHSYFNVLITVVGAGDVHSISGSRGMSRMN 205
Db 123 VSPFRVCMKGGVFTINGHSYFNVLITVVGAGDVHSISGSRGMSRMN 182
Qy 206 WQSNVYNGQSLSFQVTLSDGRTLTAYNLVPSNMQFGQTYEG 247
Db 183 WQSNVYNGQSLSFQVTLSDGRTLTAYNLVPSNMQFGQTYEG 224

RESULT 7
US-09-092-160-2
Sequence 2, Application US/09092160C
Patent No. 625466
GENERAL INFORMATION:
APPLICANT: Cosgrove, Daniel J
APPLICANT: McQueen-Mason, Simon
APPLICANT: Guiltinan, Mark J
APPLICANT: Scherban, Tatyana
APPLICANT: Shi, Jun
TITLE OF INVENTION: PURIFIED EXPANSIN PROTEINS
FILE REFERENCE: 1194/1C114US3
CURRENT APPLICATION NUMBER: US/09/092,160C
CURRENT FILING DATE: 1998-06-05
EARLIER APPLICATION NUMBER: 08/440,517
EARLIER FILING DATE: 1995-05-12
EARLIER APPLICATION NUMBER: 08/242,090
EARLIER FILING DATE: 1994-05-12
EARLIER APPLICATION NUMBER: 08/060,944
EARLIER FILING DATE: 1993-05-12
NUMBER OF SEQ ID NOS: 7
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 2
LENGTH: 228
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:

OTHER INFORMATION: Description of Artificial Sequence: rice expansin
FEATURE:
NAME/KEY: UNSURE
LOCATION: 211
OTHER INFORMATION: Xaa is unknown or other.
US-09-160-2

Query Match 73.6%; Score 1026; DB 3; Length 228;
Best Local Similarity 79.3%; Pred. No. 1.8e-92;
Matches 176; Conservative 22; Mismatches 24; Indels 0; Gaps 0;

QY 26 GGMOSGATFFYGAGDSGTMGACGYNLYSOGYGTNTALSTALFNNGLSCGACPEMFC 85
DB 3 GGMVNAHATFFYGAGDSGTMGACGYNLYSOGYGTNTALSTALFNNGLSCGACPEMFC 62
QY 86 TNDPKWCLPGTIRVTATNFCPPNFALPNNNGWCNPPLOHFDMAEPALQIAYRAGIY 145
DB 63 QNDGKMKCLPGSIYVTATNFCPPNFALPNNAGWCNPPQOHFDLSQVFORIAQYRAGIY 122
QY 146 VSPFRVPCMKKGGVFTINGHSYFNLVLTNVGAGDVHSVSIKSGRTGWSKSRNMGON 205
DB 123 VAYRRVPCVRGGIRFTINGHSYFNLVLTNVGAGDVHSAMVKSGRTGWSKSRNMGON 182
QY 206 WQSNNTYNGQSLSFQVTLSDGRTLTAYNLVPSNMQFQTYEG 247
DB 183 WQSNNTYNGQSLSFQVTLSDGRTLTAYNLVPSNMQFQTYEG 224

RESULT 8

US-09-112-498A-8
Sequence 8, Application US/09112498A
Patent No. 6458928

GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: MICROBIAL SWOLLENIN PROTEIN, DNA SEQUENCES
TITLE OF INVENTION: ENCODING SUCH SWOLLENIN AND METHOD OF PRODUCING SUCH
NUMBER OF SEQUENCES: 31
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Releasee #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/112,498A
FILING DATE:
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 98/14226
FILING DATE:
APPLICATION NUMBER: US 08/893,766
FILING DATE:
FILING DATE: 11-JUL-1997
INFORMATION FOR SEQ ID NO: 8
SEQUENCE CHARACTERISTICS:
LENGTH: 232 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULAR TYPE: protein
US-09-112-498A-8

Query Match 73.4%; Score 1022.5; DB 4; Length 232;
Best Local Similarity 78.1%; Pred. No. 4.1e-92;
Matches 178; Conservative 26; Mismatches 23; Indels 1; Gaps 1;

QY 24 DYGMOSGATFFYGAGDSGTMGACGYNLYSOGYGTNTALSTALFNNGLSCGACPEM 83
DB 5 DNGMWRGHAHTFFYGAGDSGTMGACGYNLYSOGYGTNTALSTALFNNGLSCGACPEM 64
QY 84 TCTNDPKWCLPGTIRVTATNFCPPNFALPNNNGWCNPPLOHFDMAEPALQIAYRAGI 143
DB 65 TCEDDDEWCMCPGSIYVTATNFCPPNFALPNNAGWCNPPQOHFDLSQVFORIAQYRAGI 124
QY 144 VPSFRVPCMKKGGVFTINGHSYFNLVLTNVGAGDVHSVSIKSGRTGWSKSRNMGON 202

DB 125 VPARFRVPCCKGSGIRFTINGHSYFNLVLTNVGAGDVHSVSIKSGRTGWSKSRNMGON 184
QY 203 GQNMOSNNYLNQGLSFQVTLSDGRTLTAYNLVPSNMQFQTYEGPOF 250
DB 185 GQNMOSNNYLNQGLSFQVTLSDGRTLTAYNLVPSNMQFQTYEGPOF 232

RESULT 9

US-08-440-517A-6
Sequence 6, Application US/08440517A
Patent No. 5959082

GENERAL INFORMATION:
APPLICANT: COSGROVE, DANIEL J.;
APPLICANT: GUILTINAN, MARK;
APPLICANT: SHERIDAN, TATIANA;
APPLICANT: SHI, JUN
TITLE OF INVENTION: PURIFIED EXPANSIN PROTEINS
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSER: INTELLECTUAL PROPERTY OFFICE, THE
ADDRESSEE: PENNSYLVANIA STATE UNIVERSITY
STREET: 113 TECHNOLOGY CENTER
CITY: UNIVERSITY PARK
STATE: PENNSYLVANIA
COUNTRY: UNITED STATES OF AMERICA
ZIP: 16802-7000
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: NEC 286
OPERATING SYSTEM: DOS
SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/440,517A
FILING DATE:
CLASSIFICATION: 530
INFORMATION FOR SEQ ID NO: 6
SEQUENCE CHARACTERISTICS:
LENGTH: 226
TYPE: AMINO ACID
TOPOLOGY: UNKNOWN
US-08-440-517A-6

Query Match 72.6%; Score 1011.5; DB 2; Length 226;
Best Local Similarity 77.1%; Pred. No. 4.7e-91;
Matches 175; Conservative 23; Mismatches 28; Indels 1; Gaps 1;

QY 24 DYGMOSGATFFYGAGDSGTMGACGYNLYSOGYGTNTALSTALFNNGLSCGACPEM 83
DB 1 DYSSMOSHAHTFFYGAGDSGTMGACGYNLYSOGYGTNTALSTALFNNGLSCGACPEM 59
QY 84 TCTNDPKWCLPGTIRVTATNFCPPNFALPNNNGWCNPPLOHFDMAEPALQIAYRAGI 143
DB 60 RCDNDGQWCLPGSIYVTATNFCPPNFALPNNAGWCNPPQOHFDLSQVFORIAQYRAGI 119
QY 144 VPSFRVPCMKKGGVFTINGHSYFNLVLTNVGAGDVHSVSIKSGRTGWSKSRNMGON 203
DB 120 VPSFRVPCMKKGGVFTINGHSYFNLVLTNVGAGDVHSVSIKSGRTGWSKSRNMGON 179
QY 204 QNMOSNNYLNQGLSFQVTLSDGRTLTAYNLVPSNMQFQTYEGPOF 250
DB 180 QNMOSNNYLNQGLSFQVTLSDGRTLTAYNLVPSNMQFQTYEGPOF 226

RESULT 10

US-09-092-160-6
Sequence 6, Application US/09092160C
Patent No. 6255466

GENERAL INFORMATION:
APPLICANT: COSGROVE, DANIEL J.
APPLICANT: McQUEEN-MASON, SIMON
APPLICANT: GUILTINAN, MARK J.
APPLICANT: SHERIDAN, TATIANA
APPLICANT: SHI, JUN

;; TITLE OF INVENTION: PURIFIED EXPANSIN PROTEINS
;; FILE REFERENCE: 1194/1C114US3
;; CURRENT APPLICATION NUMBER: US/09/092,160C
;; EARLIER FILING DATE: 1998-06-05
;; EARLIER APPLICATION NUMBER: 08/440,517
;; EARLIER FILING DATE: 1995-05-12
;; EARLIER APPLICATION NUMBER: 08/242,090
;; EARLIER FILING DATE: 1994-05-12
;; EARLIER APPLICATION NUMBER: 08/060,944
;; EARLIER FILING DATE: 1993-05-12
;; NUMBER OF SEQ ID NOS: 7
;; SOFTWARE: PatentIn Ver. 2.1
;; SEQ ID NO: 6
;; LENGTH: 226
;; TYPE: PRT
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: Description of Artificial Sequence: Arabidopsis
;; OTHER INFORMATION: expansin
US-09-092-160-6

Query Match 72.6%; Score 1011.5; DB 3; Length 226;
Best Local Similarity 77.1%; Pred. No. 4.7e-91;
Matches 175; Conservative 23; Mismatches 28; Indels 1; Gaps 1;

QY 24 DYGMOSGHATFYGGDASGTMGACGYGNLYSQYGTNTVALSTALFNNGLSCGACFEM 83
DB 1 DYSWQSAHATFYGGDASGTMGACGYGNLYSQYGTNTVALSTALFNNGLSCGACFEL 59
QY 84 TCTNDPRMCLPGTIRVATATNFCPPNFALPNNNGMCPNLPQHEDMAEPALQIAQYRAGI 143
DB 60 RCDNDGWCMLPGSVTVATATNLCPPNFALPNDGGMCPNPRHFMAPAFQIAQYRAGI 119
QY 144 VPVSFRVPCMKKGAVFTINGHSYFNLVLTITVAGAGDVHSVSIKSRGCMQMSRNMW 203
DB 120 VPVSFRVPCMKKGAVFTINGHSYFNLVLTITVAGAGDVHSVSIKSRGCMQMSRNMW 179
QY 204 QNMQSNNTYLDGQSLSFQVTLSDGRTLTAVNLVPSNMQFGQTEGPOF 250
DB 180 QNMQSNNTYLDGQSLSFQVTLSDGRTLTAVNLVPSNMQFGQTEGPOF 226

RESULT 11
US-08-440-517A-5
;; Sequence 5, Application US/08440517A
;; Patent No.: 5959082
;; GENERAL INFORMATION:
;; APPLICANT: COSGROVE, DANIEL J.;
;; APPLICANT: GUILTINAN, MARK;
;; APPLICANT: SHCHERBAN, TATYANA;
;; APPLICANT: SHI, JUN
;; TITLE OF INVENTION: PURIFIED EXPANSIN PROTEINS
;; NUMBER OF SEQUENCES: 6
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: INTELLECTUAL PROPERTY OFFICE, THE
;; ADDRESS: PENNSYLVANIA STATE UNIVERSITY
;; STREET: 113 TECHNOLOGY CENTER
;; CITY: UNIVERSITY PARK
;; STATE: PENNSYLVANIA
;; COUNTRY: UNITED STATES OF AMERICA
;; ZIP: 16802-7000
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: FLOPPY DISK
;; COMPUTER: NEC 286
;; OPERATING SYSTEM: DOS
;; SOFTWARE: WORDPERFECT 5.1
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/440,517A
;; FILING DATE:
;; CLASSIFICATION: 530
;; INFORMATION FOR SEQ ID NO: 5:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 225

;; TYPE: AMINO ACID
;; TOPOLOGY: UNKNOWN
US-08-440-517A-5

Query Match 69.0%; Score 962; DB 2; Length 225;
Best Local Similarity 75.0%; Pred. No. 3.2e-86;
Matches 171; Conservative 26; Mismatches 27; Indels 4; Gaps 2;

QY 24 DYGMOSGHATFYGGDASGTMGACGYGNLYSQYGTNTVALSTALFNNGLSCGACFEM 83
DB 1 DNGMERGHATFYGGDASGTMGACGYGNLYSQYGTNTVALSTALFNNGLSCGACFEL 60
QY 84 TCTNDPRMCLPGTIRVATATNFCPPNFALPNNNGMCPNLPQHEDMAEPALQIAQYRAGI 143
DB 61 TCDDPEWCIPGSIIV---RYNLANFALANDNGMCPNLPKHFDLAEPAFLQIAQYRAGI 117
QY 144 VPVSFRVPCMKKGAVFTINGHSYFNLVLTITVAGAGDVHSVSIKSRGCMQMSRNMW 202
DB 118 VPVSFRVPCMKKGAVFTINGHSYFNLVLTITVAGAGDVHSVSIKSRGCMQMSRNMW 177
QY 203 GNMQSNNTYLDGQSLSFQVTLSDGRTLTAVNLVPSNMQFGQTEGPOF 250
DB 178 GNMQSNNTYLDGQSLSFQVTLSDGRTLTAVNLVPSNMQFGQTEGPOF 225

RESULT 12
US-09-092-160-5
;; Sequence 5, Application US/09092160C
;; Patent No. 6235466
;; GENERAL INFORMATION:
;; APPLICANT: Cosgrove, Daniel J
;; APPLICANT: McQueen-Mason, Simon
;; APPLICANT: Guiltinan, Mark J
;; APPLICANT: Scherban, Tatyana
;; APPLICANT: Shi, Jun
;; TITLE OF INVENTION: PURIFIED EXPANSIN PROTEINS
;; FILE REFERENCE: 1194/1C114US3
;; CURRENT APPLICATION NUMBER: US/09/092,160C
;; CURRENT FILING DATE: 1998-06-05
;; EARLIER APPLICATION NUMBER: 08/440,517
;; EARLIER FILING DATE: 1995-05-12
;; EARLIER APPLICATION NUMBER: 08/242,090
;; EARLIER FILING DATE: 1994-05-12
;; EARLIER APPLICATION NUMBER: 08/060,944
;; EARLIER FILING DATE: 1993-05-12
;; NUMBER OF SEQ ID NOS: 7
;; SOFTWARE: PatentIn Ver. 2.1
;; SEQ ID NO: 5
;; LENGTH: 225
;; TYPE: PRT
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: Description of Artificial Sequence: Arabidopsis
;; OTHER INFORMATION: expansin
US-09-092-160-5

Query Match 69.0%; Score 962; DB 3; Length 225;
Best Local Similarity 75.0%; Pred. No. 3.2e-86;
Matches 171; Conservative 26; Mismatches 27; Indels 4; Gaps 2;

QY 24 DYGMOSGHATFYGGDASGTMGACGYGNLYSQYGTNTVALSTALFNNGLSCGACFEM 83
DB 1 DNGMERGHATFYGGDASGTMGACGYGNLYSQYGTNTVALSTALFNNGLSCGACFEL 60
QY 84 TCTNDPRMCLPGTIRVATATNFCPPNFALPNNNGMCPNLPQHEDMAEPALQIAQYRAGI 143
DB 61 TCDDPEWCIPGSIIV---RYNLANFALANDNGMCPNLPKHFDLAEPAFLQIAQYRAGI 117
QY 144 VPVSFRVPCMKKGAVFTINGHSYFNLVLTITVAGAGDVHSVSIKSRGCMQMSRNMW 202
DB 118 VPVSFRVPCMKKGAVFTINGHSYFNLVLTITVAGAGDVHSVSIKSRGCMQMSRNMW 177
QY 203 GNMQSNNTYLDGQSLSFQVTLSDGRTLTAVNLVPSNMQFGQTEGPOF 250

Db 178 GQMOSNTYLRGQSLSFQVTLSDGRIVSVDPVPHMQGQIFEGQF 225

RESULT 13
US-09-112-498A-10
Sequence 10, Application US/09112498A
Patent No. 6458928

GENERAL INFORMATION:

APPLICANT:

TITLE OF INVENTION: MICROBIAL SWOLLENIN PROTEIN, DNA SEQUENCES

TITLE OF INVENTION: ENCODING SUCH SWOLLENINS AND METHOD OF PRODUCING SUCH

TITLE OF INVENTION: SWOLLENINS

NUMBER OF SEQUENCES: 31

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent in Release #1.0, Version #1.25 (EPO)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/112,498A

FILING DATE:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 98/14226

FILING DATE:

APPLICATION NUMBER: US 08/893,766

FILING DATE: 11-JUL-1997

INFORMATION FOR SEQ ID NO: 10:

SEQUENCE CHARACTERISTICS:

LENGTH: 241 amino acids

TYPE: amino acid

TOPOLOGY: unknown

MOLECULE TYPE: protein

US-09-112-498A-10

Query Match 67.4%; Score 939; DB 4; Length 241;

Best Local Similarity 70.9%; Pred. No. 6.2e-84;

Matches 161; Conservative 29; Mismatches 35; Indels 2; Gaps 1;

QY 26 GQMOSGHATFYGGDASGTMGACGYGNLYSQGYGNTVALSTALFNNGLSCGACFEMTC 85

Db 13 GQMETAHATFYGGSDASGTMGACGYGNLYSQGYGNTVALSTALFNNGLSCGACFELKC 72

QY 86 TNDPKKCLPG--TIRVATNFCPPNFALPNNNGWCNPELQHPDMAEPALQIAQYRAGI 143

Db 73 ASDPKWCHSGSPSIFLTATNFCPPNPAQPSDNGWCNPPPHDLAMPFLKIAEYRAGI 132

QY 144 VEVSPFRVPCMKKGVRFTINGHSYFNVLITVNVGAGDVHVSIGKSRGTGQMSGRNMG 203

Db 133 VEVSPFRVPCMKKGVRFTINGHSYFNVLITVNVGAGDVHVSIGKSRGTGQMSGRNMG 192

QY 204 QNMOSNNYLNQGLSFQVTLSDGRITLTVANLVPSNMQFGQTEGPOF 250

Db 193 QNMOSNVLVQGLSFRVTSSDRSSTSNVIAANMKFGQTEGKNF 239

RESULT 14
US-09-112-498A-13
Sequence 13, Application US/09112498A
Patent No. 6458928

GENERAL INFORMATION:

APPLICANT:

TITLE OF INVENTION: MICROBIAL SWOLLENIN PROTEIN, DNA SEQUENCES

TITLE OF INVENTION: ENCODING SUCH SWOLLENINS AND METHOD OF PRODUCING SUCH

TITLE OF INVENTION: SWOLLENINS

NUMBER OF SEQUENCES: 31

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent in Release #1.0, Version #1.25 (EPO)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/112,498A

FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 98/14226

FILING DATE: US 08/893,766

FILING DATE: 11-JUL-1997

INFORMATION FOR SEQ ID NO: 13:

SEQUENCE CHARACTERISTICS:

LENGTH: 258 amino acids

TYPE: amino acid

TOPOLOGY: unknown

MOLECULE TYPE: protein

US-09-112-498A-13

Query Match 67.2%; Score 937; DB 4; Length 258;

Best Local Similarity 72.7%; Pred. No. 1.1e-83;

Matches 165; Conservative 21; Mismatches 39; Indels 2; Gaps 1;

QY 26 GQMOSGHATFYGGDASGTMGACGYGNLYSQGYGNTVALSTALFNNGLSCGACFEMTC 85

Db 30 GQWTAHATFYGGSDASGTMGACGYGNLYSQGYGNTVALSTALFNNGLSCGACFELKC 89

QY 86 TNDPKKCLPG--TIRVATNFCPPNFALPNNNGWCNPELQHPDMAEPALQIAQYRAGI 143

Db 90 DQDPKCNPNPSILITATNFCPPNPAQPSDNGWCNPPPHDLAMPFLKIAEYRAGI 149

QY 144 VEVSPFRVPCMKKGVRFTINGHSYFNVLITVNVGAGDVHVSIGKSRGTGQMSGRNMG 203

Db 150 VEVSPFRVPCMKKGVRFTINGHSYFNVLITVNVGAGDVHVSIGKSRGTGQMSGRNMG 209

QY 204 QNMOSNNYLNQGLSFQVTLSDGRITLTVANLVPSNMQFGQTEGPOF 250

Db 210 QNMOSNAVFGQLSFRVTGSDRISTSNVAVPPIHQGQITGKNF 256

RESULT 15
US-09-112-498A-9

Sequence 9, Application US/09112498A

Patent No. 6458928

GENERAL INFORMATION:

APPLICANT:

TITLE OF INVENTION: MICROBIAL SWOLLENIN PROTEIN, DNA SEQUENCES

TITLE OF INVENTION: ENCODING SUCH SWOLLENINS AND METHOD OF PRODUCING SUCH

TITLE OF INVENTION: SWOLLENINS

NUMBER OF SEQUENCES: 31

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent in Release #1.0, Version #1.25 (EPO)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/112,498A

FILING DATE:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 98/14226

FILING DATE:

APPLICATION NUMBER: US 08/893,766

FILING DATE: 11-JUL-1997

INFORMATION FOR SEQ ID NO: 9:

SEQUENCE CHARACTERISTICS:

LENGTH: 233 amino acids

TYPE: amino acid

TOPOLOGY: unknown

MOLECULE TYPE: protein

US-09-112-498A-9

Query Match 63.8%; Score 889.5; DB 4; Length 233;

Best Local Similarity 69.5%; Pred. No. 4e-79;

Matches 157; Conservative 26; Mismatches 34; Indels 9; Gaps 2;

QY 26 GQMOSGHATFYGGDASGTMGACGYGNLYSQGYGNTVALSTALFNNGLSCGACFEMTC 85

Db 14 GQWTAHATFYGGSDASGTMGACGYGNLYSQGYGNTVALSTALFNNGLSCGACFELKC 73

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: December 18, 2003, 17:49:54 ; Search time 32 Seconds
(without alignments)
1459.052 Million cell updates/sec

Title: US-09-383-579C-10

Perfect score: 1394

Sequence: 1 MAFYSFSSFLPLPFV.....AYNLVSNMFGQTYGPGP 250

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 696363 seqs, 186758610 residues

Total number of hits satisfying chosen parameters: 696363

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:*

1: /cgn2_6/ptodata/2/pubppaa/US07_PUBCOMB.pep:*

2: /cgn2_6/ptodata/2/pubppaa/PCT_NEW_PUB.pep:*

3: /cgn2_6/ptodata/2/pubppaa/US06_NEW_PUB.pep:*

4: /cgn2_6/ptodata/2/pubppaa/US06_PUBCOMB.pep:*

5: /cgn2_6/ptodata/2/pubppaa/US07_NEW_PUB.pep:*

6: /cgn2_6/ptodata/2/pubppaa/PCTUS_PUBCOMB.pep:*

7: /cgn2_6/ptodata/2/pubppaa/US08_NEW_PUB.pep:*

8: /cgn2_6/ptodata/2/pubppaa/US08_PUBCOMB.pep:*

9: /cgn2_6/ptodata/2/pubppaa/US09_PUBCOMB.pep:*

10: /cgn2_6/ptodata/2/pubppaa/US09_PUBCOMB.pep:*

11: /cgn2_6/ptodata/2/pubppaa/US09_PUBCOMB.pep:*

12: /cgn2_6/ptodata/2/pubppaa/US09_NEW_PUB.pep:*

13: /cgn2_6/ptodata/2/pubppaa/US10_PUBCOMB.pep:*

14: /cgn2_6/ptodata/2/pubppaa/US10_PUBCOMB.pep:*

15: /cgn2_6/ptodata/2/pubppaa/US10_PUBCOMB.pep:*

16: /cgn2_6/ptodata/2/pubppaa/US10_NEW_PUB.pep:*

17: /cgn2_6/ptodata/2/pubppaa/US60_NEW_PUB.pep:*

18: /cgn2_6/ptodata/2/pubppaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1265	90.7	227	10 US-09-896-301-7	Sequence 7, Appl1
2	1228	88.1	225	15 US-10-197-294A-6	Sequence 6, Appl1
3	1131	81.1	223	15 US-10-197-294A-4	Sequence 4, Appl1
4	1109.5	79.6	222	15 US-10-197-294A-5	Sequence 5, Appl1
5	1044	74.9	258	12 US-10-150-559-4	Sequence 4, Appl1
6	1035	74.2	233	15 US-10-197-294A-12	Sequence 12, Appl1
7	1027	73.7	253	12 US-10-409-701-9	Sequence 9, Appl1
8	1026	73.6	228	15 US-09-896-301-2	Sequence 2, Appl1
9	1017.5	72.0	236	15 US-10-197-294A-8	Sequence 8, Appl1
10	1013.5	72.7	232	15 US-10-197-294A-9	Sequence 9, Appl1
11	1011.5	72.6	225	10 US-09-896-301-6	Sequence 6, Appl1
12	962	69.0	225	10 US-09-896-301-5	Sequence 5, Appl1
13	940	67.4	241	15 US-10-197-294A-11	Sequence 11, Appl1
14	937	67.2	237	15 US-10-197-294A-14	Sequence 14, Appl1
15	889.5	63.8	233	15 US-10-197-294A-10	Sequence 10, Appl1

16	884	63.4	234	15 US-10-197-294A-7	Sequence 7, Appl1
17	857.5	61.5	222	10 US-09-896-301-3	Sequence 3, Appl1
18	814	58.4	232	15 US-10-197-294A-13	Sequence 13, Appl1
19	773.5	55.5	227	10 US-09-896-301-4	Sequence 4, Appl1
20	362.5	26.0	227	15 US-10-125-001-20	Sequence 20, Appl1
21	302.5	21.7	239	15 US-10-125-001-22	Sequence 22, Appl1
22	294	21.1	308	15 US-10-125-001-14	Sequence 4, Appl1
23	273	19.6	245	15 US-10-125-001-14	Sequence 14, Appl1
24	266.5	19.1	282	12 US-10-102-349-2	Sequence 2, Appl1
25	266.5	19.1	282	12 US-10-102-349-4	Sequence 4, Appl1
26	266.5	19.1	282	15 US-10-125-001-2	Sequence 2, Appl1
27	262.5	18.8	265	15 US-10-125-001-12	Sequence 12, Appl1
28	253.5	18.2	239	12 US-10-259-165-276	Sequence 276, App
29	246	17.6	283	12 US-10-409-701-11	Sequence 11, Appl1
30	239	17.1	263	9 US-09-811-572-10	Sequence 10, Appl1
31	239	17.1	263	11 US-09-847-208-138	Sequence 138, App
32	236.5	17.0	240	9 US-09-949-888-2	Sequence 2, Appl1
33	232.5	16.7	265	11 US-09-847-208-107	Sequence 107, App
34	232	16.6	231	15 US-10-125-001-11	Sequence 11, Appl1
35	229	16.4	263	11 US-09-847-208-112	Sequence 112, App
36	220.5	15.8	269	11 US-09-847-208-133	Sequence 133, Appl
37	206.5	14.8	222	12 US-10-259-165-392	Sequence 44, Appl
38	206.5	14.8	222	12 US-10-259-165-392	Sequence 392, App
39	192.5	13.8	263	11 US-09-847-208-127	Sequence 127, App
40	185.5	13.3	180	15 US-10-125-001-13	Sequence 13, Appl1
41	185	13.3	191	11 US-09-847-208-173	Sequence 173, App
42	150.5	10.8	332	15 US-10-197-294A-3	Sequence 3, Appl1
43	150.5	10.8	483	15 US-10-197-294A-2	Sequence 2, Appl1
44	109.5	7.9	138	15 US-10-125-001-19	Sequence 19, Appl1
45	100.5	7.2	54	12 US-10-161-660-12	Sequence 12, Appl1

ALIGNMENTS

RESULT 1

US-09-896-301-7

Sequence 7, Application US/09896301

Patent No. US20020103355A1

GENERAL INFORMATION:

APPLICANT: Cosgrove, Daniel J

APPLICANT: McQueen-Mason, Simon

APPLICANT: Gullitman, Mark J

APPLICANT: Shcherban, Tatyana

APPLICANT: Shi, Jun

TITLE OF INVENTION: PURIFIED EXPANSIN PROTEINS

FILE REFERENCE: 1194/1C114US3

CURRENT APPLICATION NUMBER: US/09/896,301

PRIOR FILING DATE: 2001-06-29

PRIOR APPLICATION NUMBER: 09/092,160

PRIOR FILING DATE: 1998-06-05

PRIOR APPLICATION NUMBER: 08/440,517

PRIOR FILING DATE: 1995-05-12

PRIOR APPLICATION NUMBER: 08/242,090

PRIOR FILING DATE: 1994-05-12

PRIOR APPLICATION NUMBER: 08/060,944

PRIOR FILING DATE: 1993-05-12

NUMBER OF SEQ ID NOS: 7

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 7

LENGTH: 227

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Description of Artificial Sequence: cucumber

OTHER INFORMATION: expansin

US-09-896-301-7

Query Match 90.7%; Score 1265; DB 10; Length 227;

Best Local Similarity 99.1%; Pred. No. 2.4e-118;

Matches 225; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

CY 24 DYGMOSGHATFYGGDASGTWAGAGYGNLYSGYGTNTVALSTALFNNGLSGACFEM 83

```

Db      1 DYGGWOSGATPYGGDDAGTGMGACGYGNLYSGYGTNTVALSTLFPNNGLSGCACFEM 60
        |||
Qy      84 TCTNDPKMCLPGTIRVTATNFCPPNFALPNNNGMWCNPPLOHFDMAEPALQIAYRAGI 143
        |||
Db      61 TCTNDPKMCLPGTIRVTATNFCPPNFALPNDGMCNPPLOHFDMAEPALQIAYRAGI 120
        |||
Qy      144 VVVSFRVRCMKKGGVRFITNGHSYFNVLITNVGAGADVHSVSIKSGRTGQMSRRNG 203
        |||
Db      121 VVVSFRVRCMKKGGVRFITNGHSYFNVLITNVGAGADVHSVSIKSGRTGQMSRRNG 180
        |||
Qy      204 QMWOSNNYLNQGLSFQVTLSDGRTLTAYNLVPSNMQFGQTYEGPOF 250
        |||
Db      181 QMWOSNNYLNQGLSFQVTLSDGRTLTAYNLVPSNMQFGQTYEGPOF 227
        |||

```

RESULT 2 US-10-197-294A-6

```

; Sequence 6, Application US/10197294A
; Publication No. US20030104546A1
; GENERAL INFORMATION:
; APPLICANT: Swanson, Barbara A.
; APPLICANT: Ward, Michael
; APPLICANT: Penttila, Merja
; APPLICANT: Pere, Jaakko
; APPLICANT: Saloheimo, Markku
; TITLE OF INVENTION: Microbial Swollenin Protein, DNA
; TITLE OF INVENTION: Sequences Encoding Such Swollenins and Method of Producing
; FILE REFERENCE: GC378-2-D1
; CURRENT APPLICATION NUMBER: US/10/197,294A
; CURRENT FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: US 09/112,498
; PRIOR FILING DATE: 1998-07-09
; PRIOR APPLICATION NUMBER: US 08/893,766
; PRIOR FILING DATE: 1997-07-11
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FaastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 225
; TYPE: PRT
; ORGANISM: Plant/eukaryotic
US-10-197-294A-6

```

Query Match 88.1%; Score 1228; DB 15; Length 225;
Best Local Similarity 98.2%; Pred. No. 1.2e-114;
Matches 223; Conservative 1; Mismatches 1; Indels 2; Gaps 2;

```

Qy      24 DYGGWOSGATPYGGDDAGTGMGACGYGNLYSGYGTNTVALSTLFPNNGLSGCACFEM 83
        |||
Db      1 DYGGWOSGATPYGGDDAGTGMGACGYGNLYSGYGTNTVALSTLFPNNGLSGCACFEM 60
        |||
Qy      84 TCTNDPKMCLPGTIRVTATNFCPPNFALPNNNGMWCNPPLOHFDMAEPALQIAYRAGI 143
        |||
Db      61 TCTNDPKMCLPGTIRVTATNFCPPNFALPNNNGMWCNPPLOHFDMAEPALQIAYRAGI 118
        |||
Qy      144 VVVSFRVRCMKKGGVRFITNGHSYFNVLITNVGAGADVHSVSIKSGRTGQMSRRNG 203
        |||
Db      119 VVVSFRVRCMKKGGVRFITNGHSYFNVLITNVGAGADVHSVSIKSGRTGQMSRRNG 178
        |||
Qy      204 QMWOSNNYLNQGLSFQVTLSDGRTLTAYNLVPSNMQFGQTYEGPOF 250
        |||
Db      179 QMWOSNNYLNQGLSFQVTLSDGRTLTAYNLVPSNMQFGQTYEGPOF 225
        |||

```

RESULT 3 US-10-197-294A-4

```

; Sequence 4, Application US/10197294A
; Publication No. US20030104546A1
; GENERAL INFORMATION:
; APPLICANT: Swanson, Barbara A.
; APPLICANT: Ward, Michael
; APPLICANT: Penttila, Merja

```

```

; APPLICANT: Pere, Jaakko
; APPLICANT: Saloheimo, Markku
; TITLE OF INVENTION: Microbial Swollenin Protein, DNA
; TITLE OF INVENTION: Sequences Encoding Such Swollenins and Method of Producing
; FILE REFERENCE: GC378-2-D1
; CURRENT APPLICATION NUMBER: US/10/197,294A
; CURRENT FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: US 09/112,498
; PRIOR FILING DATE: 1998-07-09
; PRIOR APPLICATION NUMBER: US 08/893,766
; PRIOR FILING DATE: 1997-07-11
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FaastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 223
; TYPE: PRT
; ORGANISM: Trichoderma reesei
US-10-197-294A-4

```

Query Match 81.1%; Score 1131; DB 15; Length 223;
Best Local Similarity 88.4%; Pred. No. 5.8e-105;
Matches 199; Conservative 16; Mismatches 8; Indels 2; Gaps 2;

```

Qy      26 DYGGWOSGATPYGGDDAGTGMGACGYGNLYSGYGTNTVALSTLFPNNGLSGCACFEM 85
        |||
Db      1 DYGGWOSGATPYGGDDAGTGMGACGYGNLYSGYGTNTVALSTLFPNNGLSGCACFEM 60
        |||
Qy      86 TNDPKMCLPGTIRVTATNFCPPNFALPNNNGMWCNPPLOHFDMAEPALQIAYRAGI 145
        |||
Db      61 DNDPKMCLPGTIRVTATNFCPPNFALPNNNGMWCNPPLOHFDMAEPALQIAYRAGI 120
        |||
Qy      146 VVVSFRVRCMKKGGVRFITNGHSYFNVLITNVGAGADVHSVSIKSGRTGQMSRRNG 205
        |||
Db      121 VVVSFRVRCMKKGGVRFITNGHSYFNVLITNVGAGADVHSVSIKSGRTGQMSRRNG 180
        |||
Qy      206 QMWOSNNYLNQGLSFQVTLSDGRTLTAYNLVPSNMQFGQTYEGPOF 250
        |||
Db      181 QMWOSNNYLNQGLSFQVTLSDGRTLTAYNLVPSNMQFGQTYEGPOF 223
        |||

```

RESULT 4 US-10-197-294A-5

```

; Sequence 5, Application US/10197294A
; Publication No. US20030104546A1
; GENERAL INFORMATION:
; APPLICANT: Swanson, Barbara A.
; APPLICANT: Ward, Michael
; APPLICANT: Penttila, Merja
; APPLICANT: Pere, Jaakko
; APPLICANT: Saloheimo, Markku
; TITLE OF INVENTION: Microbial Swollenin Protein, DNA
; TITLE OF INVENTION: Sequences Encoding Such Swollenins and Method of Producing
; FILE REFERENCE: GC378-2-D1
; CURRENT APPLICATION NUMBER: US/10/197,294A
; CURRENT FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: US 09/112,498
; PRIOR FILING DATE: 1998-07-09
; PRIOR APPLICATION NUMBER: US 08/893,766
; PRIOR FILING DATE: 1997-07-11
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FaastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 222
; TYPE: PRT
; ORGANISM: Plant/eukaryotic
US-10-197-294A-5

```

Query Match 79.6%; Score 1109.5; DB 15; Length 222;
Best Local Similarity 88.0%; Pred. No. 8.1e-103;
Matches 198; Conservative 16; Mismatches 8; Indels 3; Gaps 3;

```

Qy      26 GGMOSGHATFYGGDASGTMGACGYGNLYSGYGTNTVALSTALFNNGLSCGACFEMTC 85
        1 GGMOSAHATFYGGDASGTMGACGYGNLYSGYGTNTVALSTALFNNGLSCGACFELTC 60
Db      86 TNDKMCPLPGTIRYATATNFCPPNFALPNNNGMGCNPPLOHFDMAEPALQIAOYRAGIVP 145
        61 DNDK-CLPGSITVATNFCPPNFALPNNNGMGCNPPLOHFDMAEPALQIAOYRAGIVP 119
Qy      146 VSPRVRVCMKKGVRFITNGHSYFNLYLITNVGAGDVHSVIGSRITGQMSMRNGON 205
        120 VAYRVRVCKKRGGRFTNGHSYFNLYLITNVGAGDVHSVIGSRITGQMSMRNGON 179
Db      206 WQSNNYLNGGSLSFQVTLSDGRITLTAVALVPSNMQFCQTYGPOF 250
        180 WQSNYLNNGGSLSFQVTLSDGRITLTAVALVPSNMQFCQTF-GGQF 222

```

```

RESULT 5
US-10-150-559-4
; Sequence 4, Application US/10150559
; Publication No. US20030221218A1
; GENERAL INFORMATION:
; APPLICANT: Wilkins, Thea A.
; TITLE OF INVENTION: The Regence of the University of California
; FILE REFERENCE: 023070-116500US
; CURRENT APPLICATION NUMBER: US/10/150,559
; CURRENT FILING DATE: 2002-05-17
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: Patentn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 258
; TYPE: PRT
; ORGANISM: Geosyrium hirsutum
US-10-150-559-4

```

```

Query Match      74.9%; Score 1044; DB 12; Length 258;
Best Local Similarity 74.3%; Pred. No. 3.4e-96;
Matches 182; Conservative 27; Mismatches 26; Indels 10; Gaps 1;

```

```

Qy      16 FFFVFTFA-----DYGMOSGHATFYGGDASGTMGACGYGNLYSGYGTNTVA 65
        14 FFFLFISCNSTIFLGANGDDNGMOTAHATFYGADATGTMGACGYGNLYSGYGTSTAA 73
Db      66 LSTALFNNGLSCGACFEMTCNDKMCPLPGTIRYATATNFCPPNFALPNNNGMGCNPPLOH 125
        74 LSTALFNNGLSCGACFEMTCNDKMCPLPGTIRYATATNFCPPNFALPNNNGMGCNPPREH 133
Qy      126 FDMAEPALQIAOYRAGIVPVSFRRVPCMKKGVRFITNGHSYFNLYLITNVGAGDVHS 185
        134 FDMAEPALQIAOYRAGIVPVSFRRVPCMKKGVRFITNGHSYFNLYLITNVGAGDVHS 193
Db      186 VSIKSGRTGQMSMRNGONWQSNNYLNGGSLSFQVTLSDGRITLTAVALVPSNMQFCQTY 245
        194 VSIKSGRTGWLPMSSRNNGQWQSNNYLNGGSLSFQVTLSDGRITLTAVALVPSNMQFCQTF 253
Qy      246 EGPOF 250
        254 EGQOF 258
Db

```

```

RESULT 6
US-10-197-294A-12
; Sequence 12, Application US/10197294A
; Publication No. US20030104546A1
; GENERAL INFORMATION:
; APPLICANT: Swanson, Barbara A.
; APPLICANT: Ward, Michael
; APPLICANT: Penttila, Merja
; APPLICANT: Pere, Jaako
; APPLICANT: Saloheimo, Markku
; TITLE OF INVENTION: Microbial Swollenin Protein, DNA
; TITLE OF INVENTION: Sequences Encoding Such Swollenins and Method of Producing

```

```

; TITLE OF INVENTION: Such Swollenins
; FILE REFERENCE: GC378-2-D1
; CURRENT APPLICATION NUMBER: US/10/197,294A
; CURRENT FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: US 09/112,498
; PRIOR FILING DATE: 1998-07-09
; PRIOR APPLICATION NUMBER: US 08/893,766
; PRIOR FILING DATE: 1997-07-11
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12
; LENGTH: 233
; TYPE: PRT
; ORGANISM: Plant/eukaryotic
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (1)...(233)
; OTHER INFORMATION: Xaa = Any Amino Acid
US-10-197-294A-12

```

```

Query Match      74.2%; Score 1035; DB 15; Length 233;
Best Local Similarity 78.1%; Pred. No. 2.4e-95;
Matches 178; Conservative 23; Mismatches 27; Indels 0; Gaps 0;

```

```

Qy      23 ADYGMOSGHATFYGGDASGTMGACGYGNLYSGYGTNTVALSTALFNNGLSCGACFE 82
        6 ADYGMOSAHATFYGGDASGTMGACGYGNLYSGYGTNTVALSTALFNDGAACRCGYE 65
Db      83 MCTNDKMCPLPGTIRYATATNFCPPNFALPNNNGMGCNPPLOHFDMAEPALQIAOYRAG 142
        66 LRCNDQMCPLPGSVTVATNTLCPNFALPNDQGMGCNPPRPHDMAEPALQIGYRAG 125
Qy      143 IVPSPRRVPCMKKGVRFITNGHSYFNLYLITNVGAGDVHSVIGSRITGQMSMRNW 202
        126 IVPSTRVPCVKKGVRFITNGHSYFNLYLITNVAGPQVQSVISGSSITGQPMSSRNW 185
Db      203 GQWQSNNYLNGGSLSFQVTLSDGRITLTAVALVPSNMQFCQTYGPOF 250
        186 GQWQSNYSYLDGSLSFQVAVSDGRITLTAVALVPSNMQFCQTFBGGQF 233

```

```

RESULT 7
US-10-409-701-9
; Sequence 9, Application US/10409701
; Publication No. US20030221224A1
; GENERAL INFORMATION:
; APPLICANT: Zinselmeier, Chris
; APPLICANT: Helentjaris, Timothy G.
; TITLE OF INVENTION: Enhanced Silk Excretion Under Stress
; FILE REFERENCE: 1421
; CURRENT APPLICATION NUMBER: US/10/409,701
; CURRENT FILING DATE: 2003-04-08
; PRIOR APPLICATION NUMBER: US 60/370,796
; PRIOR FILING DATE: 2002-04-08
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 253
; TYPE: PRT
; ORGANISM: Zea mays
US-10-409-701-9

```

```

Query Match      73.7%; Score 1027; DB 12; Length 253;
Best Local Similarity 78.0%; Pred. No. 1.7e-94;
Matches 177; Conservative 25; Mismatches 25; Indels 0; Gaps 0;

```

```

Qy      24 DYGMOSGHATFYGGDASGTMGACGYGNLYSGYGTNTVALSTALFNNGLSCGACFEM 83
        27 DYGMOSAHATFYGGDASGTMGACGYGNLYSGYGTNTVALSTALFNDGAACGCTEL 86
Db      84 TCTNDKMCPLPGTIRYATATNFCPPNFALPNNNGMGCNPPLOHFDMAEPALQIAOYRAGI 143
        87 RCNDNGQSLPGTITVATNFCPPNFALPNDQGMGCNPPRPHDMAEPALQIAOYRAGI 146

```

QY 144 VPSRPRVPCMKKGVRTFTINGHSYFNLVLTITVVGAGDVHSVSIKSGRTGQMSRRNG 203
 DB 147 VVAVYRVPCVKKGGIRFTINGHSYFNLVLTITVVGAGDVHSVSIKSGRTGQMSRRNG 206
 QY 204 QNMOSNNYINGQSLSPQVTLSDGRTLTAVNLVPSNMQFGQYEGPQF 250
 DB 207 QNMOSNLLDGQSLSPQVTLSDGRTLTAVNLVPSNMQFGQYEGPQF 253

RESULT 8

US-09-896-301-2
 ; Sequence 2, Application US/09896301
 ; Patent No. US20020103355A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Cosgrove, Daniel J
 ; APPLICANT: McQueen-Mason, Simon
 ; APPLICANT: Guillean, Mark J
 ; APPLICANT: Shcherban, Tatyana
 ; APPLICANT: Shi, Jun
 ; TITLE OF INVENTION: PURIFIED EXPANSIN PROTEINS
 ; FILE REFERENCE: 1194/1C114US3
 ; CURRENT APPLICATION NUMBER: US/09/896,301
 ; CURRENT FILING DATE: 2001-06-29
 ; PRIOR APPLICATION NUMBER: 09/092,160
 ; PRIOR FILING DATE: 1998-06-05
 ; PRIOR APPLICATION NUMBER: 08/440,517
 ; PRIOR FILING DATE: 1995-05-12
 ; PRIOR APPLICATION NUMBER: 08/242,090
 ; PRIOR FILING DATE: 1994-05-12
 ; PRIOR APPLICATION NUMBER: 08/060,944
 ; PRIOR FILING DATE: 1993-05-12
 ; NUMBER OF SEQ ID NOS: 7
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 2
 ; LENGTH: 228
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence: rice expansin
 ; NAME/KEY: UNSURE
 ; LOCATION: 211
 ; OTHER INFORMATION: Xaa is unknown or other.
 US-09-896-301-2

Query Match 73.6%; Score 1026; DB 10; Length 228;
 Best Local Similarity 79.3%; Pred. No. 1.9e-94;
 Matches 176; Conservative 22; Mismatches 24; Indels 0; Gaps 0;

QY 26 GGMOSGHATFYGGDASGTMGACGYGNLYSGYGTNTVALSTALFNNGLSGACCEBMT 85
 DB 3 GGMVNAHAATFYGGDASGTMGACGYGNLYSGYGTNTVALSTALFNNGLSGACCEBMT 62
 QY 86 TNDPKKCLPCTIRVTATNFCPPNFALPNNNGMCPNLPLOHFMABAPFLOIAGYRGIYV 145
 DB 63 QNDGKMC-PSISIVTATNFCPPNFALPNNNGMCPNLPLOHFMABAPFLOIAGYRGIYV 122
 QY 146 VSFRRVPCMKKGVRTFTINGHSYFNLVLTITVVGAGDVHSVSIKSGRTGQMSRRNG 205
 DB 123 VAVRVPVCRRGIRFTINGHSYFNLVLTITVVGAGDVHSVSIKSGRTGQMSRRNG 182
 QY 206 WOSNNYINGQSLSPQVTLSDGRTLTAVNLVPSNMQFGQYEG 247
 DB 183 WOSNNYINGQSLSPQVTLSDGRTLTAVNLVPSNMQFGQYEG 224

RESULT 9

US-10-197-294A-8
 ; Sequence 8, Application US/10197294A
 ; Publication No. US20030104546A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Swanson, Barbara A.
 ; APPLICANT: Ward, Michael

APPLICANT: Penttila, Merja
 APPLICANT: Pere, Jaakko
 APPLICANT: Saloheimo, Markku
 TITLE OF INVENTION: Microbial Swollenin Protein, DNA
 TITLE OF INVENTION: Sequences Encoding Such Swollenins and Method of Producing
 TITLE OF INVENTION: Such Swollenins
 FILE REFERENCE: GC378-2-D1
 CURRENT APPLICATION NUMBER: US/10/197,294A
 CURRENT FILING DATE: 2002-07-17
 PRIOR APPLICATION NUMBER: US 09/112,498
 PRIOR FILING DATE: 1998-07-09
 PRIOR APPLICATION NUMBER: US 08/893,766
 PRIOR FILING DATE: 1997-07-11
 NUMBER OF SEQ ID NOS: 40
 SOFTWARE: FastSeq for Windows Version 4.0
 SEQ ID NO 8
 LENGTH: 236
 TYPE: PRT
 ORGANISM: Plant/eukaryotic
 US-10-197-294A-8

Query Match 73.0%; Score 1017.5; DB 15; Length 236;
 Best Local Similarity 78.6%; Pred. No. 1.4e-93;
 Matches 176; Conservative 23; Mismatches 24; Indels 1; Gaps 1;

QY 26 GGMOSGHATFYGGDASGTMGACGYGNLYSGYGTNTVALSTALFNNGLSGACCEBMT 85
 DB 12 GGMVNAHAATFYGGDASGTMGACGYGNLYSGYGTNTVALSTALFNNGLSGACCEBMT 71
 QY 86 TNDPKKCLPCTIRVTATNFCPPNFALPNNNGMCPNLPLOHFMABAPFLOIAGYRGIYV 145
 DB 72 QNDGKMC-PSISIVTATNFCPPNFALPNNNGMCPNLPLOHFMABAPFLOIAGYRGIYV 130
 QY 146 VSFRRVPCMKKGVRTFTINGHSYFNLVLTITVVGAGDVHSVSIKSGRTGQMSRRNG 205
 DB 131 VAVRVPVCRRGIRFTINGHSYFNLVLTITVVGAGDVHSVSIKSGRTGQMSRRNG 190
 QY 206 WOSNNYINGQSLSPQVTLSDGRTLTAVNLVPSNMQFGQYEGPQF 249
 DB 191 WOSNNYINGQSLSPQVTLSDGRTLTAVNLVPSNMQFGQYEGPQF 234

RESULT 10

US-10-197-294A-9
 ; Sequence 9, Application US/10197294A
 ; Publication No. US20030104546A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Swanson, Barbara A.
 ; APPLICANT: Ward, Michael
 ; APPLICANT: Penttila, Merja
 ; APPLICANT: Pere, Jaakko
 ; APPLICANT: Saloheimo, Markku
 TITLE OF INVENTION: Microbial Swollenin Protein, DNA
 TITLE OF INVENTION: Sequences Encoding Such Swollenins and Method of Producing
 TITLE OF INVENTION: Such Swollenins
 FILE REFERENCE: GC378-2-D1
 CURRENT APPLICATION NUMBER: US/10/197,294A
 CURRENT FILING DATE: 2002-07-17
 PRIOR APPLICATION NUMBER: US 09/112,498
 PRIOR FILING DATE: 1998-07-09
 PRIOR APPLICATION NUMBER: US 08/893,766
 PRIOR FILING DATE: 1997-07-11
 NUMBER OF SEQ ID NOS: 40
 SOFTWARE: FastSeq for Windows Version 4.0
 SEQ ID NO 9
 LENGTH: 232
 TYPE: PRT
 ORGANISM: Plant/eukaryotic
 US-10-197-294A-9

Query Match 72.7%; Score 1013.5; DB 15; Length 232;
 Best Local Similarity 77.6%; Pred. No. 3.4e-93;
 Matches 177; Conservative 25; Mismatches 25; Indels 1; Gaps 1;

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: December 18, 2003, 22:33:47 ; Search time 2802 Seconds
(without alignments)
3650.038 Million cell updates/sec

Title: US-09-383-579c-10

Perfect score: 1394
Sequence: 1 MAFSYSPFSSLLFLPPFFVF.....AYNLVPSNMWQGTGTEGPPQ 250

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 2888711 seqs, 2045481386 residues

Total number of hits satisfying chosen parameters: 5777422

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
-MODEL=frame+ p2n.model -DEV=xld
-O=/cgr2.1/USPTO_spool_p/US93353579/runat_18122003_171927_28772/app_query.fasta_1.391
-DB=GenBml -OPMT=faetap -SUFFIX=rge -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS-bits -START=1 -END=1 -MATRIX=Diosum62 -TRANS=human40.cdi -LIST=45
-DOCALLGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pct -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USBR=US09383579 @CGN 1.1 4958 @runat_18122003_171927_28772 -NCPU=6 -ICPU=3
-NO_MMP -LARGEOUTERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -MANN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : GenBml:*
1: gb_ba:*
2: gb_hgt:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vl:*
15: em_da:*
16: em_fun:*
17: em_hum:*
18: em_in:*
19: em_mu:*
20: em_om:*
21: em_or:*
22: em_ov:*
23: em_pat:*
24: em_ph:*
25: em_pl:*
26: em_ro:*
27: em_sts:*
28: em_un:*

29: em_vl:*
30: em_hgt_hum:*
31: em_hgt_inv:*
32: em_hgt_other:*
33: em_hgt_mus:*
34: em_hgt_pln:*
35: em_hgt_rtd:*
36: em_hgt_man:*
37: em_hgt_vrt:*
38: em_sy:*
39: em_hgt_hum:*
40: em_hgt_mus:*
41: em_hgt_other:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1394	100.0	952	8	CSU30382
2	1275	91.5	681	6	AR076514
3	1275	91.5	681	6	AR161478
4	1275	91.5	681	6	AX306492
5	1275	91.5	684	6	AX306490
6	1160.5	83.2	1109	8	PAU93167
7	1152.5	82.6	1035	8	CAR291817
8	1151.5	82.6	1048	8	AF297521
9	1151.5	82.6	1109	8	AF350937
10	1143.5	82.0	1088	8	AF230332
11	1141	81.9	1180	8	AB104443
12	1140	81.8	1283	8	AB093028
13	1138	81.6	1195	8	AB104444
14	1137.5	81.6	1153	8	AB093029
15	1133.5	81.3	1118	8	AB093030
16	1130.5	81.1	1142	8	AF428174
17	1125	80.7	1147	8	AF086776
18	1120	80.3	1108	8	AF083166
19	1118	80.2	1177	8	AF049354
20	1117.5	80.1	1180	8	AF159563
21	1116.5	80.1	1173	8	AF167360
22	1113.5	79.9	1233	8	AF350936
23	1113	79.8	1262	8	AY079206
24	1112	79.8	1070	8	AY079208
25	1111	79.7	1220	8	AB029083
26	1108	79.5	1117	8	AF428175
27	1105	79.3	1252	8	AF038815
28	1102.5	79.1	1098	8	AY083168
29	1101.5	79.0	998	8	AF085330
30	1100	78.9	1175	8	AB104445
31	1092	78.3	919	8	PTU64891
32	1092	78.3	1169	8	AY299692
33	1087	78.0	923	8	PTU64890
34	1085	77.8	762	6	AX506393
35	1085	77.8	762	6	AX651951
36	1085	77.8	891	8	PTU64893
37	1085	77.8	1016	8	AY086770
38	1077	77.3	923	8	PTU64892
39	1076.5	77.2	1191	8	AY079205
40	1071.5	76.9	1144	6	AX392019
41	1063	76.3	1497	8	CAR89608
42	1055	75.7	1245	8	AB104442
43	1054.5	75.6	1340	8	AB093031
44	1054	75.6	1355	8	AB093032
45	1053	75.5	1419	8	AF448467

RESULT 1

ALIGNMENTS

Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 91.46% Indels: 0
 DB: 6 Gaps: 0

US-09-383-579c-10 (1-250) x AR076514 (1-681)

QY	24	AspTyrGlyGlyTTPGlnSerGlyHisAlaThrPheTyrGlyGlyAspAlaSerGly	43
DB	1	GACTACGGTGGCTGGCAGAGCGGCACGCCACTTTATGTGTGGTGAAGCATCTGGC	60
QY	44	ThrMetGlyGlyAlaCySGlyTyrGlyAsnLeuTyrSerGlnGlyTyrGlyThrAsnThr	63
DB	61	ACCATGGGTGGAGCTGTGGGTATGGGATTATTAACGCCAAGGATGGACCAACACG	120
QY	64	ValAlaLeuSerThrAlaLeuPheAsnAsnGlyLeuSerCySGlyAlaCySPheGluMet	83
DB	121	GTGGCGCTGACACTGGCGCTATTAAACATGATTAAGTTGTGTGCTTCTTGAATG	180
QY	84	ThrCysThrAsnAspProLysTyrCysLeuProGlyThrIleArgValThrAlaThrAsn	103
DB	181	ACTGTACAAACGACCTTAATGGTGCCTTCGGGAACCTATTAGGTCACCTGCCACAC	240
QY	104	PheCysProProAsnPheAlaLeuProAsnAsnAsnGlyGlyTyrCysAsnProProLeu	123
DB	241	TTTGGCCCTCTTAATCTTCTCTCTCCCTTAACAAATGGTGGATGGTCAACCTCTCTC	300
QY	124	GlnHisPheAspMetAlaGluProAlaPheLeuGlnIleAlaGlnTyrArgAlaGlyIle	143
DB	301	CAACACTTCGACATGGCTGACCTGCTCTTCAAAATCGTCAATACCGAGCTGGATC	360
QY	144	ValProValSerPheArgValProCysMetLysGlyGlyValArgPheThrIle	163
DB	361	GTCCCGCTCTCTTCGAGGGTACATGATGAAGAAAGTGGAGGTTTACATC	420
QY	164	AsnGlyHisSerTyrPheAsnLeuValLeuIleThrAsnValGlyValArgPheVal	183
DB	421	AATGGCCACTCATCTTCAACCTGTTTGAATCAAAACGTGGTGGCGCAGCAGCTC	480
QY	184	HisSerValSerIleLysGlySerArgThrGlyTyrPginSerMetSerArgAsnTyrGly	203
DB	481	CACCTGTGTGATTAAGGGGTCTCGAATGGATGGCAATCATGCTAGAAATGGGGC	540
QY	204	GlnAsnTyrPginSerAsnAsnTyrLeuAsnGlyGlnGlyLeuSerPheGlnValThrLeu	223
DB	541	CAAAACCTGGCAAGCAACATATCTCATATGCCAAGGCTTCTTCAAGTCACTCTT	600
QY	224	SerAspGlyArgThrLeuThrAlaTyrAsnLeuValProSerAsnTyrPginPheGlyGln	243
DB	601	AGTATGTGTGCACTCTCATCTGCTATATCTGTTCTTCAATGGCAATTTGGCCAA	660
QY	244	ThrTyrGluGlyProGlnPhe 250	
DB	661	ACCTATGAAAGCCCTCAATTC 681	

RESULT 3
 ARI61478 681 bp DNA linear PAT 17-OCT-2001
 LOCUS ARI61478
 DEFINITION Sequence 1 from patent US 6255466.
 ACCSSION ARI61478 GI:16227385
 VERSION ARI61478.1
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unclassified.
 REFERENCE 1 (bases 1 to 681)
 AUTHORS Cosgrove,D.J., McQueen-Mason,S., Gullitnan,M., Shcherban,T. and Shi,J.
 TITLE Purified plant expansion proteins and DNA encoding same
 JOURNAL Patent: US 6255466-A 1 03-JUL-2001;
 FEATURES Location/Qualifiers
 source 1..681
 /organism="unknown"

BASE COUNT 161 a 179 c 164 g 177 t

ORIGIN

Alignment Scores:
 Pred. No.: 1,71e-115 Length: 681
 Score: 1275.00 Matches: 227
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 91.46% Indels: 0
 DB: 6 Gaps: 0

US-09-383-579c-10 (1-250) x ARI61478 (1-681)

QY	24	AspTyrGlyGlyTTPGlnSerGlyHisAlaThrPheTyrGlyGlyAspAlaSerGly	43
DB	1	GACTACGGTGGCTGGCAGAGCGGCACGCCACTTTATGTGTGGTGAAGCATCTGGC	60
QY	44	ThrMetGlyGlyAlaCySGlyTyrGlyAsnLeuTyrSerGlnGlyTyrGlyThrAsnThr	63
DB	61	ACCATGGGTGGAGCTGTGGGTATGGGATTATTAACGCCAAGGATGGACCAACACG	120
QY	64	ValAlaLeuSerThrAlaLeuPheAsnAsnGlyLeuSerCySGlyAlaCySPheGluMet	83
DB	121	GTGGCGCTGACACTGGCGCTATTAAACATGATTAAGTTGTGTGCTTCTTGAATG	180
QY	84	ThrCysThrAsnAspProLysTyrCysLeuProGlyThrIleArgValThrAlaThrAsn	103
DB	181	ACTGTACAAACGACCTTAATGGTGCCTTCGGGAACCTATTAGGTCACCTGCCACAC	240
QY	104	PheCysProProAsnPheAlaLeuProAsnAsnAsnGlyGlyTyrCysAsnProProLeu	123
DB	241	TTTGGCCCTCTTAATCTTCTCTCTCCCTTAACAAATGGTGGATGGTCAACCTCTCTC	300
QY	124	GlnHisPheAspMetAlaGluProAlaPheLeuGlnIleAlaGlnTyrArgAlaGlyIle	143
DB	301	CAACACTTCGACATGGCTGACCTGCTCTTCAAAATCGTCAATACCGAGCTGGATC	360
QY	144	ValProValSerPheArgValProCysMetLysGlyGlyValArgPheThrIle	163
DB	361	GTCCCGCTCTCTTCGAGGGTACATGATGAAGAAAGTGGAGGTTTACATC	420
QY	164	AsnGlyHisSerTyrPheAsnLeuValLeuIleThrAsnValGlyValArgPheVal	183
DB	421	AATGGCCACTCATCTTCAACCTGTTTGAATCAAAACGTGGTGGCGCAGCAGCTC	480
QY	184	HisSerValSerIleLysGlySerArgThrGlyTyrPginSerMetSerArgAsnTyrGly	203
DB	481	CACCTGTGTGATTAAGGGGTCTCGAATGGATGGCAATCATGCTAGAAATGGGGC	540
QY	204	GlnAsnTyrPginSerAsnAsnTyrLeuAsnGlyGlnGlyLeuSerPheGlnValThrLeu	223
DB	541	CAAAACCTGGCAAGCAACATATCTCATATGCCAAGGCTTCTTCAAGTCACTCTT	600
QY	224	SerAspGlyArgThrLeuThrAlaTyrAsnLeuValProSerAsnTyrPginPheGlyGln	243
DB	601	AGTATGTGTGCACTCTCATCTGCTATATCTGTTCTTCAATGGCAATTTGGCCAA	660
QY	244	ThrTyrGluGlyProGlnPhe 250	
DB	661	ACCTATGAAAGCCCTCAATTC 681	

RESULT 4
 AX306492 681 bp DNA linear PAT 11-DEC-2001
 LOCUS AX306492
 DEFINITION Sequence 3 from Patent WO018163.
 ACCSSION AX306492 GI:17645712
 VERSION AX306492.1
 KEYWORDS
 SOURCE Cucumis sativus (cucumber)
 ORGANISM Cucumis sativus
 REFERENCE 1
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids I; Cucurbitales; Cucurbitaceae; Cucumis.

Db	301	CACACCTTCGACATGCGTGAAGCTCCCTTCCTTCAAAATCGCTCATATACCGAGCTGGTATC	360
QY	144	ValProValSerPheArgArgValProCysMetIysIysGIyValAlaArgPheThrIle	163
Db	361	GTCCCGCTCTCTTCGTAGAGGTACCATGTATGAAGAAAGGTGGAGTGAAGTTTAAATC	420
QY	164	AsnGIyHisSerTyrPheAsnLeuValLeuIleThrAsnValGIyGIyValGIyAspVal	183
Db	421	AAATGGCACTCACTACTTCAACTCTGTTTGATCAAAACGTGGGGGCGAGGCAAGCTC	480
QY	184	HisSerValSerIleIysGIySerArgThrGIyTPGIInSerMetSerArgAsnTPdGIy	203
Db	481	CACCTGTGTGTGATAAAGGGGTCTGGAAGTGGATGCATCATCATCTTAAATTTGGGGC	540
QY	204	GIInAsnTPGIInSerAsnAsnTyrLeuAsnGIyGIyIleuSerPheGIInValThrIleu	223
Db	541	CAAACTGGCAAGCAACAACTATCTCATGTGGCCAAAGGCTTTCCTTCAAGTCACTCTT	600
QY	224	SerAspGIyArgThrIleuThrAlaTyrAsnLeuValProSerAsnTPGIInPheGIyIn	243
Db	601	AGTATGATGTGGACCTCTCACTGCTCATATCTCGTTCCTTCAATGGCAATTTGGCCAA	660
QY	244	ThrTyrGIyGIyProGIInPhe	250
Db	661	ACCTATGAAGGCCCTCAATTC	681
RESULT 6			
PAU93167		1109 bp	mRNA
LOCUS			linear
DEFINITION			PLN 01-SEP-1998
ACCESSION	U93167		complete cds.
VERSION	U93167.1		GI:3510537
KEYWORDS			
SOURCE			
ORGANISM			Prunus armeniaca (apricot)
			Prunus armeniaca
			Eumariotyta, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
			Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
			rosidae; eutrosidae I; Rosales; Rosaceae; Amygdaloidae; Prunus.
REFERENCE			1 (bases 1 to 1109)
AUTHORS			Mbeguile-A-Mbeguile,D., Gomez,R.-M. and Fils-Lycaon,B.
TITLE			Molecular cloning and nucleotide sequence of expansin 1 (PA-Expi1)
			from apricot fruit
JOURNAL			unpublished
REFERENCE			2 (bases 1 to 1109)
AUTHORS			Mbeguile-A-Mbeguile,D., Gomez,R.-M. and Fils-Lycaon,B.
TITLE			Submitted (12-MAR-1997) Station de Technologie des Produits
JOURNAL			Direct Submission
REFERENCE			3 (bases 1 to 1109)
AUTHORS			Mbeguile-A-Mbeguile,D., Gomez,R.-M. and Fils-Lycaon,B.
TITLE			Submitted (12-DEC-1997) Station de Technologie des Produits
JOURNAL			Vegetaux, INRA, Site AGRORPARC, Avignon 84914 Cedex 9, France
REMARK			Sequence update by submitter
FEATURES			Location/Qualifiers
			1..1109
source			/organism="Prunus armeniaca"
			/mol_type="mRNA"
			/strain="Bergeron"
			/db_xref="taxon:36596"
			/clone="PAPRI45"
			/tissue_type="mesocarp plus exocarp"
			/dev_stage="ripe fruit"
			1..1109
			/gene="PA-Expi1"
			74..838
			/gene="PA-Expi1"
			/codon_start=1
			/product="expansin"
			/protein_id="AAC33529.1"
			/db_xref="GI:3510538"
			/translation="MAFQALSILAPLALSLVIFNLHLGAFADYGVGMEGAHATFYGGSD
gene			
CDS			

BASE COUNT	301 a	254 c	242 g	312 t	
ORIGIN	ASGFMGACCGAGNLTGSGGAGTATLSTALPNNMLSGGSCYEMKCNNDPRACRPESS VTANRCPENRPNAGSNDNGMKCNPEPLQGFHDLAPFLQIAQYRAQIVPTFRVRPEMK GGIFPTNGHSYFWLVLTINVGAGDVHSAVSKSRRTGMDPMSRNMGNOSNNYLANC QSLSEQVTTSGRVTISYNAAPGMWGGQFFSGQF"				
Alignment Scores:					
Pred. No.:	4.92e-104	Length:	1109		
Score:	1160.50	Matches:	206		
Percent Similarity:	88.40%	Conservative:	15		
Best Local Similarity:	82.40%	Mismatches:	28		
Query Match:	83.25%	Indels:	1		
DB:	8	Gaps:	1		
US-09-383-579C-10 (1-250) x PAU93167 (1-1109)					
QY	2	AlaPheSerTyrrSerProPheSer---SerLeuPheLeuLeuProPhePheValPhe	20		
Db	86	GCAATTCCTTATAGCTCCCTACGCCCTCTCTTGTCTCTTCAATCTTCATCTTCATGCT	145		
QY	21	ThrPheAlaAepTyrglygyltyrtpginserglyhisalathrphetyrglygyltyrAsp	40		
Db	146	GCTTTTGGTGATTAATGAGTGGCGGGAAGGCCCTCATGCATTTTAAATGAGCGCGTAT	205		
QY	41	AlaSerglyThrMetglyValAlaCysglytyrtyrglybaleuTyrrSerGlnGlytyrgly	60		
Db	206	GCCTCGGGAACCAATGGGGGGAGCATGTGGGATAGGAACTTGTCACGCCAAGGATATGA	265		
QY	61	ThrAsnThrValAlaAlaSerThrAlaLeuPheAsnAsnGlyLeuSerCysglyValaCys	80		
Db	266	ACCACACTGCAGCTTTAAGACAGCCTTGTTTAAACAATGGCTTGAGCTGTGCTTGT	325		
QY	81	PheGlnMetThrCysThrAsnAspProLysTyrCysLeuProGlyThrIleArgValThr	100		
Db	326	TATGAATAGATGCACAAATGACCCCTAGATGCTGCTCTGGAAGATCATTTGTTACT	385		
QY	101	AlaThrAsnPheCysProProAsnPheAlaLeuProAsnAsnAsnGlytyrtyrCysAsn	120		
Db	386	GCCCAAAACTTTTCCCACTTAACCTTTGCTCAGTCCAAACGACAAATGGCGGCTGGTGCAT	445		
QY	121	ProProLeuGlnHisPheAsnMetAlaGlnProAlaPheLeuGlnIleAlaGlnTyrArg	140		
Db	446	CTTCCTCCCTCCAGCACTTGATTTGGCTGAGCTGCTCTTCTTCAAAATGGCCCAATACCGC	505		
QY	141	AlaGlyIleValProValSerPheArgArgValProCysMetIleBlyGlyValArg	160		
Db	506	GCTGGGATTTGGCTGCTTACTCTTACAAAGAGTGCCTGTATGAAGAGGAGGAATTCGA	565		
QY	161	PheThrIleAsnGlyHisSerTyrrPheAsnLeuValIleuIleThrAsnValGlyValAla	180		
Db	566	TTTCAACATCATAGGCCACTCTTACTTCAACTGTTTTTGAATCAACAACTGGTGGTGC	625		
QY	181	GlyAspValHisSerValSerIleBlyGlySerArgThrGlytyrtpginserMetSerArg	200		
Db	626	GGAACGCGCACTCAGTTTCAATCAATCAAGGGGTCCGAACAGGGTGGCAACCATGTCCAGA	685		
QY	201	AsnTyrtpginAsnTyrtpginSerAsnAsnTyrLeuAsnGlyGlnGlyLeuSerPheGln	220		
Db	686	AACCTGGGGGGCAAACTGGCAGAGCAACAATTACTTCATAGGCCAGAGCCTTCTCCAA	745		
QY	221	ValThrLeuSerAspGlyArgThrLeuThrAlaTyrrAsnLeuValProSerAsnTyrpGln	240		
Db	746	GTGACCAACCAAGTACGGAAGAAGCTTAAACAAGCTAACAAAGTGGGCCCTGTAATTTGGAG	805		
QY	241	PheGlyGlnThrTyrglygylProGlnPhe	250		
Db	806	TTTGTTCAGACTTCTCAGGGGGTCAATTT	835		

ACCESSION AJ291817 GI:11932091
 VERSION AJ291817.1
 KEYWORDS expansin.
 SOURCE Cicer arietinum (chickpea)
 ORGANISM Cicer arietinum
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Ciceraceae; Cicer.
 REFERENCE 1
 Dopicco, B., Sanchez, M.A. and Labrador, E.
 An second expansin is expressed in chickpea epicotyls
 JOURNAL Unpublished
 REFERENCE 2 (bases 1 to 1035)
 Labrador, E.
 Direct Submision
 Submitted (15-DEC-2000) Labrador E., Dpto. Fisiologia Vegetal, Univ. Salamanca, Campus Miguel de Unamuno. Pza. Doctores de la Reina s/n, E-37007, SPAIN
 FEATURES
 source
 1.1035
 /organism="Cicer arietinum"
 /mol_type="mRNA"
 /cultivar="Castellana"
 /db_xref="taxon:3827"
 /clone="Canexp-2"
 /cissue_type="etiolated epicotyls"
 /clone_1ib="CAN-5"
 /dev_stage="5 days old seedling"
 /country="Spain"
 30.812
 /codon_start=1
 /product="expansin"
 /protein_id="CAC19184.1"
 /db_xref="GI:11932092"
 /translation="MAOKLRMAHOEFIVLKGILPFPNNMNSAIADYGEAGAHAT
 EYGGDASGTMGACGGYGLYSGYGTNTALSTALFNNGISCGSCYEMRCNDPRMC
 KRGSTIVTATNFCPPNPISLANNNGKCNPLPHFDMAEPAFLQIAEYRGIYPSVFR
 VPCMKGGIRFTINGHSYFNVLVTNVGAGDVSVISKGRFGMSRNGQWQWS
 NSYLNGQPSFVNTSDGRTSYNVAPEPNMFGQTFQGAQF"
 BASE COUNT 312 a 168 c 213 g 342 t
 ORIGIN
 Alignment Scores:
 Pred. No.: 2,74e-103 Length: 1035
 Score: 1152.50 Matches: 203
 Percent Similarity: 89.11% Conservative: 18
 Best Local Similarity: 81.85% Mismatches: 20
 Query Match: 82.68% Indels: 7
 DB: 8 Gaps: 1
 US-09-383-579c-10 (1-250) x CAR291817 (1-1035)
 QY 10 SerLeuPheLeuLeuProPhePheValPhe-----ThrPhe 22
 Db 66 TCATTGTTCTTAAAGGCTCTAATTTTATTATTTTAACTGATATGCAAGTGTATTA 125
 QY 23 ALaSPYrIGLyGlyTyrPheInserGlyHsAlaThrPheTyrGlyGlyAlaSPaLaser 42
 Db 126 GCGATTATGAGTGTGGAGAGGCTCATGCCACTTCTTATGATGGGGGTATGTTCT 185
 QY 43 GlyThMetGlyGlyAlaCySgLyTyrGlyAsnLeuTyrSerGlnGlyTyrGlyThraAn 62
 Db 186 GGCACAAATGGGTGACATGTGATATGTTATTTATATGCAAGATATGCAACCAAC 245
 QY 63 ThrValAlaLeuSerThrAlaLeuPheAsnGlyLeuSerCySgLyAlaCySPheGlu 82
 Db 246 AAGGACGACCTAAGCCTGTTATTCACAAATGGTTAAGTTGTGATCTTGCTATGAA 305
 QY 83 MetThCySThrAsnAPrOlySTrPcySLeuPrgLyThrIleArgValThralaThr 102
 Db 306 ATGAGATGCAATGATATCCAGATGTGTCAACCTGCTCTATTTATTTGTTACTGCA 365

QY 103 AenPheCyProPAsnPheAlaLeuProAsnAsnGlyLyTyrCyAsnProPro 122
 Db 366 AATTTTGTCCACCAATCCATCTTGGCTAATTAATTAATGAGTGTGGTACCTCT 425
 QY 123 LeuGlnHisPheAspMetAlaGluProAlaPheLeuGlnIleAlaGlnTyrArgAlaGly 142
 Db 426 TTGCACAACTTTGATATGCTGTAACCTGCTTCCCTCAATGCTGCAATATATGGCTGGA 485
 QY 143 IleValProValSerPheArgArgValProCySmetLySlyGlyGlyValArgPheThr 162
 Db 486 ATTGCGCTGTGCTCTTATGAAAGTGCATGATGAAAGGAGGATATGAGTTTCA 545
 QY 163 IleAsnGlyHisSerTyrPheAsnLeuValLeuIleThrAsnValGlyValAlaGlyAsp 182
 Db 546 ATCAATGACACTCTTACTTCACTCACTAGTTTGGTCACTAATGTTGGTGCTGAGAT 605
 QY 183 ValHisSerValSerIleLyGlySerArgThrGlyTyrPheInserMetSerArgAsnTyr 202
 Db 606 GTTCATTCAGTTTCCATAAAGTTCAAGACTGGGTGGCAATCATGTCAGAATATGG 665
 QY 203 GlyIleAsnTyrPheInserAsnAsnTyrLeuAsnGlyGlnGlyLeuSerPheGlnValThr 222
 Db 666 GGCACAAATTTGGCAAGCAATCTTCACTTAATGTTCAACCCCTTCAATTCAGTCAAC 725
 QY 223 LeuSerAspGlyArgThrLeuThrAlaTyrAsnLeuValProSerAsnTyrGlnPheGly 242
 Db 726 ACAATGTATGTAGTACATATGCAATGATGATGATGATGATGATGATGATGATGAT 785
 QY 243 GlnThrTyrGlyGlyProGlnPhe 250
 Db 786 CAACATTTCAAGAGGCTCAATTT 809
 RESULT 8
 AF297521 1048 bp mRNA linear PLN 17-SEP-2000
 LOCUS Prunus avium expansin 1 (Exp1) mRNA, complete cds.
 DEFINITION AF297521
 ACCESSION AF297521 GI:10180016
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM
 Prunus avium (sweet cherry)
 Prunus avium
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosids; eurosids I; Rosales; Rosaceae; Amygdaloideae; Prunus.
 1 (bases 1 to 1048)
 Wu, Z. and Wiersma, P.A.
 Differential Expression of Expansin Genes Isolated from Sweet Cherry (Prunus avium L.) During Fruit Ripening
 JOURNAL Unpublished
 REFERENCE 2 (bases 1 to 1048)
 Wiersma, P.A.
 Direct Submision
 Submitted (18-AUG-2000) Agriculture and Agri-Food Canada, Pacific Agri-Food Research Centre, 4200 Highway 97, Summerland, British Columbia V0H 1Z0, Canada
 FEATURES
 source
 1.1048
 /organism="Prunus avium"
 /mol_type="mRNA"
 /db_xref="taxon:42229"
 1.1048
 /gene="Exp1"
 81.845
 /gene="Exp1"
 /note="PrunExp1"
 /codon_start=1
 /product="expansin 1"
 /protein_id="PAG13982.1"
 /db_xref="GI:10180017"
 /translation="MAAPALSLAPLALSLVFNLIHNGAFADYGMGEGAHATFYGGD
 ASGTGACGGYGLYSGYGTNTALSTALFNNGISCGSCYEMRCNDPRMCPSII
 VTATNFCPPNPISLANNNGKCNPLPHFDMAEPAFLQIAEYRGIYPSVFR
 GGIPTINGHSYFNVLVTNVGAGDVSVISKGRFGMSRNGQWQWSNTYLVG

QY 121 ProProLeuGlnHisPheaspMetAlaGluProAlaPheLeuGlnIleAlaGlnIleTyrArg 140
 DB 447 CCTCCTCTCCAGACACTTATTTGGCCAGCCGCTTTCTTGGCAATTCGCCAATTCGCC 506
 QY 141 AlAGlyIleValProValSerPheArgValProCysMetLeuValGlyValArg 160
 DB 507 GCTGGGATTTGCTCTTTCCTTTCAGAAAGTGCCCTGTATGAAAGAGAGATTAAGA 566
 QY 161 PheThrIleAsnGlyHisSerTyrPheAsnLeuValIleThrAsnValGlyValArg 180
 DB 567 TTCACCATCAATGGCCACTCTCACTCACTGTTTGTATGCCAACGCGGTGTGTGA 626
 QY 181 GlyAspValHisSerValSerIleGlySerArgTyrGlyTyrGlnSerMetSerArg 200
 DB 627 GGAGAGCTCCATTCATTCATTCATTCATTCATTCATTCATTCATTCATTCATTCAT 686
 QY 201 AsnTTPGlyValAsnTTPGlyInserAsnAsnTyrLeuAsnGlyValGlnIleLeuSerPheGln 220
 DB 687 AACTGGGGGCAAACTGGGAGCAAACTTACTTAAATGGCCAGACCTCTCTCCAA 746
 QY 221 ValThrLeuSerAspGlyArgThrLeuThrAlaTyrAsnLeuValProSerAsnTyrGln 240
 DB 747 GTGACCAACGAGCGAGAGAACTGTACAAACTACAGTGGCCCTGTATTCGACG 806
 QY 241 PheGlyGlnThrTyrGlyGlyProGlnPhe 250
 DB 807 TTTGGTCAGACTTCTCAGGGGGGTCAATTT 836
 RESULT 10
 AF230332 1088 bp mRNA linear PLN 26-JUN-2000
 LOCUS Zinnia elegans expansin 2 mRNA, complete cds.
 DEFINITION AF230332
 VERSION AF230332.1 GI:7025492
 KEYWORDS
 SOURCE Zinnia elegans
 ORGANISM Zinnia elegans
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 Asteridae; campanulids; Asterales; Asteraceae; Asteroideae;
 Heliantheae; Zinnia.
 REFERENCE 1 (bases 1 to 1088)
 AUTHORS Im,K.H., Cosgrove,D.J. and Jones,A.M.
 TITLE Subcellular localization of expansin mRNA in xylem cells
 JOURNAL Plant Physiol. 123 (2), 463-470 (2000)
 MEDLINE 20317189
 PUBMED 10859177
 REFERENCE 2 (bases 1 to 1088)
 AUTHORS Im,K.-H., Cosgrove,D.J. and Jones,A.M.
 TITLE Direct Subcellular
 JOURNAL Submitted (02-FEB-2000) Biology, University of North Carolina,
 Chapel Hill, NC 27599, USA
 FEATURES
 source Location/Qualifiers
 1..1088
 /organism="Zinnia elegans"
 /mol_type="mRNA"
 /db_xref="taxon:34245"
 16..753
 /codon_start=1
 /product="expansin 2"
 /protein_id="AAF35901.1"
 /db_xref="GI:7025493"
 /translation="MALSTFTIVSLVSSFNVVYGGWENGHATFYGGGASGTMGAC
 GGNLYSGQYNTALSTALFNNGLSGSSCYEMCNDDPKMCLPGSIVTATNFCPP
 NGLSNDNGMCNPNLOHFDLAEPALQIAOYRAGIVPISFPRVCVKKGQYRTING
 HSEFNILITLVAGAGDVHSVSIKSKTQMSKRMGMQMSNTSLNGQSIFVYTT
 SDGRITTSYNVAPSNMFGOTRQGGQF"
 BASE COUNT 299 a 205 c 237 g 347 t
 ORIGIN
 Alignment Scores: 2.21e-102 Length: 1088
 Pred. No.:

Score: 1143.50 Matches: 203
 Percent Similarity: 89.20% Conservative: 20
 Best Local Similarity: 81.20% Mismatches: 22
 Query Match: 82.03% Indels: 5
 DB: 8 Gaps: 1
 US-09-383-579c-10 (1-250) x AF230332 (1-1088)
 QY 1 MetAlaPheSerTyrSerProPheSerSerLeuPheLeuLeuProPhePheValPhe 20
 DB 16 ATGGCCCTTTCAACATTATACCATTTGTTCTACTACTATCTCTCTCAATGTTTC-- 72
 QY 21 ThrPheAlaAspTyrGlyValTyrGlnSerGlyHisAlaThrPheTyrGlyValGlyAsp 40
 DB 73 -----TAAGAGGTGGGAAATGTCATGCGACCTTTTACGGTGGCGAGAT 120
 QY 41 AlaSerGlyThrMetGlyValAlaCysGlyTyrGlyAsnLeuTyrSerGlnIleTyrGly 60
 DB 121 GCTCTGGACAAATGGGTGTGCTGTGTGATATGAAACTTGTATACCGCAAGATATGC 180
 QY 61 ThrAsnThrValAlaLeuSerThrAlaLeuPheAsnAsnGlyLeuSerCysGlyValAcys 80
 DB 181 ACTAACACTGGCGCATTAAGTACGGCTTTTCAACAATGGGTAAAGTTGTGTGATGT 240
 QY 81 PheGlyMetThrCysThrAsnAspProIleTyrCysLeuProGlyThrIleArgValThr 100
 DB 241 TACGAGATGAGATGAGCAACGACCTTAATGTCCTTGGCGGTTCATATGTTGTGACC 300
 QY 101 AlaThrAsnPheCysProProAsnPheAlaLeuProAsnAsnAsnGlyValTyrCysAsn 120
 DB 301 GCAACAACTTTGGCCACCTTACCTGCTGTGTATACGACAAATGGTGGTGTGCAAC 360
 QY 121 ProProLeuGlnHisPheaspMetAlaGluProAlaPheLeuGlnIleAlaGlnIleTyrArg 140
 DB 361 CCTCCTTCAACAATTGATTTGATTCAGAACCTGCTTCTTGGCAATTCACAAATATGA 420
 QY 141 AlAGlyIleValProValSerPheArgValProCysMetLeuValGlyValArg 160
 DB 421 GCTGGAATTTGCTTATATCATTCACAAAGGCTCCATGTGTCAAAAGAGAGAGTGA 480
 QY 161 PheThrIleAsnGlyHisSerTyrPheAsnLeuValIleThrAsnValGlyValArg 180
 DB 481 TTTACTATTAATAGTCATTCATTCATTCATTCATTCATTCATTCATTCATTCATTCAT 540
 QY 181 GlyAspValHisSerValSerIleGlySerArgTyrGlyTyrGlnSerMetSerArg 200
 DB 541 GGGGATGTTCACTCAGTATCAATCAAGGATCAAAACCGGGGTGCAATCCATGTCAAG 600
 QY 201 AsnTTPGlyValAsnTTPGlyInserAsnAsnTyrLeuAsnGlyValGlnIleLeuSerPheGln 220
 DB 601 AACTGGGGGCAAACTGGGCAAACTTATATCTTAACGGTCAAAAGCTTATCATTCACG 660
 QY 221 ValThrLeuSerAspGlyArgThrLeuThrAlaTyrAsnLeuValProSerAsnTyrGln 240
 DB 661 GTACGACTATGAGAGAGAAACATCAACAGCTTAAAGTTGGCCGCTTACTACGGCA 720
 QY 241 PheGlyGlnThrTyrGlyGlyProGlnPhe 250
 DB 721 TTTGGGAGACCTTCCAAAGGGGACAAATTT 750
 RESULT 11
 AB104443 1180 bp mRNA linear PLN 01-APR-2003
 LOCUS Vitis labrusca x Vitis vinifera Vexp-2 mRNA for expansin, complete
 DEFINITION cds.
 ACCESSION AB104443
 VERSION AB104443.1 GI:29421119
 KEYWORDS
 ORGANISM Vitis labrusca x Vitis vinifera
 Vitis labrusca x Vitis vinifera
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 Rosidae; Vitaceae; Vitis.

REFERENCE
AUTHORS
TITLE
JOURNAL
REFERENCE
AUTHORS
TITLE
JOURNAL

1
Ishimaru, M. and Kobayashi, S.
Expression of expansin genes is related grape berry softening
Unpublished
2 (bases 1 to 1180)
Ishimaru, M.
Direct Submission
Submitted (21-FEB-2003) Megumi Ishimaru, Osaka Prefecture
University, Graduate School of Agriculture and Biological Sciences;
1-1, Gakuen-cho, Sakai, Osaka 599-8531, Japan
(E-mail: m.ishimaru@plant.osakafu-u.ac.jp, Tel: 81-72-254-9419,
Fax: 81-72-254-9418)
Location/Qualifiers

FEATURES
Source
1. 1180
/organism="Vitis labrusca x Vitis vinifera"
/mol_type="mRNA"
/cultivar="Kyoho"
/db_xref="taxon:105599"
/clone_id="Uni-Zap XR grape berry cDNA"
/dev_stage="veraison"
/country="Japan"
1. 1180
/gene="Vexp-2"
42. 800
/gene="Vexp-2"
/codon_start=1
/product="expansin"
/protein_id="BAC6695.1"
/db_xref="GI:29421120"
/translation="MAITAFSSISLALFLFCLQGTNGDYGMEGHATFYGGDAS
GTMGAGCYGNLYSOQGYNTALSTLFDNSGSCGACYEMKNDPFCPLTIVT
ATNFCPNNLALSTNGGMCNPLQHPDLAPAKIQAQYRAQIVPVSFRVPCVKKG
IRFTNGHSYFNILITNVAGADVAIVSIKGSNTGQPMRNMGNQMSNYLNGQT
LSFOVTASDQRITSLNVAPAGNMFQGTGAGP"

BASE COUNT 299 a 279 c 301 g 301 t

ALIGNMENT SCORES:
Pred. No.: 4 29e-102 Length: 1180
Score: 1141.00 Matches: 202
Percent Similarity: 87.40% Conservative: 20
Best Local Similarity: 79.53% Mismatches: 28
Query Match: 81.85% Indels: 4
DB: 8 Gaps: 1

US-09-383-579c-10 (1-250) x ABI04443 (1-1180)

QY 1 MetAlaPheSerTySerProPheSerSerLeuPheLeuProPhePheValPhe 20
Db 36 CTCTCAATGGCTACTGACGATTTTCTTATCTCTTGCCTTTCTTCTGCTA 95
QY 21 -----ThrPheAlaSerTyGlyGlyTyTrpGlnSerGlyHisAlaThrPheTy 36
Db 96 TGCCTCCAGGCAAAATGCTATGATGGGGGAGAGTGGGCATGCCACATTTAT 155
QY 37 G1G1G1G1YAspAlaSerGlyThrMetGlyGlyValaCysGlyTyTrpGlnSerGly 56
Db 156 GGGGGTGGTACCGCTTACGACAAATGGGAGTGGGCTTGTGGATAGCAACCTGTACG 215
QY 57 G1G1G1TyGlyGlyThrSerThrValAlaLeuSerThrAlaLeuPheAsnAnGlyLeuSer 76
Db 216 CAAGGGATGGGACCAACATGACGCTCTGACGACCGCTCTTCAACACATGGGGCTAGC 275
QY 77 CysGlyValaCysPheGlyMetThrCysThrAsnAspProTyTrpCysLeuProGlyThr 96
Db 276 TGTGGGGCATGTACGATGAATGCAACATGACACCCAAATGGTGTCTCCAGGGAGCC 335
QY 97 ILAryValaThrAlaThrAsnPheCysProAsnAspPheAlaLeuProAsnAnGly 116
Db 336 CTAAACCTGACCTGCAAACTTCTGCTCTTACTTGGCTTGTCCAAACCAACGAGC 395
QY 117 G1TyTrpCysAsnProLeuGlnHisPheAspMetAlaGluProAlaPheLeuGlnIle 136

Db 396 GGATGTGCATCCCCCTTCAGCACTTCGATCTAGTACGCTGCTCTTCAGATT 455
QY 137 AlAG1TyTrpAlaGlyIleValProValSerPheArgArgValProCysMetIleVal 156
Db 456 GCCAGTACCGAGCTGAACTGTAACCTGTCTTCAAGAGAGCCCCCTGTGAAGAA 515
QY 157 G1G1YValArpPheThrIleAsnGlyHisSerTyTrpPheAsnLeuValIleThrAsn 176
Db 516 GAGAGGATCGCTTTTACATCAACGAGCACTCTACTTCAACTTGGCTCATCAAAAC 575
QY 177 ValG1GlyAlaGlyAspValHisSerValSerIleGlyGlySerArgThrGlyTrpGln 196
Db 576 GTGGCCGAGCGGAGACGTCAGGCAATGATCAATAAGGGGCTTAAGACCGGGGTGCAG 635
QY 197 SerMetSerArgAsnTrpGlyGlnAsnTrpGlnSerPheAsnTyTrpLeuAnGlyGlnGly 216
Db 636 CCCATGCAAGAACTGGGGCCGAAGCTGCAAGCAACATCAATCAACGCGCAGACC 695
QY 217 LeuSerPheGlnValThrIleuSerAspGlyArgThrIleuThrAlaTyAsnLeuValPro 236
Db 696 CTCTCATTCCAACTCAGACAGCAACGATGCCGAGCAGATGCAACGCTCATGTGGCCT 755
QY 237 SerAsnTrpGlnPheGlyGlnThrTyGlyGlyProGlnPhe 250
Db 756 GCTGCTGGCAGTTTGGGCAACATATGAGGGGCTCAGTTTC 797

RESULT 12
AB093028 1243 bp mRNA linear PLN 02-APR-2003
LOCUS
DEFINITION
AB093028
AB093028
AB093028.1 GI:29467498
VERSION
KEYWORDS
SOURCE
ORGANISM
Pyrus communis (pear)
Pyrus communis
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids I; Rosales; Rosaceae; Maloideae; Pyrus.
1
Hiwasa, K., Rose, J. K., Nakano, R., Inaba, A. and Kubo, Y.
Differential expression of seven alpha-expansin genes during growth
and ripening of pear fruit
Unpublished
2 (bases 1 to 1243)
JOURNAL
AUTHORS
TITLE
JOURNAL
Direct Submission
Submitted (08-OCT-2002) Kyoto Hiwasa, Okayama University, Graduate
School of Natural Science and Technology; Tsuchima-naka 1-1-1,
Okayama, Okayama 700-8530, Japan
(E-mail: k-hiwasac@okayama-u.ac.jp, Tel: 81-86-251-8338,
Fax: 81-86-251-8338)
Location/Qualifiers

FEATURES
Source
1. 1243
/organism="Pyrus communis"
/mol_type="mRNA"
/cultivar="La France"
/db_xref="taxon:23211"
/c1seu_type="softening fruit"
/dev_stage="ripening fruit"
/country="Japan"
1. 1243
/gene="PcExp1"
40. 804
/gene="PcExp1"
/codon_start=1
/product="expansin"
/protein_id="BAC67188.1"
/db_xref="GI:29467498"
/translation="MAFTLSHTIALFLVNLICLOGTGDTGGEGHATFYGGD
ASGTGAGAGCYGNLYSOQGYNTALSTLFDNSGSCGACYEMKNDPFCPLTIVT
ATNFCPNNLALSTNGGMCNPLQHPDLAPAKIQAQYRAQIVPVSFRVPCVKKG
GVVRFVTHSHSYFNILITNVAGADVAIVSIKGSNTGQPMRNMGNQMSNYLNGQT
LSFOVTASDQRITSLNVAPAGNMFQGTGAGP"

ACCESSION	AB010444.4						
VERSION	AB010444.4.1 GI:29421121						
KEYWORDS							
SOURCE	<i>Vitis labrusca</i> x <i>Vitis vinifera</i>						
ORGANISM	<i>Vitis labrusca</i> x <i>Vitis vinifera</i> Eukaryote; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; Vitaceae; Vitis.						
REFERENCE	1 Ishimaru,M. and Kobayahi,S. <i>Ectomorphology of expansion genes is related grape berry softening</i> Unpublished 2 (bases 1 to 1195) Ishimaru,M. Direct Submission Submitted (21-FEB-2003) Megumi Ishimaru, Osaka Prefecture University, Graduate School of Agriculture and Biological Sciences; 1-1, Gakuen-cho, Sakai, Osaka 599-8531, Japan [E-mail:m.ishimaru@plant.osakaifu-u.ac.jp, Tel.:81-72-254-9419, Fax:81-72-254-9418]						
FEATURES	Location/Qualifiers						
source	1..1195						/organism="Vitis labrusca x Vitis vinifera"
	/mol_type="mRNA"						
	/cultivar="Kyoho"						
	/db_xref="taxon:105599"						
	/clone_id="Uni-Zap XR grape berry cDNA"						
	/dev_stage="veraison"						
	/country="Japan"						
gene	1..1195						/gene="Vexp-3"
CDS	55..813						/gene="Vexp-3"
	/codon_start=1						
	/product="expansin"						
	/protein_id="BAC66696.1"						
	/db_xref="GI:29421122"						
	/translation="MATAPRSSISLALFLFCLLOGANGDYGBEGHATFYGGDAS GTMAGCGGNLYSQGVNTAIALSTALEFNLSGCACYEMKNDPDKLPGLVTAT ATNFCPPNLAINSTMGMWCPLOHPDLAEPAFOIAOYRAGIVPSFRVPCKKGQ IRTIINYSFNI.VLTINVAGDVRAVSIGSKTGQPMWRMGMWGNSYLNGQT LSQVTAADSDRMVTSLNVAPMGQFGTYGAQP"						
BASE COUNT	306 a 284 C 306 g 299 t						
ORIGIN							
Alignment Scores:							
Pred. No.:	8,56e-102		length:		1195		
Score:	1138.00		Matches:		201		
Percent Similarity:	87.01%		Conservative:		20		
Best Local Similarity:	79.13%		Mismatches:		29		
Query Match:	81.64%		Indels:		4		
DB:	8		Gaps:		1		
US-09-383-579C-10 (1-250) X AB010444.4 (1-1195)							
OY	1 MetalaPheserTySerPropheserSeLeunpheleunProphetheValPhe 20						
Db	::: :: :: :						
OY	49 CTCTCAATGGCTACTGACGATTTCCTTATCTCTCCCTCTTTCTCTGTCTA 108						
OY	21 ThrPhe-----AlaaPyrGYlTYTrglnserGYhsalatrnhetyr 36						
Db	109 TGCCTCCAMAGGCCAAATGTGTACTAATGGTGGGAMAAGCGGGCATGACACATTGTAT 168						
OY	37 GLVGlyVaPaLaSaSerGYThMeTGLyVALAcysGLyTYrgLyAnLeuTySer 56						
Db	169 GGCGGTGTACACCCTCAGCACAAATGGGTGGGCTTGTGGRTATGGCACTTGTACAGC 228						
OY	57 GlngLYTyriGLyThrAsnthrValAlaLeuSerThraAlaLeuPheaAnaNglyLeuSer 76						
Db	229 CAAGGGATATGGACAACAACCTGACAGCTCTCAGCACCGCTCTTCAACAGTGGGCTGAGC 288						
OY	77 CyegLYAlaCyPheglwtehtmrCYsrThraMaSpProLystrPYcylseuProglyThr 96						
	:						

Db 289 TGTGGGCGATGTTACGAGATGAATGCAACAGTACCCCAATGTGCTCCCGAGGACC 348
 Qy 97 11eargvalThralaThrasnPhesCysProproAsnPhelaLeuProAsnAsnGly 116
 Db 349 CTAAACGTGACTGCGCAAACTTCTGCTCTCTTAACCTTGCGCTTGTCACACACAGGCG 408
 Qy 117 GlyTTPCysAnpProProLeuGlnHisPheAspMetAlaGluProAlaPheLeuGlnIle 136
 Db 409 GGATGTGTCATCCCGCTTCAGACACTTGATCTAGCTGAGCTGCTGCTCTCTCAAGTT 468
 Qy 137 AlAGlnIYrArGAlaGlyIleValProValSerPheArGArValProCysMetIYLeu 156
 Db 469 GCCCAGTACCGAGCTGGAATGCTGCTGCTTTCAGAAAGAGTCCCTGTGTCAAGAAA 528
 Qy 157 GlyValAlaArgPheThrIleAsnGlyHisSerTyrPheAsnLeuValIleThrAsn 176
 Db 529 GGAAGGATCCGCTTACCATCAACGCGCACTCTCTCACTTCACTTGTCATACAAAC 588
 Qy 177 ValGlyValAlaGlyAspValHisSerValSerIleLeuGlySerArGThrGlyTTPGln 196
 Db 589 GTGGCCGAGAGAGAGAGTCAAGACAGTATCAATAAAGGGGTCTAAGACCGGCTGGCAG 648
 Qy 197 SerMetSerArGArGArGArGArGArGArGArGArGArGArGArGArGArGArG 216
 Db 649 CCCATGTCAAGGAAGTGGGGCCAGACCTGCGAGAGCACTCATCTCAACGCGCAGACC 708
 Qy 217 LeuSerPheGlnValThrLeuSerAspGlyArGThrLeuThrAlaIYrAsnLeuValPro 236
 Db 709 CTCCTCATTCAGACGACGACGAGCGAGCGGACCATGACAGACCTTCATGTGGCCTT 768
 Qy 237 SerAsnTrpGlnPheGlyGlnThrTyrGlyGlyProGlnPhe 250
 Db 769 GCTGCTGGCGAGTGTGGGCAACATATGAGGGGCTCATGTT 810

RESULT 14
 AB093029 1153 bp mRNA linear PLAN 02-APR-2003
 LOCUS Pyrus communis Pcbxp2 mRNA for expansin, complete cds.
 DEFINITION AB093029
 ACCESSION AB093029
 VERSION AB093029.1 GI:29467500
 KEYWORDS
 SOURCE
 ORGANISM
 Pyrus communis (pear)
 Pyrus communis
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 rosids; eurosids I; Rosales; Rosaceae; Maloideae; Pyrus.

REFERENCE
 AUTHORS
 TITLE
 JOURNAL
 REFERENCE
 AUTHORS
 TITLE
 JOURNAL
 1 Hiwasa, K., Rose, J. K., Nakano, R., Inaba, A. and Kubo, Y.
 Differential expression of seven alpha-expansin genes during growth
 and ripening of pear fruit
 Unpublished
 2 (bases 1 to 1153)
 Hiwasa, K., Kubo, Y., Nakano, R. and Inaba, A.
 Direct Submission
 Submitted (08-OCT-2002) Kyoto Hiwasa, Okayama University, Graduate
 School of Natural Science and Technology, Tsushima-naka 1-1-1,
 Okayama, Okayama 700-8530, Japan
 (E-mail: hiwasa@cc.okayama-u.ac.jp, Tel: 81-86-251-8338,
 Fax: 81-86-251-8338)

FEATURES
 source
 location/Qualifiers
 1..1153
 /organism="Pyrus communis"
 /mol_type="mRNA"
 /cultivar="La France"
 /db_xref="taxon:23211"
 /tissue_type="softening fruit"
 /dev_stage="ripening fruit"
 /country="Japan"
 1..1153
 /gene="Pcbxp2"
 59..820
 /gene="Pcbxp2"
 /codon_start=1

gene
 CDS
 59..820
 /gene="Pcbxp2"
 /codon_start=1

/product="expansin"
 /protein_id="BAC67189.1"
 /db_xref="GI:29467501"
 /translation="MAFTSHSTTALLPFLVNLCLQGFGDYGGGWEGHAPYGGGDA
 SGTMGACAGTGNLYSOGSCTGNALSTALPNNLSGSGCTEMKCGSPKRCLESTIV
 TATNFCPNAQNDNGWNCNPLQHFDLAEPFLKIQAGI VPISTFRVSCVKRG
 GIFTNGHSYFNLVLTIVGAGDVHSVSKSKTGMQPLSRNMGQNSNLSYLNQ
 SLSPQYTTSDGRILTANNVAPGMWQFGQTFEGSQF"
 59..133
 /gene="Pcbxp2"
 /evidence=not_experimental

BASE COUNT 309 a 258 c 281 g 305 t
 ORIGIN

Alignment Scores:
 Pred. No.: 9 17e-102 length: 1153
 Score: 1137.50 matches: 206
 Percent Similarity: 88.93% conservative: 19
 Best Local Similarity: 81.42% mismatches: 25
 Query Match: 81.60% indels: 3
 DB: 8 gaps: 3

US-09-383-579c-10 (1-250) x AB093029 (1-1153)

Qy 1 MetAlaPhe---SerTyrSerProPheSerSerLeu---PheLeuLeuProPhePhe 18
 Db 59 ATGGCTTTTACTTCTCACTCCACCATTCGCTCTTGTCTTGTCTTCATCTATGCTT 118
 Qy 19 ValPheThrPheAlaAspIYr---GlyGlyTTPGlnSerGlyHisAlaThrPheTyrGly 37
 Db 119 CAAGTCTCTTTTGCTGCTCTGTGAGGTGATGGAGGCGCGCCATGCAATTTATAGT 178
 Qy 38 GlyGlyAspAlaSerGlyThrMetGlyValAlaCysGlyTyrGlyAsnLeuTyrSerGln 57
 Db 179 GGTGGTATGCTCTTGACAAATGAGAGGCTGTGTGATATGGAACTTGACGCCAA 238
 Qy 58 GlyTyrGlyThrAsnThrValAlaLeuSerThrAlaLeuPheAsnAsnGlyLeuSerCys 77
 Db 239 GGGTACGGAACCAACATGACGACGACGACGACGACGACGACGACGACGACGACG 298
 Qy 78 GlyAlaCysPheGluMetThrCysThrAsnAspProIYrTyrCysLeuProGlyThrIle 97
 Db 299 GGGCTCTGTATAGATGAATGTGGCAGTGGACCCCAATATGTGCTCCCGGCGAGCATC 358
 Qy 98 ArgValThrAlaThrAsnPhesCysProproAsnPhelaLeuProAsnAsnAsnGlyGly 117
 Db 359 ATGCTACCGCCACCACTTCTGCTCCCACTTGGCGAGGCCAACGACATGTGGC 418
 Qy 118 TrpCysAnpProProLeuGlnHisPheAspMetAlaGluProAlaPheLeuGlnIleAla 137
 Db 419 TGGTGCAACCTCTCTCTCCAGCACTTGATTTGGCTGAGCTGCTTTCTGAAATGGCC 478
 Qy 138 GlnTyrArGAlaGlyIleValProValSerPheArGArValProCysMetIYLeuGly 157
 Db 479 CAATACAGACGTGAATGTGCCCATCTCTTCAGAGGGTTGCTGTGAGAAAGGA 538
 Qy 158 GlyValAlaArgPheThrIleAsnGlyHisSerTyrPheAsnLeuValIleThrAsnVal 177
 Db 539 GGAATAGAGTTCACAAACACGCGCACTTCACTCAACTGCTTTGATGATCAACAGCTC 598
 Qy 178 GlyValAlaGlyAspValHisSerValSerIleYserIYSerArGThrGlyTTPGlnSer 197
 Db 599 GGAAGAGCAGAGACGTCCTCTGTCTGTCAATCAAGGTTCCAAAGAGGTGCAACC 658
 Qy 198 MetSerArGArGArGArGArGArGArGArGArGArGArGArGArGArGArG 217
 Db 659 CTGTCAGAAATGTTGGGCGCAGAACTGGCAGAGCAACTTACCTCAACGCGCAGAGCTC 718
 Qy 218 SerPheGlnValThrLeuSerArGArGArGArGArGArGArGArGArGArGArGAr 237
 Db 719 TCCTTCAGGTTCACACACGAGGAGGAGAACTTCAACCGCAACATGTTGCGCGGGA 778
 Qy 238 AsnTrpGlnPheGlyGlnThrTyrGlyGlyProGlnPhe 250

```

Db      779 AACTGCACTCGACAAACATTGAGGCACTCAATTC 817
RESULT 15
AB093030      1118 bp  mRNA  linear  PLN 02-APR-2003
LOCUS      Pyrus communis Pcedxp3 mRNA for expansin, complete cds.
DEFINITION
ACCESSION  AB093030
VERSION    AB093030.1 GI:29467502
KEYWORDS
SOURCE
ORGANISM   Pyrus communis (pear)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            rosids; eurosids I; Rosales; Rosaceae; Maloideae; Pyrus.
REFERENCE
AUTHORS    Hiwasa,K., Rose,U.K., Nakano,R., Inaba,A. and Kubo,Y.
TITLE      Differential expression of seven alpha-expansin genes during growth
            and ripening of pear fruit
JOURNAL    Unpublished
            2 (bases 1 to 1118)
AUTHORS    Hiwasa,K., Kubo,Y., Nakano,R. and Inaba,A.
TITLE      Direct Submission
JOURNAL    Submitted (08-OCT-2002) Kyoto Hiwasa, Okayama University, Graduate
            School of Natural Science and Technology; Tsubhima-naka 1-1-1,
            Okayama, Okayama 700-8530, Japan
            (E-mail:k-hiwasaecc.okayama-u.ac.jp, Tel:81-86-251-8338,
            Fax:81-86-251-8338)
FEATURES
source
            1..1118
            /location/Qualifiers
            /organism="Pyrus communis"
            /mol_type="mRNA"
            /cultivar="La France"
            /db_xref="taxon:32311"
            /cissue_type="softening fruit"
            /dev_stage="ripening fruit"
            /country="Japan"
            1..1118
            /gene="Pcedxp3"
            /gene="Pcedxp3"
            /CDS
            74..838
            /gene="Pcedxp3"
            /codon_start=1
            /product="expansin"
            /protein_id="BAC67190.1"
            /db_xref="GI:29467503"
            /translation="MAAAHLSFAPIALSVLLENLHAGVAVYGSMEGAHATFYGGSD
            ASGTMGACAGNLYSGGYNTALSTLALFNNGLSCGCEMRCDNDRMCRPGSII
            VTAIINCPENPAOSNDNGMCNPLQHPFLABPAFLQIQAIVPSPFRVPCVK
            GGIIRPTNGHSYFNLVLTNNVAGAGDVHSVSKGARTGQPMRNMGNQMSNYLNG
            QALSFOVITSDGRTVTSNVAPGNMFGQTFSGGP"
            74..154
            /gene="Pcedxp3"
            /evidence=not experimental
sig_peptide
            /evidence=not experimental
BASE COUNT  309 a 253 c 240 g 316 t
ORIGIN
Alignment Scores:
Pred. No.:      2.17e-101      Length:      1118
Score:          1133.50      Matches:      201
Percent Similarity: 87.60%      Conservative: 18
Best Local Similarity: 80.40%      Mismatches:  30
Query Match:    81.31%      Indels:      1
DB:             8      Gaps:      1
US-09-383-579c-10 (1-250) x AB093030 (1-1118)
QY      2 AAlphaserTyserPropheser---SerleuPheleuLeuProPhePheValphe 20
DB      86 GCATTGCTTTTGTCTTATGACCTCTGTGTTCTTTATCTACATCTGCATGGT 145
QY      21 ThrPheAlaSerTyrglyGlyTyrGlnSerGlyHisAlaThrPheTyrglyGlyAap 40
DB      146 GATATTGCTGTTTAATGAGTACTGGAGAGCGCTCATGCCAATTTTACGGTGGCGGTGAT 205

```

```

QY      41 AlaSerGlyThrMetGlyGlyAlaAcylGlyTyrGlyAaenLeuTyrSerGlnGlyTyrGly 60
DB      206 GCTTCGTGCACAAATGGAGAGCATGTGTATGGAAATTTGTACAGCCAGGGATATGGA 265
QY      61 ThrAenThrValAlaLeuSerThrAlaLeuPheAaenAnglyLeuSerCysGlyAlaCys 80
DB      266 ACCAACACTGCAGCTTTAGACACACATGTTTCACAAATGCTTAAGCTGTGGCTTGT 325
QY      81 PheGlnMetThrCysThrAaenAaPProlySTyrCysLeuProGlyThrIleArgValThr 100
DB      326 TATGAATGAGATGGAGCAATGACCCGAGATGTCCTCCCTCGATCCATCATTTGTAAT 385
QY      101 AlaThrAenPheCysProProAaenPheAlaLeuProAaenAaenAnglyGlyTyrCysAaen 120
DB      386 GCTACAAACTTTTGGCCCTCTTAACCTTCTCAGTCCACGACAAATGCGGATGTGCAT 445
QY      121 ProProLeuGlnHisPheAaenPheAlaGluProAlaPheLeuGlnIleAlaGlnTyrArg 140
DB      446 CTTCTCTCCACATTTGCAATTTGGCTGAGCTGCTTTCTTCCAAATTCGCCAATACCT 505
QY      141 AlaGlyIleValProValSerPheArgArgValProCysMetLeuGlyGlyValArg 160
DB      506 GCTGGAATCGTCCCGGTTTCTTCAAGAGTACCTGTGTGAAGAAAGAGGATTAAGA 565
QY      161 PheThrIleAenGlyHisSerTyrrPheAaenLeuValIleThrAaenValGlyGlyAla 180
DB      566 TTCACCATCAACAGGCGACCTCTTCAACCTGGTTTGTATACCAACGCTGGCTGGGCA 625
QY      181 GlyAaenValHisSerValSerIleLeuGlySerAaGlnGlyTyrGlnSerMetSerArg 200
DB      626 GAGACGTCATTCATGTTTCATCAAGGGGTCCAAACAGGGTGCAACCCATGTCACAGA 685
QY      201 AaenTyrGlyAaenTyrGlnSerAaenAaenTyrrLeuAaenGlyGlnGlyLeuSerPheGln 220
DB      686 AACTGGGGGCAAAACTGGGAGAGCAACTTACCTCAATGCGCAAGCCCTCTCTCCAA 745
QY      221 ValThrLeuSerAaenGlyArgThrLeuThrAlaTyrrAaenLeuValProSerAaenTyrGln 240
DB      746 GTACACACACAGTACGAGTGAACCGTCAACAGCTCAACAGTCCGCTGTGTAATGGCAG 805
QY      241 PheGlyGlnThrTyrrGlyGlyProGlnPhe 250
DB      806 TTTGCTACACATTCCTCGGGGGGTCAATTT 835

```

Search completed: December 19, 2003, 00:28:23
 Job time : 2807 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: December 18, 2003, 22:32:07 ; Search time 258 Seconds
(without alignments)
2615.735 Million cell updates/sec

Title: US-09-383-579c-10
Perfect score: 1394
Sequence: 1 MAFSYSPFSSILFLPFVF.....AYNLVSNMWFQGTGEGPQR 250

Scoring table:
BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 2552756 seqs, 1349719017 residues

Total number of hits satisfying chosen parameters: 5105512

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
-MODE=frame+ p2n.model -DEV=x1p
-Q=Cgrr2.1/USFTO.spool_p/US0933579/runat.18122003.171926.28762/app.query.fasta.1.391
-DB=N-Geneseq.15Jun03 -OPMT=faetap -SUFFIX=ring -MINMATCH=0.1 -LOOPEXT=0
-LOOPEXT=0 -UNITS=b1ts -START=1 -END=-1 -MATRIX=b1osunet2 -TRANS=human40.cdi
-LIST=45 -DOCALLIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=plc -NORM=ext -HEAPSIZE=500 -MINLEN=2000000000
-USRR=US09383579 @CNC 1.1 490 @runat.18122003.171926.28762 -NCPU=6 -ICPU=3
-NO_MMAP -IARSEQUTRY -NEG_SCORES=0 -WAIT -DSPBLOC=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :
N-Geneseq.15Jun03.*
1: /SIDS1/gcgdata/geneseg/geneseqn-emb1/NA1980.DAT.*
2: /SIDS1/gcgdata/geneseg/geneseqn-emb1/NA1981.DAT.*
3: /SIDS1/gcgdata/geneseg/geneseqn-emb1/NA1982.DAT.*
4: /SIDS1/gcgdata/geneseg/geneseqn-emb1/NA1983.DAT.*
5: /SIDS1/gcgdata/geneseg/geneseqn-emb1/NA1984.DAT.*
6: /SIDS1/gcgdata/geneseg/geneseqn-emb1/NA1985.DAT.*
7: /SIDS1/gcgdata/geneseg/geneseqn-emb1/NA1986.DAT.*
8: /SIDS1/gcgdata/geneseg/geneseqn-emb1/NA1987.DAT.*
9: /SIDS1/gcgdata/geneseg/geneseqn-emb1/NA1988.DAT.*
10: /SIDS1/gcgdata/geneseg/geneseqn-emb1/NA1989.DAT.*
11: /SIDS1/gcgdata/geneseg/geneseqn-emb1/NA1990.DAT.*
12: /SIDS1/gcgdata/geneseg/geneseqn-emb1/NA1991.DAT.*
13: /SIDS1/gcgdata/geneseg/geneseqn-emb1/NA1992.DAT.*
14: /SIDS1/gcgdata/geneseg/geneseqn-emb1/NA1993.DAT.*
15: /SIDS1/gcgdata/geneseg/geneseqn-emb1/NA1994.DAT.*
16: /SIDS1/gcgdata/geneseg/geneseqn-emb1/NA1995.DAT.*
17: /SIDS1/gcgdata/geneseg/geneseqn-emb1/NA1996.DAT.*
18: /SIDS1/gcgdata/geneseg/geneseqn-emb1/NA1997.DAT.*
19: /SIDS1/gcgdata/geneseg/geneseqn-emb1/NA1998.DAT.*
20: /SIDS1/gcgdata/geneseg/geneseqn-emb1/NA1999.DAT.*
21: /SIDS1/gcgdata/geneseg/geneseqn-emb1/NA2000.DAT.*
22: /SIDS1/gcgdata/geneseg/geneseqn-emb1/NA2001A.DAT.*
23: /SIDS1/gcgdata/geneseg/geneseqn-emb1/NA2001B.DAT.*
24: /SIDS1/gcgdata/geneseg/geneseqn-emb1/NA2002.DAT.*
25: /SIDS1/gcgdata/geneseg/geneseqn-emb1/NA2003.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed.

and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1275	91.5	681	17	AAT13320
2	1275	91.5	681	24	ABA97162
3	1275	91.5	684	24	ABA97161
4	1085	77.8	762	24	AB213283
5	1085	77.8	1015	21	AA48712
6	1085	77.8	1016	21	AA48712
7	1071.5	76.9	1144	24	AA40777
8	1041	74.7	780	21	AA32964
9	1041	74.7	1198	21	AA30628
10	1041	74.7	1233	21	AA33521
11	1036.5	74.4	753	24	AA30633
12	1030	73.9	687	24	AB21286
13	1026.5	73.6	1334	21	ABA97164
14	1024.5	73.5	1336	21	AA47530
15	1024	73.5	1336	21	AA40169
16	1024	73.5	747	24	AB213264
17	1011.5	72.6	1236	21	AA40035
18	1009.5	72.4	1212	21	AA47991
19	999	71.7	1167	22	AA45165
20	993	71.2	774	24	AA03713
21	993	71.2	1319	21	AB212284
22	970	69.6	1205	21	AA44930
23	965	69.2	1201	21	AA43121
24	944	67.7	824	21	AA44975
25	942	67.6	1276	24	AA42473
26	939	67.4	774	24	AA43263
27	939	67.4	1037	21	AB213037
28	938	67.3	893	24	AA42618
29	934	67.0	1236	21	AB298723
30	928	66.6	1213	22	AA34714
31	919.5	66.0	2415	17	AA03711
32	919.5	66.0	2415	17	AA30268
33	919.5	66.0	2415	17	AA31053
34	889.5	63.8	2415	18	AA770039
35	889.5	63.8	1291	21	AA50400
36	870	62.4	1233	21	AA37064
37	857.5	61.5	980	21	AA41263
38	838.5	60.2	1103	22	AA03712
39	836.5	60.0	768	24	AB213241
40	831	59.6	702	20	AA68446
41	826.5	59.3	488	21	AA68446
42	795	57.0	1132	21	AA293525
43	786	56.4	537	20	AA38981
44	771	55.3	475	21	AA68448
45	732	52.5	695	21	AA293526
			501	20	AA41531
					AA68447

ALIGNMENTS

RESULT 1
AAT13320
ID AAT13320 standard; DNA; 681 BP.
XX
XX
AC AAT13320;
XX
XX
DT 25-MAR-2003 (updated)
DT 08-JUL-1996 (first entry)
XX
XX
DE Cucurbit expansin-29 cDNA.
XX
KW Expansin-29; plant cell wall; cellulose; paper recycling; de-inking;
KW polyaccharide; cucumber; ss.
XX
XX
OS Cucumis sativus var. Burpee Pickler.
XX
XX
PN AU9540262-A.

XX 04-APR-1996.
 PD 06-DEC-1995; 95AU-0040262.
 XX
 PF 12-MAY-1993; 93US-0060944.
 PR 12-MAY-1995; 95US-0440517.
 PR 12-MAY-1994; 94AU-0068320.
 XX
 (PENN-) PENN STATE RES FOUND.
 PA Cosgrove DJ, McQueen-Mason S;
 PI WPI, 1996-201150/21.
 DR P-PSDB; AAR94527.
 XX
 PT Expansin proteins which alter the mechanical strength of
 PT poly:saccharide(s) - useful in paper mfr. and recycling
 PS Disclosure; Page 30; 60pp; English.
 XX
 CC A cDNA clone (AAT13320) codes for cucumber expansin-29 (AAR94527),
 CC a member of a novel class of proteins that catalyse the extension of
 CC plant cell walls and the weakening of the hydrogen bonds in pure
 CC cellulose. It was obcd. by PCR amplification of cucumber seedling
 CC cDNA using primers based on isolated peptide fragments of the protein.
 CC The gene can be expressed in bacterial or other systems for use in
 CC recombinant expansin prodn. Expression of the gene in transgenic
 CC plants may allow alteration of plant growth characteristics,
 CC while expression in plant tissue cultures may allow improved prodn.
 CC of useful chemicals
 CC (Updated on 25-MAR-2003 to correct PF field.)
 CC (Updated on 25-MAR-2003 to correct PR field.)
 CC
 SQ Sequence 681 BP; 161 A; 179 C; 164 G; 177 T; 0 other;

Alignment Scores:
 Pred. No.: 1,48e-125 Length: 681
 Score: 1275.00 Matches: 227
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 91.46% Indels: 0
 DB: 17 Gaps: 0

US-09-383-579c-10 (1-250) x AAT13320 (1-681)

QY 24 AAPTYYGLVGLYTRDQINSERGLYHISALATNRPHEHYRGLVGLVYASPAIASERGLY 43
 DB 1 GACTACGGTGGCTGGAGAGCGGCCACGCTTTATGCGTGGTGTACCGCATCTGGC 60
 QY 44 ThrMetGLVGLVYALACysGLYTYRGLYaaNLeuTYRserGLInGLYTYRGLYThrAsnThr 63
 DB 61 ACCATGGGGTGGAGCTTGTGGGTATGGGAATTATACAGCCAAAGGATGGCAGAAACAG 120
 QY 64 ValAlaLeuSerThrAlaLeuPheAsnAsnGLYLeuSerCysGLYALACysPheGLYMet 83
 DB 121 GGGGGCTAGACATGGCTGCTATTTAACAATGATTAAGTTGGTGGCTTGGCAATG 180
 QY 84 ThrCysThrAsnAspProLysTrpCysLeuProGLYThrLlArgValThrAlaThrAsn 103
 DB 181 ACTTGACAAAGCAGCCCTAAATGGTGCCTTCGGGAACTATTAGGGTCACTGCCACCAAC 240
 QY 104 PheCysProProAsnBheAlaLeuProAsnAsnAsnGLYTYRProCysAsnProProLeu 123
 DB 241 TTTTGGCCCTCAATCTTGTCTCTCCCTAACAAATGGATGGATGGCAACCTCCTCTC 300
 QY 124 GlnHisPheAspMetKlaGluProAlaPheLeuGlnIleAlaGlnIlyrArgAlaGlyIle 143
 DB 301 CAACACTTGTGACATGGCTGAGCTGCTCTTCCTCAATGCTCAATACCGACCTGGTATC 360
 QY 144 ValProValSerPheArgArgValProCysMetLysLysGLYGLYValArgPheThrIle 163
 DB 361 GTCCCGCTCTCTTTTGGTGGGTACCATGATGAGAAAGGTGGAGTGAAGTTTACATTC 420

QY 164 AenGLYHisSerTYRPhenAsnLeuValLeuIleThrAsnValGLYValAGLYAspVal 183
 DB 421 AATGGCCACTCACTCACTCACTCTTTTGATCACAAAAGTCGGTGGCGAGGCACGTC 480
 QY 184 HisSerValSerIleLysGLYSerArgThrGLYTPGINSerMetSerArgAsnTrpGLY 203
 DB 481 CACTCTGTGTGATTAAGGGGTCTCGAACTGGATGGCAATCCATGTCTAGAAATTGGGGC 540
 QY 204 GlnAsnTrpGlnSerAsnAsnTYRLeuAsnGLYngInGLYLeuSerPheGlnValThrLeu 223
 DB 541 CAAACTGCAAAAGCAACACTATCTCAATGGCCAGGCTTTCCTTCAAGTCACTCTT 600
 QY 224 SerAspGLYArgThrLeuThrAlaTYRAsnLeuValProSerAsnTrpGlnPheGLYGln 243
 DB 601 AGTGATGTGTGACACTCACTCACTCAATATCTGTTCTTCCAAATGGCAATTGGCCAA 660
 QY 244 ThrTYRGLUGLYProGlnPhe 250
 DB 661 ACTTATGAAGGCTCAATTC 681

RESULT 2
 ABA97162
 ID ABA97162 standard; DNA; 681 BP.
 XX
 AC ABA97162;
 XX
 DT 19-APR-2002 (first entry)
 XX
 DE C. sativus DNA encoding expansin csexp1a.
 XX
 KW Expansin; cellulose-based textile; cotton; paper recycling; csexp1a;
 KM paper pulp; plant tissue; papermaking; gene; cucumber; de.
 XX
 OS Cucumis sativus.
 XX
 FH Key Location/Qualifiers
 FT CDS 1..681
 FT /*tag= a
 FT /partial
 FT /product= "csexp1a"
 FT /note= "No start or stop codon given"
 XX
 PN DE10032630-A1.
 XX
 PD 22-NOV-2001.
 XX
 PF 05-JUL-2000; 2000DE-1032630.
 XX
 PR 16-MAY-2000; 2000DE-1023561.
 XX
 PA (FARB) BAYER AG.
 XX
 DR Berendes F, Rast HG, Vogt U, Gouloudis C;
 XX
 DR WPI, 2002-155755/21.
 XX
 DR P-PSDB; AAG80769.
 XX
 PT Vector encoding an expansin, useful in treatment of cellulosic
 PT materials for paper recycling, providing large-scale production
 PS Claim 2; Page 14-16; 22pp; German.

This invention describes a novel vector (A) comprising (i) nucleic acid (II) encoding an expansin (II) and (ii) coupled sequences that allow expression of (I) in microorganisms. The recombinant expansins described in the invention are used in preparation, treatment and finishing of cellulose-based textiles (e.g. cotton) or in recycling of paper or for preparation of pulp from plant tissue, as a substitute for corrosive chemicals currently used in papermaking. Recombinant methods make possible large scale production of expansins possible. This sequence encodes the Cucumis sativus (cucumber) expansin, csexp1a, described in the invention.

XX Sequence 681 BP; 161 A; 178 C; 164 G; 178 T; 0 other;

Alignment Scores:

Pred. No.:	1,48e-125	Length:	681
Score:	1275.00	Matches:	227
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	91.46%	Indels:	0
DB:	24	Gaps:	0

US-09-383-579c-10 (1-250) x ABA97161 (1-681)

```

Qy 24 AspTyrGlyGlyTyrGlnSerGlyHleAlaThrPheTyrGlyGlyIleAspAlaSerGly 43
    |||||
Db 1 GACTACGGTGGCTGGAGAGCGGCGCACCCCTTTATGCGTGGTGCATCGCATCGGC 60
Qy 44 ThMeGlyGlyIleAlaCysGlyTyrGlyAsnLeuTyrSerGlnGlyTyrGlyThrAsnThr 63
    |||||
Db 61 ACCATGGGTGGAGCTGTGGGTATGGGAATTATATACGCCAAGGCTATGGCAGCAACAG 120
Qy 64 ValAlaLeuSerThrAlaLeuPheAsnAsnGlyLeuSerCysGlyIleAlaCysPheGluMet 83
    |||||
Db 121 GTGGCGGTGACACTGGCTATTACAAATGATTAAGTGTGCTGCTTCCGAATG 180
Qy 84 ThCysThrAsnAspProlySTyrCysLeuProGlyThrIleArgValThrAlaThrAsn 103
    |||||
Db 181 ACTTGTCACAAACGATCTTAATGTCCTTCCGGAACTATTAGGTCACGACCAAC 240
Qy 104 PheCysProProAsnPheAlaLeuProAsnAsnGlyIleTyrCysAsnProProLeu 123
    |||||
Db 241 TTTTGCCCTCTTAATCTTGGCTCTCCCTTAACAAATGATGTCACACCCCTCTC 300
Qy 124 GlnHisPheAsnMetAlaGluProAlaPheLeuGlnIleAlaGlnTyrArgAlaGlyIle 143
    |||||
Db 301 CAACATTTCCAAACGCTGAGCCCTGCTTCCCTCAATCGCTCAATCCGAGCCGATC 360
Qy 144 ValProValSerPheAsnArgValProCysMetLeuLeuGlyIleValArgPheThrIle 163
    |||||
Db 361 GTCCCTCTCTCTTCTTCTGAGGTACCATGATGAAAGAGGTGAGGTATTAACATC 420
Qy 164 AsnGlyHisSerTyrPheAsnLeuValLeuIleThrAsnValGlyIleAlaGlyAspVal 183
    |||||
Db 421 AATGGCCACTCATCTTCAACCTCGTTTGTATCAAAACGTCGGTGGCGAGGAGCTC 480
Qy 184 HisSerValSerIleLeuGlySerArgThrGlyTyrGlnSerMetSerArgAsnTyrGly 203
    |||||
Db 481 CACTCTGTCTGATMAAGGGGTCTCGAACTGATGCAATCCATGCTAGAAATTTGGGCG 540
Qy 204 GlnAsnTyrGlnSerAsnAsnTyrLeuAsnGlyIleGlnIleLeuSerPheGlnValThrLeu 223
    |||||
Db 541 CAATACTGGCAAGCAACACTATCTCAATGGCCAAAGGCTCTTCTTCAAGTACACTT 600
Qy 224 SerAspGlyArgThrLeuThrAlaTyrAsnLeuValProSerAsnTyrGlnPheGlyGln 243
    |||||
Db 601 AGTATGTGTGCACTCTCACTGCTATATCTCTTCTTCCATTTGGCAATTTGGCAG 660
Qy 244 ThrTyrGlnGlyProGlnPhe 250
    |||||
Db 661 ACCATGAGAGGCTCTCAATTC 681

```

RESULT 3

ABA97161 standard; DNA; 684 BP.

XX ABA97161;
 AC 19-APR-2002 (first entry)
 XX
 DE C. sativus DNA encoding SI expansin homologue.
 XX Expansin; SI; cellulose-based textile; cotton; paper recycling;
 KW paper pulp; plant tissue; papermaking; gene; cucumber; ds.

XX OS Cucumis sativus.

XX Key Location/Qualifiers

FT CDS 1..684
 FT /tag= a
 FT /partial
 FT /product= "SI expansin homologue"
 FT /note= "No start codon given"

XX DE10032630-A1.

XX PD 22-NOV-2001.

XX PF 05-JUL-2000; 2000DE-1032630.

XX FR 16-MAY-2000; 2000DE-1023561.

XX PA (PARB) BAYER AG.

XX PI Berendes F, Rast HG, Vogt U, Gouloudis C;

XX DR WPI; 2002-155755/21.

XX DR P-PSDB; AAG80768.

XX PT Vector encoding an expansin, useful in treatment of cellulosic

XX materials for paper recycling, providing large-scale production

XX PS Claim 2; Page 11-14; 22pp; German.

XX CC This invention describes a novel vector (A) comprising (i) nucleic acid
 CC (i) encoding an expansin (II) and (ii) coupled sequences that allow
 CC expression of (I) in microorganisms. The recombinant expansins described
 CC in the invention are used in preparation, treatment and finishing of
 CC cellulose-based textiles (e.g. cotton) or in recycling of paper or for
 CC preparation of pulp from plant tissue, as a substitute for corrosive
 CC chemicals currently used in papermaking. Recombinant methods make
 CC possible large scale production of expansins possible. This sequence
 CC encodes the Cucumis sativus (cucumber) SI expansin homologue described in
 CC the invention.

XX SQ Sequence 684 BP; 163 A; 179 C; 164 G; 178 T; 0 other;

Alignment Scores:

Pred. No.:	1,49e-125	Length:	684
Score:	1275.00	Matches:	227
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	91.46%	Indels:	0
DB:	24	Gaps:	0

US-09-383-579c-10 (1-250) x ABA97161 (1-684)

```

Qy 24 AspTyrGlyGlyTyrGlnSerGlyHleAlaThrPheTyrGlyGlyIleAspAlaSerGly 43
    |||||
Db 1 GACTACGGTGGCTGGAGAGCGGCGCACCCCTTTATGCGTGGTGCATCGCATCGGC 60
Qy 44 ThMeGlyGlyIleAlaCysGlyTyrGlyAsnLeuTyrSerGlnGlyTyrGlyThrAsnThr 63
    |||||
Db 61 ACCATGGGTGGAGCTGTGGGTATGGGAATTATATACGCCAAGGCTATGGCAGCAACAG 120
Qy 64 ValAlaLeuSerThrAlaLeuPheAsnAsnGlyLeuSerCysGlyIleAlaCysPheGluMet 83
    |||||
Db 121 GTGGCGGTGACACTGGCTATTACAAATGATTAAGTGTGCTGCTTCCGAATG 180
Qy 84 ThCysThrAsnAspProlySTyrCysLeuProGlyThrIleArgValThrAlaThrAsn 103
    |||||
Db 181 ACTTGTCACAAACGATCTTAATGTCCTTCCGGAACTATTAGGTCACGACCAAC 240
Qy 104 PheCysProProAsnPheAlaLeuProAsnAsnGlyIleTyrCysAsnProProLeu 123
    |||||
Db 241 TTTTGCCCTCTTAATCTTGGCTCTCCCTTAACAAATGATGTCACACCCCTCTC 300

```

QY 124 GlnHisPheAspMetAlaGluProAlaPheLeuGlnIleAlaGlnTyrArgAlaGlyIle 143
 Db 301 CAACACTTCGACATGCGTACGCTCTTCCTTCAATGCTCAATACCGAGCTGATTC 360
 QY 144 ValProValSerPheArgValProCysMetLysLysGlyValArgPheThrIle 163
 Db 361 GTCCCGTCTCTTCGTAGGGATACATATGAAAGAGTGGAGTGGATTACAAATC 420
 QY 164 AenGlyHisSerTyrPheAsnLeuValLeuIleThrAsnValGlyValAlaGlyAspVal 183
 Db 421 AATGGCCACTCATCTTCAACCTCGTTTGATCACAAGCTGGTGGCCAGCGACGTC 480
 QY 184 HisSerValSerIleLysLysSerArgThrGlyTyrGlnSerMetSerArgSerThrIle 203
 Db 481 CACTCTGTCATTAAGGGGTCCTCGAACCTGATGGCAATCCATGCTGAATAATGGGGC 540
 QY 204 GlnAsnTrpGlnSerAsnAsnTyrLeuAsnGlyGlnGlyLeuSerPheGlnValThrLeu 223
 Db 541 CAAAAGTGGCAAGCAACAATATCTCATATGGCCAAAGGCTTCCCTTCAAGTCACTCTT 600
 QY 224 SerAspGlyArgThrLeuThrAlaTyrAsnLeuValProSerAsnTrpGlnPheGlyGln 243
 Db 601 ACTGATGGTGGCACTCTCACTGCTATATCTGTTCTTCCCAATGGCAATTTGGCCAA 660
 QY 244 ThrTyrGlnGlyProGlnPhe 250
 Db 661 ACCTATGAAGGCCCTCAATTC 681
 RESULT 4
 AB213283
 ID AB213283 standard; DNA; 762 BP.
 AC AB213283;
 DT 21-JAN-2003 (first entry)
 XX Arabidopsis thaliana stress regulated gene SEQ ID NO 1088.
 DE Arabidopsis thaliana; plant; gene; stress; transgenic; ds.
 XX Arabidopsis thaliana.
 OS Arabidopsis thaliana.
 XX MO20021655-A2.
 PN 28-FEB-2002.
 XX 24-AUG-2001; 2001WO-US26685.
 PF 24-AUG-2000; 2000US-227866P.
 PR 26-JAN-2001; 2001US-264647P.
 PR 22-JUN-2001; 2001US-300111P.
 XX (SCR1) SCRIPPS RES INST.
 PA (SYGN) SYNGENTA PARTICIPATIONS AG.
 XX Harper JF, Kreps J, Wang X, Zhu T;
 PI WPI; 2002-304127/34.
 DR Identifying a stress condition to which a plant cell has been exposed
 PT and producing plants with increased tolerance to these abiotic stresses
 PT -
 XX Claim 144; SEQ ID NO 1088; 577bp + Sequence Listing; English.
 XX The invention relates to identifying a stress condition to which a plant
 CC cell has been exposed, comprising:
 CC (a) contacting nucleic acid representative of expressed polynucleotides
 CC in the plant cell with an array or probes representative of the plant
 CC cell genome; and
 CC (b) detecting a profile of expressed polynucleotides in the plant cell
 CC characteristic of a stress response. The method is useful in the
 CC production of transgenic plants, cells and seeds and in producing plants

CC with increased tolerance to abiotic stress. The present sequence is that
 CC of an Arabidopsis thaliana stress regulated gene (AB212196-AB217574) used
 CC in methods of the invention.
 CC Note: The sequence data for this patent is not represented in the printed
 CC specification but is based on sequence information supplied to Derwent by
 CC the European Patent Office.

XX Sequence 762 BP; 202 A; 196 C; 184 G; 180 T; 0 other;

Alignment Scores:

Alignment Scores:	2,35e-105	Length:	762
Pred. No.:	1085.00	Matches:	194
Score:	86.75%	Conservative:	22
Percent Similarity:	77.91%	Mismatches:	31
Best Local Similarity:	77.83%	Indels:	2
Query Match:	24	Gaps:	2

US-09-383-579C-10 (1-250) x AB213283 (1-762)

QY 4 SerTyrSerProPheSerSerLeuPheLeuLeuProPhePheVal---PheThrPhe 22
 Db 13 TCATCTTAAATATATTCATATATTCATATATTCGATTATTCCTCCAAAGAACTCAT 72
 QY 23 AlaAspTyrGlyValTyrGlnSerGlyHisAlaThrPheTyrGlyValAspAlaSer 42
 Db 73 GGAGACGACGAGGTGGCGAAGTGTGATGCAAGCCGCTTTACGGCGGCAAGATCTTCC 132
 QY 43 GlyThrMetGlyValAlaCysGlyTyrGlyAsnLeuTyrSerGlnGlyTyrGlyThrAsn 62
 Db 133 GGCAACATGAGGGCGAGCTTGTGCTATGGAATTTGTATGGCCAAGTTACCGAGCAAC 192
 QY 63 ThrValAlaLeuSerThrAlaLeuPheAsnAsnGlyLeuSerCysGlyValAspPheGlu 82
 Db 193 ACGGGCGCTTAAAGTACGCTCTATTCACAACGAGCTCACCTGTGGCGCTGTATGAG 252
 QY MetThrCysThrAsnAspProLysTrpCysLeuProGlyThrIleArgValThrAlaThr 102
 Db 253 ATGAAGTGTACGATGACCCGAGGTGTCTCGGGTCAACCATCACTCCACACTACA 312
 QY 103 AsnPheCysProProAsnPheAlaLeuProAsnAsnAsnGlyValTyrCysAsnProPro 122
 Db 313 AACTTTGGCCACCTAACCTCGCTCTTCACAGATATGAGGTTGGTCAATCCTCCT 372
 QY 123 LeuGlnHisPheAspMetAlaGluProAlaPheLeuGlnIleAlaGlnTyrArgAlaGly 142
 Db 373 CTTGACATTTTCGACCTCGCCGAGCAGCACTTTCTTCAGATCGCTCAGATGTCGCGC 432
 QY 143 IleValProValSerPheArgValProCysMetLysLysGlyValArgPheThr 162
 Db 433 ATTTGTTCTGTTCTTTCCGAGATGATGATGAAAGAGAAATAGGTTTACG 492
 QY 163 IleAsnGlyHisSerTyrPheAsnLeuValLeuIleThrAsnValGlyValAlaGlyAsp 182
 Db 493 ATCAACGAGCACTCATCTTCAACCTCGTTGATCTCCAAAGTGAAGAGACAGAGAC 552
 QY 183 ValHisSerValSerIleLysLysSerArgThr---GlyTyrGlnSerMetSerArgAsn 201
 Db 553 GTACACGGCGTCTCATCAAAAGGCTCAAAAACAGCTGTGCAAGCAATGCTGAAC 612
 QY 202 TrpGlyGlnAsnTrpGlnSerAsnAsnTyrLeuAsnGlyGlnGlyLeuSerPheGlnVal 221
 Db 613 TGGGACAAACTGGCAGACGCAATTCATCATGAACGACCAAGCCTTCTCCAGATA 672
 QY 222 ThrLeuSerAspGlyArgThrLeuThrAlaTyrAsnLeuValProSerAsnTrpGlnPhe 241
 Db 673 ACGACAGGAGGTGGCACTCGTTAGCAACAGACGTGGCTCTTATTTGGCAGATTG 732
 QY 242 GlyGlnThrTyrGlnGlyProGlnPhe 250
 Db 733 GGACAAACCTACCAAGGTGTCAAGTTG 759
 RESULT 5
 AAC48712

ID AAC48712 standard; DNA, 1015 BP.
XX AAC48712;
AC
XX 18-OCT-2000 (first entry)
DT
XX
DE Arabidopsis thaliana DNA fragment SEQ ID NO: 58484.
XX
KW Hybridisation assay; genetic mapping; gene expression control;
KW protein identification; signal transduction pathway;
KW metabolic pathway; promoter; termination sequence; ss.
XX
OS Arabidopsis thaliana.
PN
XX EP1033405-A2.
XX
PD 06-SEP-2000.
XX
PF 25-FEB-2000; 2000EP-0301439.
XX
XX 25-FEB-1999; 99US-0121825.
PR 05-MAR-1999; 99US-0123180.
PR 09-MAR-1999; 99US-0123548.
PR 22-MAR-1999; 99US-0125788.
PR 25-MAR-1999; 99US-0126264.
PR 29-MAR-1999; 99US-0126785.
PR 01-APR-1999; 99US-0127462.
PR 06-APR-1999; 99US-0128234.
PR 08-APR-1999; 99US-0128714.
PR 16-APR-1999; 99US-0129845.
PR 19-APR-1999; 99US-0130077.
PR 21-APR-1999; 99US-0130449.
PR 23-APR-1999; 99US-0130510.
PR 28-APR-1999; 99US-0130891.
PR 30-APR-1999; 99US-0132048.
PR 30-APR-1999; 99US-0132407.
PR 04-MAY-1999; 99US-0132484.
PR 05-MAY-1999; 99US-0132485.
PR 06-MAY-1999; 99US-0132486.
PR 07-MAY-1999; 99US-0132487.
PR 11-MAY-1999; 99US-0132863.
PR 14-MAY-1999; 99US-0134256.
PR 14-MAY-1999; 99US-0134219.
PR 14-MAY-1999; 99US-0134221.
PR 14-MAY-1999; 99US-0134370.
PR 18-MAY-1999; 99US-0134768.
PR 19-MAY-1999; 99US-0134941.
PR 20-MAY-1999; 99US-0135124.
PR 21-MAY-1999; 99US-0135353.
PR 24-MAY-1999; 99US-0135629.
PR 25-MAY-1999; 99US-0136021.
PR 27-MAY-1999; 99US-0136392.
PR 28-MAY-1999; 99US-0136782.
PR 01-JUN-1999; 99US-0137222.
PR 03-JUN-1999; 99US-0137528.
PR 04-JUN-1999; 99US-0137529.
PR 07-JUN-1999; 99US-0137724.
PR 08-JUN-1999; 99US-0138094.
PR 10-JUN-1999; 99US-0138540.
PR 10-JUN-1999; 99US-0138847.
PR 14-JUN-1999; 99US-0139119.
PR 16-JUN-1999; 99US-0139462.
PR 17-JUN-1999; 99US-0139463.
PR 18-JUN-1999; 99US-0139464.
PR 18-JUN-1999; 99US-0139455.
PR 18-JUN-1999; 99US-0139456.
PR 18-JUN-1999; 99US-0139457.
PR 18-JUN-1999; 99US-0139458.
PR 18-JUN-1999; 99US-0139459.
PR 18-JUN-1999; 99US-0139460.
PR 18-JUN-1999; 99US-0139461.
PR 18-JUN-1999; 99US-0139462.
PR 18-JUN-1999; 99US-0139463.
PR 18-JUN-1999; 99US-0139750.
PR 18-JUN-1999; 99US-0139763.
PR 21-JUN-1999; 99US-0139817.
PR 22-JUN-1999; 99US-0139899.
PR 23-JUN-1999; 99US-0140353.
PR 24-JUN-1999; 99US-0140354.
PR 24-JUN-1999; 99US-0140685.
PR 28-JUN-1999; 99US-0140823.
PR 29-JUN-1999; 99US-0140991.
PR 30-JUN-1999; 99US-0141287.
PR 01-JUL-1999; 99US-0141842.
PR 01-JUL-1999; 99US-0142154.
PR 06-JUL-1999; 99US-0142205.
PR 08-JUL-1999; 99US-0142380.
PR 09-JUL-1999; 99US-0142803.
PR 12-JUL-1999; 99US-0142920.
PR 13-JUL-1999; 99US-0143542.
PR 14-JUL-1999; 99US-0143624.
PR 15-JUL-1999; 99US-0144005.
PR 16-JUL-1999; 99US-0144085.
PR 19-JUL-1999; 99US-0144325.
PR 19-JUL-1999; 99US-0144331.
PR 19-JUL-1999; 99US-0144332.
PR 19-JUL-1999; 99US-0144333.
PR 19-JUL-1999; 99US-0144334.
PR 19-JUL-1999; 99US-0144335.
PR 20-JUL-1999; 99US-0144332.
PR 20-JUL-1999; 99US-0144632.
PR 21-JUL-1999; 99US-0144884.
PR 21-JUL-1999; 99US-0144814.
PR 21-JUL-1999; 99US-0145086.
PR 22-JUL-1999; 99US-0145088.
PR 22-JUL-1999; 99US-0145085.
PR 22-JUL-1999; 99US-0145087.
PR 22-JUL-1999; 99US-0145089.
PR 22-JUL-1999; 99US-0145192.
PR 23-JUL-1999; 99US-0145145.
PR 23-JUL-1999; 99US-0145218.
PR 23-JUL-1999; 99US-0145224.
PR 26-JUL-1999; 99US-0145276.
PR 27-JUL-1999; 99US-0145513.
PR 27-JUL-1999; 99US-0145918.
PR 27-JUL-1999; 99US-0145919.
PR 28-JUL-1999; 99US-0145951.
PR 02-AUG-1999; 99US-0146386.
PR 02-AUG-1999; 99US-0146388.
PR 02-AUG-1999; 99US-0146389.
PR 03-AUG-1999; 99US-0147038.
PR 04-AUG-1999; 99US-0147204.
PR 05-AUG-1999; 99US-0147192.
PR 05-AUG-1999; 99US-0147260.
PR 06-AUG-1999; 99US-0147303.
PR 06-AUG-1999; 99US-0147316.
PR 09-AUG-1999; 99US-0147493.
PR 09-AUG-1999; 99US-0147935.
PR 10-AUG-1999; 99US-0148171.
PR 11-AUG-1999; 99US-0148319.
PR 12-AUG-1999; 99US-0148341.
PR 13-AUG-1999; 99US-0148565.
PR 13-AUG-1999; 99US-0148684.
PR 16-AUG-1999; 99US-0149368.
PR 17-AUG-1999; 99US-0149175.
PR 18-AUG-1999; 99US-0149426.
PR 20-AUG-1999; 99US-0149723.
PR 20-AUG-1999; 99US-0149929.
PR 23-AUG-1999; 99US-0149902.

```

PR 23-AUG-1999; 99US-0149930.
PR 25-AUG-1999; 99US-0150566.
PR 26-AUG-1999; 99US-0150884.
PR 27-AUG-1999; 99US-0151065.
PR 27-AUG-1999; 99US-0151066.
PR 27-AUG-1999; 99US-0151080.
PR 30-AUG-1999; 99US-0151303.
PR 31-AUG-1999; 99US-0151438.
PR 01-SEP-1999; 99US-0151930.
PR 07-SEP-1999; 99US-0152363.
PR 10-SEP-1999; 99US-0153070.
PR 13-SEP-1999; 99US-0153758.
PR 15-SEP-1999; 99US-0154018.
PR 16-SEP-1999; 99US-0154039.
PR 20-SEP-1999; 99US-0154779.
PR 22-SEP-1999; 99US-0155139.
PR 23-SEP-1999; 99US-0155486.
PR 24-SEP-1999; 99US-0155659.
PR 28-SEP-1999; 99US-0156458.
PR 29-SEP-1999; 99US-0156596.
PR 04-OCT-1999; 99US-0157117.
PR 05-OCT-1999; 99US-0157753.
PR 06-OCT-1999; 99US-0157865.
PR 07-OCT-1999; 99US-0158029.
PR 08-OCT-1999; 99US-0158232.
PR 12-OCT-1999; 99US-0158369.
PR 13-OCT-1999; 99US-0159293.
PR 13-OCT-1999; 99US-0159294.
PR 13-OCT-1999; 99US-0159295.
PR 14-OCT-1999; 99US-0159329.
PR 14-OCT-1999; 99US-0159330.
PR 14-OCT-1999; 99US-0159331.
PR 14-OCT-1999; 99US-0159637.
PR 18-OCT-1999; 99US-0159638.
PR 18-OCT-1999; 99US-0159584.
PR 21-OCT-1999; 99US-0160741.
PR 21-OCT-1999; 99US-0160767.
PR 21-OCT-1999; 99US-0160768.
PR 21-OCT-1999; 99US-0160770.
PR 21-OCT-1999; 99US-0160814.
PR 21-OCT-1999; 99US-0160815.
PR 22-OCT-1999; 99US-0160980.
PR 22-OCT-1999; 99US-0160981.
PR 22-OCT-1999; 99US-0160989.
PR 25-OCT-1999; 99US-0161404.
PR 25-OCT-1999; 99US-0161405.
PR 25-OCT-1999; 99US-0161406.
PR 26-OCT-1999; 99US-0161359.
PR 26-OCT-1999; 99US-0161360.
PR 26-OCT-1999; 99US-0161361.
PR 28-OCT-1999; 99US-0161920.
PR 28-OCT-1999; 99US-0161920.
PR 28-OCT-1999; 99US-0161993.
PR 29-OCT-1999; 99US-0162142.

```

Alignment Scores:

Pred. No.:	3,52e-105	Length:	1015
Score:	1085.00	Matches:	194
Percent Similarity:	86.75%	Conservative:	22
Best Local Similarity:	77.91%	Mismatches:	31
Query Match:	77.83%	Indels:	2
DB:	21	Gaps:	2

US-09-383-579c-10 (1-250) x AAC48712 (1-1015)

```

QY 4 SerTyrSerProPheSerSerLeuPheLeuLeuProPhePheVal---PheThrPhe 22
DB 98 TCATACTTAAATAATTCATATCATATTAATTCGTAATTCCTCCAGGAAGACTCAT 157
QY 23 AlaAspTyrGlyGlyTyrPheGlnSerGlyHisAlaThrPheTyrGlyGlyGlyAspAlaSer 42
DB 158 GGAGACGACGAGGAGTGGCAGGTGTGTACGCCACGCTTTACGGCGGAGAGATGCTTCC 217

```

```

QY 43 GlyThrMetGlyGlyAlaCysGlyTyrGlyAsnLeuTyrSerGlnGlyTyrThrAsn 62
DB 218 GGCACCAATGGCGGAGCTTGTGGCTATGAGAAATTTGATGGCCAGAGTTACGGAGCGAAGC 277
QY 63 ThrValAlaLeuSerThrAlaLeuPheAsnAsnGlyLeuSerCysGlyAlaCysAsnGlu 82
DB 278 ACGGGCGCTTTAAGTACGGCTCTATTCAACACGACCTCAGCTGTGGCGCGGTATGAG 337
QY 83 MetThrCysThrAsnAspProLysTyrPhePheProGlyThrThrAlaGlyAlaThr 102
DB 338 ATGAAGTGTAGACGAGACCGCGGTGTGTCTGGGTCAACCATACCGTCAACCTTCA 397
QY 103 AsnPheCysProProAsnPheAlaLeuProAsnAsnAsnGlyGlyTyrPheAsnProPro 122
DB 398 AACTTTGCCACCTTAACCTTGGCTCTTCCACAGTAATGAGAGTTGGTGCATCTCTCT 457
QY 123 LeuGlnHisPheAsnMetAlaGluProAlaPheLeuGlnHisAlaGlnTyrArgAlaGly 142
DB 458 CTTGACGATTTGACCTCGCGGAGCCAGCTTTTCTTCAGATCGCTCAGATCGTCCGCGC 517
QY 143 IleValProValSerPheArgArgValProCysMetGlyGlyGlyValArgPheThr 162
DB 518 ATGTCTCTGTCTCTTCCGAAAGTACCATGTATGAAGAAAGGAGATAGGTTTACG 577
QY 163 IleAsnGlyHisSerTyrPheAsnLeuValLeuIleThrAsnValGlyValArgGlyAsp 182
DB 578 ATCAACGACGACCTACTTCACTCACTCGTCTGATCTCCAGTTCAGAGAGACGACGAGAGC 637
QY 183 ValHisSerValSerIleGlyGlySerArgThr---GlyTyrPheGlnSerMetSerArgAsn 201
DB 638 GTACACGCGCTCATCAATCAAAAGGCTCAAAACACAGCTGTGGCAGACGATGCTGAAGC 697
QY 202 TrpGlyGlnAsnTrpGlnSerAsnAsnTyrLeuAsnGlyGlnGlyLeuSerPheGlnVal 221
DB 698 TGGGACAAACCTGGCAGAGCATATCATACGAAACGAAAGCCCTTCTCCAGGTA 757
QY 222 ThrLeuSerAspGlyArgThrLeuThrAlaTyrAsnLeuValProSerAsnTrpGlnPhe 241
DB 758 ACGACGAGGATGTGCGACACTCGTTAGCAACGAGTGGCTCTTCTTATTTGGCAGTTTC 817
QY 242 GlyGlnThrTyrGluGlyProGlnPhe 250
DB 818 GGACAAACCTACCAAGGTGTGCACTTC 844

```

RESULT 6
AAC40777 standard; DNA; 1016 BP.

AAC40777;
XX
AC AAC40777;
XX
XX 17-OCT-2000 (first entry)
DT
DE Arabidopsis thaliana DNA fragment SEQ ID NO: 29509.
XX
KW Hybridization assay; genetic mapping; gene expression control;
KW Protein identification; signal transduction pathway;
KW metabolic pathway; promoter; termination sequence; ss.
XX Arabidopsis thaliana.
XX
PN EP1033405-A2.
XX
XX 06-SEP-2000.
PD
XX 25-FEB-2000; 2000BP-0301439.
PF
XX 25-FEB-1999; 99US-0121825.
PR 05-MAR-1999; 99US-0123180.
PR 09-MAR-1999; 99US-0123548.
PR 23-MAR-1999; 99US-0125788.
PR 25-MAR-1999; 99US-0126264.
PR 29-MAR-1999; 99US-0126785.
PR 01-APR-1999; 99US-0127462.

CC The present invention relates to novel genes which encode cell wall
 CC hydrolases such as beta-galactosidase (beta-Gal), pectin methylsterase
 CC (PME), polygalacturonase (PG) and cell wall proteins such as expansin
 CC (Exp1) and expansin2 (Exp2) proteins from pear fruit. The nucleic acids
 CC are useful for regulating fruit ripening and for suppressing endogenous
 CC beta-gal, PME, PG, Exp1 and Exp2 genes in any fruit or other plant
 CC organs, thus modifying the structure of the cell walls of the fruit or
 CC plant and providing for ripe yet firm fruit and vegetables. The genes
 CC may be used to screen a cDNA library or a genomic library from any
 CC species, to inhibit or enhance gene expression or to produce transgenic
 CC plants. The present sequence is a cDNA encoding pear expansin 2 protein.
 XX
 SO Sequence 1144 BP, 325 A; 258 C; 242 G; 319 T; 0 other;

Alignment Scores:
 Pred. NO.: 1.12e-103 Length: 1144
 Score: 1071.50 Matches: 199
 Percent Similarity: 86.17% Conservative: 19
 Best Local Similarity: 78.66% Mismatches: 30
 Query Match: 76.87% Indels: 5
 DB: 24 Gaps: 1

US-09-383-579c-10 (1-250) x AABD2964 (1-1144)

QY 2 AlapheserYrSerProPheser--SerleuPheleuProPhePheValPhe 20
 DB 95 GCATTGCTTTGCTCTATAGCCCTCTCTGTTGCTTAACTACATCGCATGCT 154
 QY 21 ThrPheAlaApyTYRGLYTYRGLNserLYHsAlaThrPheTYRGLYGLYAsp 40
 DB 155 GTATTGCTGTTATGTAGTGGAGGCGCCTCATGCAATTTACGGGGGGTGAT 214
 QY 41 AlaserGLYThrmGLYGLYAlaCYesGLYTYRGLYAsnLeuTYRserGLNGLYTYRGLY 60
 DB 215 GCTTGTGGCAAAAGGAGGAGCATGTGTTATGGAAATTTGTCAGCCGAGTATGGA 274
 QY 61 ThraThrValAlaLeuSerThr-AlaLeuPheAsnAsnGLYLeuSerCYesGLYAlaCY 80
 DB 275 ACCAACACTGACGCTTGGAGCAAGCATGTTCAACATGGCTTAAAGCTGTGGTCTG 334
 QY 80 ePhGLuMetThrCYthrAsnAapProLYsTYRLeuProGLYThrIleArgValTh 100
 DB 335 TTAAGAAATGAGATGCGAATGACCCGAGTGTGCCGTCTGATCCATCATTTGTAAC 394
 QY 100 rAlaThraSnPheCYsPProAsnPheAlaLeuProAsnAsnAsnGLYTYRProCYsAs 120
 DB 395 TGTCAACAACCTTTGCCCTCTTAACCTTGTCTCACTCCACAGCAATGGGATGTGCA 454
 QY 120 nProProLeuGLNHisPheAspMetAlaGLUProAlaPheLeuGLNleAlaGLNtyrAr 140
 DB 455 TCCTCCTCTCCAGCATTTGATTTGGTGGAGCTGCTTCTTGCAANTGGCCATACCA 514
 QY 140 g-AlaGLYIle-ValPro-ValSerPheArgValProCYsMetLYsLYsGLYIle 159
 DB 515 GTGCTGGAATCAGGCGAGGTTTCTTCAGAAAGTACTTGTGTGAAGAAAGAGAGAAAT 574
 QY 159 lArgPheThrIleAsnGLYHisSerTYRPhAsnLeuValleuIleThrAsnValGLY 179
 DB 575 AAGATTCACATCAACGGCCACTCTTAACCTGGTTTGTATCCCAACGAGGCTGG 634
 QY 179 yAlaGLYAspValHisSerValSerIleLYsGLYSerArgThrGLYTYRGLNserMetSe 199
 DB 635 GGCAGAGAGCGTTCATTCAGTTCAATCAAGGGGTCCAGAAACAGGGTGGCAACCATGTC 694
 QY 199 rArgAsnTTPGLYGLNAsnTTPGLNserAsnAsnTYRleuAsnGLYGLNGLYLeuSerPh 219
 DB 695 AAGAAACTGGGGTCAAAACTGGCAGAGCACTTACTCACTCAAGCCCTCTCTCTT 754
 QY 219 eGLNValThrLeuSerAspGLYArgTYRleuThrAlaTYRAsnLeuValProSerAsnTr 239
 DB 755 CCAAGTACACCAACGATGAGGATGAGTACAGACGTTCAACAGTCCGCGCTGGTAATTG 814
 QY 239 gAlnPhesGLYGLNThrTYRGLNGLYProGLN 249

DB 815 GCATTGCTGACAGCATTTCCGGGGGTCAA 845
 RESULT 8
 ID AAC50628 standard; DNA, 780 BP.
 XX
 AC AAC50628;
 XX
 DT 18-OCT-2000 (first entry)
 XX
 DE Arabidopsis thaliana DNA fragment SEQ ID NO: 65548.
 XX
 KW Hybridisation assay; genetic mapping; gene expression control;
 KW protein identification; signal transduction pathway;
 KW metabolic pathway; promoter; termination sequence; BR.
 OS Arabidopsis thaliana.
 XX
 PN EP1033405-A2.
 XX
 PD 06-SEP-2000.
 XX
 PF 25-FEB-2000; 2000EP-0301439.
 XX
 PR 25-FEB-1999; 99US-0121825.
 PR 05-MAR-1999; 99US-0123180.
 PR 09-MAR-1999; 99US-0123548.
 PR 23-MAR-1999; 99US-0125788.
 PR 25-MAR-1999; 99US-0126264.
 PR 29-MAR-1999; 99US-0126785.
 PR 01-APR-1999; 99US-0127462.
 PR 06-APR-1999; 99US-0128274.
 PR 08-APR-1999; 99US-0128314.
 PR 16-APR-1999; 99US-0129845.
 PR 19-APR-1999; 99US-0130077.
 PR 21-APR-1999; 99US-0130449.
 PR 23-APR-1999; 99US-0130510.
 PR 23-APR-1999; 99US-0130891.
 PR 28-APR-1999; 99US-0131449.
 PR 30-APR-1999; 99US-0132048.
 PR 30-APR-1999; 99US-0132407.
 PR 04-MAY-1999; 99US-0132484.
 PR 05-MAY-1999; 99US-0132485.
 PR 06-MAY-1999; 99US-0132486.
 PR 06-MAY-1999; 99US-0132487.
 PR 07-MAY-1999; 99US-0132863.
 PR 11-MAY-1999; 99US-0134218.
 PR 14-MAY-1999; 99US-0134219.
 PR 14-MAY-1999; 99US-0134221.
 PR 14-MAY-1999; 99US-0134370.
 PR 18-MAY-1999; 99US-0134768.
 PR 19-MAY-1999; 99US-0134941.
 PR 20-MAY-1999; 99US-0135124.
 PR 21-MAY-1999; 99US-0135353.
 PR 24-MAY-1999; 99US-0135629.
 PR 25-MAY-1999; 99US-0136021.
 PR 27-MAY-1999; 99US-0136392.
 PR 28-MAY-1999; 99US-0137682.
 PR 01-JUN-1999; 99US-0137222.
 PR 03-JUN-1999; 99US-0137588.
 PR 04-JUN-1999; 99US-0137582.
 PR 07-JUN-1999; 99US-0137724.
 PR 08-JUN-1999; 99US-0138094.
 PR 10-JUN-1999; 99US-0138540.
 PR 10-JUN-1999; 99US-0138847.
 PR 14-JUN-1999; 99US-0139119.
 PR 16-JUN-1999; 99US-0139452.
 PR 16-JUN-1999; 99US-0139453.
 PR 17-JUN-1999; 99US-0139492.
 PR 18-JUN-1999; 99US-0139454.
 PR 18-JUN-1999; 99US-0139455.

```
PR 18-JUN-1999; 99US-0139456.  
PR 18-JUN-1999; 99US-0139457.  
PR 18-JUN-1999; 99US-0139458.  
PR 18-JUN-1999; 99US-0139459.  
PR 18-JUN-1999; 99US-0139460.  
PR 18-JUN-1999; 99US-0139461.  
PR 18-JUN-1999; 99US-0139462.  
PR 18-JUN-1999; 99US-0139463.  
PR 18-JUN-1999; 99US-0139750.  
PR 18-JUN-1999; 99US-0139753.  
PR 21-JUN-1999; 99US-0139817.  
PR 22-JUN-1999; 99US-0139899.  
PR 23-JUN-1999; 99US-0140353.  
PR 23-JUN-1999; 99US-0140354.  
PR 24-JUN-1999; 99US-0140695.  
PR 28-JUN-1999; 99US-0140823.  
PR 29-JUN-1999; 99US-0140891.  
PR 30-JUN-1999; 99US-0141287.  
PR 01-JUL-1999; 99US-0141842.  
PR 01-JUL-1999; 99US-0142154.  
PR 02-JUL-1999; 99US-0142055.  
PR 06-JUL-1999; 99US-0142390.  
PR 08-JUL-1999; 99US-0142803.  
PR 09-JUL-1999; 99US-0142920.  
PR 12-JUL-1999; 99US-0142977.  
PR 13-JUL-1999; 99US-0143542.  
PR 14-JUL-1999; 99US-0143624.  
PR 15-JUL-1999; 99US-0144005.  
PR 16-JUL-1999; 99US-0144085.  
PR 16-JUL-1999; 99US-0144086.  
PR 19-JUL-1999; 99US-0144325.  
PR 19-JUL-1999; 99US-0144331.  
PR 19-JUL-1999; 99US-0144332.  
PR 19-JUL-1999; 99US-0144333.  
PR 19-JUL-1999; 99US-0144334.  
PR 19-JUL-1999; 99US-0144335.  
PR 20-JUL-1999; 99US-0144352.  
PR 20-JUL-1999; 99US-0144884.  
PR 21-JUL-1999; 99US-0144814.  
PR 21-JUL-1999; 99US-0145086.  
PR 21-JUL-1999; 99US-0145088.  
PR 22-JUL-1999; 99US-0145085.  
PR 22-JUL-1999; 99US-0145087.  
PR 22-JUL-1999; 99US-0145089.  
PR 22-JUL-1999; 99US-0145192.  
PR 23-JUL-1999; 99US-0145145.  
PR 23-JUL-1999; 99US-0145218.  
PR 23-JUL-1999; 99US-0145224.  
PR 26-JUL-1999; 99US-0145276.  
PR 27-JUL-1999; 99US-0145913.  
PR 27-JUL-1999; 99US-0145918.  
PR 27-JUL-1999; 99US-0145919.  
PR 28-JUL-1999; 99US-0145951.  
PR 02-AUG-1999; 99US-0146386.  
PR 02-AUG-1999; 99US-0146388.  
PR 02-AUG-1999; 99US-0146389.  
PR 03-AUG-1999; 99US-0147038.  
PR 04-AUG-1999; 99US-0147204.  
PR 04-AUG-1999; 99US-0147302.  
PR 05-AUG-1999; 99US-0147192.  
PR 05-AUG-1999; 99US-0147260.  
PR 06-AUG-1999; 99US-0147303.  
PR 06-AUG-1999; 99US-0147416.  
PR 09-AUG-1999; 99US-0147493.  
PR 09-AUG-1999; 99US-0147935.  
PR 10-AUG-1999; 99US-0148171.  
PR 11-AUG-1999; 99US-0148319.  
PR 12-AUG-1999; 99US-0148341.  
PR 13-AUG-1999; 99US-0148565.  
PR 13-AUG-1999; 99US-0148684.  
PR 16-AUG-1999; 99US-0149368.  
PR 17-AUG-1999; 99US-0149175.  
  
PR 18-AUG-1999; 99US-0149426.  
PR 20-AUG-1999; 99US-0149722.  
PR 20-AUG-1999; 99US-0149723.  
PR 20-AUG-1999; 99US-0149929.  
PR 23-AUG-1999; 99US-0149902.  
PR 23-AUG-1999; 99US-0149930.  
PR 25-AUG-1999; 99US-0150566.  
PR 26-AUG-1999; 99US-0150884.  
PR 27-AUG-1999; 99US-0151065.  
PR 27-AUG-1999; 99US-0151066.  
PR 27-AUG-1999; 99US-0151080.  
PR 30-AUG-1999; 99US-0151303.  
PR 31-AUG-1999; 99US-0151438.  
PR 01-SEP-1999; 99US-0151930.  
PR 07-SEP-1999; 99US-0152363.  
PR 10-SEP-1999; 99US-0153070.  
PR 13-SEP-1999; 99US-0153758.  
PR 15-SEP-1999; 99US-0154018.  
PR 16-SEP-1999; 99US-0154039.  
PR 20-SEP-1999; 99US-0154779.  
PR 22-SEP-1999; 99US-0155139.  
PR 23-SEP-1999; 99US-0155486.  
PR 24-SEP-1999; 99US-0155659.  
PR 28-SEP-1999; 99US-0156458.  
PR 29-SEP-1999; 99US-0156596.  
PR 04-OCT-1999; 99US-0157117.  
PR 05-OCT-1999; 99US-0157753.  
PR 06-OCT-1999; 99US-0157865.  
PR 07-OCT-1999; 99US-0158029.  
PR 08-OCT-1999; 99US-0158232.  
PR 12-OCT-1999; 99US-0158369.  
PR 13-OCT-1999; 99US-0158293.  
PR 13-OCT-1999; 99US-0158294.  
PR 13-OCT-1999; 99US-0159295.  
PR 14-OCT-1999; 99US-0159329.  
PR 14-OCT-1999; 99US-0159330.  
PR 14-OCT-1999; 99US-0159331.  
PR 14-OCT-1999; 99US-0159637.  
PR 14-OCT-1999; 99US-0159638.  
PR 18-OCT-1999; 99US-0159584.  
PR 21-OCT-1999; 99US-0160741.  
PR 21-OCT-1999; 99US-0160767.  
PR 21-OCT-1999; 99US-0160768.  
PR 21-OCT-1999; 99US-0160770.  
PR 21-OCT-1999; 99US-0160814.  
PR 21-OCT-1999; 99US-0160815.  
PR 22-OCT-1999; 99US-0160980.  
PR 22-OCT-1999; 99US-0160981.  
PR 22-OCT-1999; 99US-0160989.  
PR 25-OCT-1999; 99US-0161404.  
PR 25-OCT-1999; 99US-0161405.  
PR 25-OCT-1999; 99US-0161406.  
PR 26-OCT-1999; 99US-0161359.  
PR 26-OCT-1999; 99US-0161360.  
PR 26-OCT-1999; 99US-0161361.  
PR 28-OCT-1999; 99US-0161920.  
PR 28-OCT-1999; 99US-0161992.  
PR 28-OCT-1999; 99US-0161993.  
PR 29-OCT-1999; 99US-0162142.  
  
Alignment Scores:  
Pred. No.: 1 11e-100  
Score: 1041.00  
Percent Similarity: 89.78%  
Best Local Similarity: 79.56%  
Query Match: 74.68%  
DB: 21  
Gaps: 0  
Matches: 179  
Conservative: 23  
Mismatches: 23  
Indels: 0  
US-09-383-579c-10 (1-250) x AAC50628 (1-780)  
QY 26 GYGIYTRPGInsercGIYHIsaIathrPheryrGIYGIYGIYAspAsaIsercIYthrMet 45  
Db 100 GCGGTGGATCAACGCTCAGCCACCTTTTACGGTGGTGGATGATCCTTCCGCAATG 159
```



```
QY 46 GlyIYAlaCysglYTYrgLYasnLeuTYrserGlnGlyTYrgLYThraSnThraValAla 65
DB 160 GGTCGCTCTTGATATGGTAATCTATATAGCCAAAGCTACGGGAGAGACGGCGGCT 219
QY 66 LeuSerThraAlaLeuPheAsnAsnGlyLeuSerCysglYAlaCysPheGluMetThrCys 85
DB 220 CTAGGCAGCTCTCTTCAACAAATGACTTAGCTGTGGTCTTCTTGTAGATTAAGATGT 279
QY 86 ThraAsnProLYSTPQYLeuProGlyThraIleArgValThraAlaThraAsnPhCys 105
DB 280 GAAACAGATGGTAATAGTGTTCCTGCAATCTGCTCAATCGTTGACCGCTACAACTTCTGC 339
QY 106 ProProAsnPheAlaLeuProAsnAsnAsnGlyTYrCysAsnProProLeuGlnHis 125
DB 340 CCGCAATATACGGCTTAGCGCAACATATAGCCGCTTGTCTATCTCTCTTGAACAC 399
QY 126 PheAsnMetAlaGluProAlaPheLeuGlnIleAlaGlnTYrArgAlaGlyIleValPro 145
DB 400 TTTGACCTTGCTCAGCTGTTTTCACGCAATGCTCAGTACAGAGCTGGAAATCGTCCT 459
QY 146 ValSerPheArgValProCysMetLYsGlyValArgPheThraIleAsnGly 165
DB 460 GTTTCCTACAGAAAGGTTCTTGCAAGAGAGAGAGAAATTAAGATTCAACATTAACGCGC 519
QY 166 HisSerTYrPheAsnLeuValLeuIleThraSnValGlyIYAlaGlyAspValHisSer 185
DB 520 CACTCATACTTCACCTTGTGCTGATCAACAACTCGGTGTCGCGAGACGTTCACTCG 579
QY 186 ValSerIleLYsGlySerArgThrgLYTTPGlnSerMetSerArgAsnTPGlyGlnAsn 205
DB 580 GCGCGCATCAAGGCTTCAAGAACAGTGTGCACACTATGTCAAGAACTGGGGGCAAAAT 639
QY 206 ThrGlnSerAsnAsnTYrLeuAsnGlyGlnGlyLeuSerPheGlnValThraLeuSerAsp 225
DB 640 TGGCAAAAGCACTTACCTTCAACGTCACGCTTCTTAAAGTCAACACCAAGCGAC 699
QY 226 GlyArgThraLeuThraIYrAsnLeuValProSerAsnTPGlnPheGlyGlnThrTYr 245
DB 700 GGCGGCACAGTGTCTCTTCAACGCGGCTCTCCGCTGTCTTATGGCCAGACTTTT 759
QY 246 GluGlyProGlnPhe 250
DB 760 GCCCGTGACAGCTTC 774

RESULT 9
AAC33521
ID AAC33521 standard; DNA, 1198 BP.
XX
AC AAC33521;
XX
DT 17-OCT-2000 (first entry)
XX
DE Arabidopsis thaliana DNA fragment SEQ ID NO: 3354.
XX
KM Hybridisation assay; genetic mapping; gene expression control;
KM protein identification; signal transduction pathway;
KM metabolic pathway; promoter; termination sequence; ss.
XX
OS Arabidopsis thaliana.
XX
EP1033405-A2.
XX
PD 06-SEP-2000.
XX
PF 25-FEB-2000; 2000EP-0301439.
XX
PR 25-FEB-1999; 99US-0121825.
PR 05-MAR-1999; 99US-0123180.
PR 09-MAR-1999; 99US-0123548.
PR 23-MAR-1999; 99US-0125788.
PR 25-MAR-1999; 99US-0126264.
PR 29-MAR-1999; 99US-0126785.
PR 01-APR-1999; 99US-0127462.
PR 06-APR-1999; 99US-0128234.
PR 08-APR-1999; 99US-0128714.
PR 16-APR-1999; 99US-0129845.
PR 19-APR-1999; 99US-0130077.
PR 21-APR-1999; 99US-0130449.
PR 23-APR-1999; 99US-0130510.
PR 23-APR-1999; 99US-0130891.
PR 28-APR-1999; 99US-0131449.
PR 30-APR-1999; 99US-0132048.
PR 30-APR-1999; 99US-0132407.
PR 04-MAY-1999; 99US-0132484.
PR 05-MAY-1999; 99US-0132485.
PR 06-MAY-1999; 99US-0132486.
PR 06-MAY-1999; 99US-0132487.
PR 07-MAY-1999; 99US-0132863.
PR 11-MAY-1999; 99US-0134256.
PR 14-MAY-1999; 99US-0134218.
PR 14-MAY-1999; 99US-0134219.
PR 14-MAY-1999; 99US-0134221.
PR 14-MAY-1999; 99US-0134370.
PR 16-MAY-1999; 99US-0134376.
PR 19-MAY-1999; 99US-0134941.
PR 20-MAY-1999; 99US-0135124.
PR 21-MAY-1999; 99US-0135353.
PR 24-MAY-1999; 99US-0135629.
PR 25-MAY-1999; 99US-0136021.
PR 27-MAY-1999; 99US-0136392.
PR 28-MAY-1999; 99US-0136782.
PR 01-JUN-1999; 99US-0137222.
PR 03-JUN-1999; 99US-0137528.
PR 04-JUN-1999; 99US-0137502.
PR 07-JUN-1999; 99US-0137724.
PR 08-JUN-1999; 99US-0138094.
PR 10-JUN-1999; 99US-0138540.
PR 10-JUN-1999; 99US-0138847.
PR 14-JUN-1999; 99US-0139119.
PR 16-JUN-1999; 99US-0139452.
PR 16-JUN-1999; 99US-0139453.
PR 17-JUN-1999; 99US-0139458.
PR 18-JUN-1999; 99US-0139454.
PR 18-JUN-1999; 99US-0139455.
PR 18-JUN-1999; 99US-0139456.
PR 18-JUN-1999; 99US-0139457.
PR 18-JUN-1999; 99US-0139458.
PR 18-JUN-1999; 99US-0139459.
PR 18-JUN-1999; 99US-0139460.
PR 18-JUN-1999; 99US-0139461.
PR 18-JUN-1999; 99US-0139462.
PR 18-JUN-1999; 99US-0139463.
PR 18-JUN-1999; 99US-0139750.
PR 18-JUN-1999; 99US-0139763.
PR 21-JUN-1999; 99US-0139817.
PR 22-JUN-1999; 99US-0139899.
PR 23-JUN-1999; 99US-0140353.
PR 23-JUN-1999; 99US-0140354.
PR 24-JUN-1999; 99US-0140695.
PR 28-JUN-1999; 99US-0140823.
PR 29-JUN-1999; 99US-0140991.
PR 30-JUN-1999; 99US-0141287.
PR 01-JUL-1999; 99US-0141842.
PR 01-JUL-1999; 99US-0142154.
PR 02-JUL-1999; 99US-0142055.
PR 06-JUL-1999; 99US-0142390.
PR 08-JUL-1999; 99US-0142803.
PR 09-JUL-1999; 99US-0142920.
PR 12-JUL-1999; 99US-0142977.
PR 13-JUL-1999; 99US-0143542.
PR 14-JUL-1999; 99US-0143624.
PR 15-JUL-1999; 99US-0144005.
PR 16-JUL-1999; 99US-0144085.
PR 16-JUL-1999; 99US-0144086.
PR 19-JUL-1999; 99US-0144325.
```

PR 19-JUL-1999: 99US-0144331.
PR 19-JUL-1999: 99US-0144332.
PR 19-JUL-1999: 99US-0144333.
PR 19-JUL-1999: 99US-0144334.
PR 19-JUL-1999: 99US-0144335.
PR 20-JUL-1999: 99US-0144332.
PR 20-JUL-1999: 99US-0144332.
PR 20-JUL-1999: 99US-0144332.
PR 21-JUL-1999: 99US-0144814.
PR 21-JUL-1999: 99US-0145086.
PR 21-JUL-1999: 99US-0145086.
PR 22-JUL-1999: 99US-0145085.
PR 22-JUL-1999: 99US-0145087.
PR 22-JUL-1999: 99US-0145089.
PR 22-JUL-1999: 99US-0145192.
PR 23-JUL-1999: 99US-0145145.
PR 23-JUL-1999: 99US-0145218.
PR 23-JUL-1999: 99US-0145224.
PR 26-JUL-1999: 99US-0145276.
PR 27-JUL-1999: 99US-0145313.
PR 27-JUL-1999: 99US-0145318.
PR 27-JUL-1999: 99US-0145319.
PR 28-JUL-1999: 99US-0145351.
PR 02-AUG-1999: 99US-0146386.
PR 02-AUG-1999: 99US-0146388.
PR 02-AUG-1999: 99US-0146389.
PR 03-AUG-1999: 99US-0147038.
PR 04-AUG-1999: 99US-0147204.
PR 04-AUG-1999: 99US-0147302.
PR 05-AUG-1999: 99US-0147312.
PR 05-AUG-1999: 99US-0147360.
PR 06-AUG-1999: 99US-0147303.
PR 06-AUG-1999: 99US-0147416.
PR 09-AUG-1999: 99US-0147493.
PR 09-AUG-1999: 99US-0147935.
PR 10-AUG-1999: 99US-0148171.
PR 11-AUG-1999: 99US-0148319.
PR 12-AUG-1999: 99US-0148341.
PR 13-AUG-1999: 99US-0148565.
PR 13-AUG-1999: 99US-0148684.
PR 16-AUG-1999: 99US-0149368.
PR 17-AUG-1999: 99US-0149175.
PR 18-AUG-1999: 99US-0149426.
PR 20-AUG-1999: 99US-0149722.
PR 20-AUG-1999: 99US-0149723.
PR 20-AUG-1999: 99US-0149929.
PR 23-AUG-1999: 99US-0149902.
PR 23-AUG-1999: 99US-0149930.
PR 25-AUG-1999: 99US-0150566.
PR 26-AUG-1999: 99US-0150884.
PR 27-AUG-1999: 99US-0151065.
PR 27-AUG-1999: 99US-0151066.
PR 27-AUG-1999: 99US-0151080.
PR 30-AUG-1999: 99US-0151303.
PR 31-AUG-1999: 99US-0151438.
PR 01-SEP-1999: 99US-0151930.
PR 07-SEP-1999: 99US-0152363.
PR 10-SEP-1999: 99US-0153070.
PR 13-SEP-1999: 99US-0153758.
PR 15-SEP-1999: 99US-0154018.
PR 16-SEP-1999: 99US-0154439.
PR 20-SEP-1999: 99US-0154779.
PR 22-SEP-1999: 99US-0155139.
PR 23-SEP-1999: 99US-0155486.
PR 24-SEP-1999: 99US-0155659.
PR 28-SEP-1999: 99US-0156458.
PR 29-SEP-1999: 99US-0156596.
PR 04-OCT-1999: 99US-0157117.
PR 05-OCT-1999: 99US-0157753.
PR 06-OCT-1999: 99US-0157865.
PR 07-OCT-1999: 99US-0158029.
PR 08-OCT-1999: 99US-0158332.
PR 12-OCT-1999: 99US-0158369.

PR 13-OCT-1999: 99US-0159293.
PR 13-OCT-1999: 99US-0159294.
PR 13-OCT-1999: 99US-0159295.
PR 14-OCT-1999: 99US-0159329.
PR 14-OCT-1999: 99US-0159330.
PR 14-OCT-1999: 99US-0159331.
PR 14-OCT-1999: 99US-0159337.
PR 14-OCT-1999: 99US-0159638.
PR 18-OCT-1999: 99US-0159584.
PR 21-OCT-1999: 99US-0160741.
PR 21-OCT-1999: 99US-0160767.
PR 21-OCT-1999: 99US-0160768.
PR 21-OCT-1999: 99US-0160770.
PR 21-OCT-1999: 99US-0160814.
PR 21-OCT-1999: 99US-0160815.
PR 22-OCT-1999: 99US-0160980.
PR 22-OCT-1999: 99US-0160981.
PR 22-OCT-1999: 99US-0160989.
PR 25-OCT-1999: 99US-0161404.
PR 25-OCT-1999: 99US-0161405.
PR 25-OCT-1999: 99US-0161406.
PR 26-OCT-1999: 99US-0161359.
PR 26-OCT-1999: 99US-0161360.
PR 26-OCT-1999: 99US-0161361.
PR 28-OCT-1999: 99US-0161920.
PR 28-OCT-1999: 99US-0161992.
PR 28-OCT-1999: 99US-0161993.
PR 29-OCT-1999: 99US-0162142.

Alignment Scores:

Prod. No.:	2, 04e-100	Length:	1198
Score:	1041.00	Matches:	179
Percent Similarity:	89.78%	Conservative:	23
Best Local Similarity:	79.56%	Mismatches:	23
Query Match:	74.68%	Indels:	0
DB:	21	Gaps:	0

US-09-383-579c-10 (1-250) x AAC33521 (1-1198)

QY 26 GlyIYTPGInserGlyHisAlaThrPheYrGlyGlyAspAlaSerGlyThrMet 45
DB 125 GCGGTTGGATCAACGCTCACCCCACTTTTACGGTGGTGGATGCTTCCGGCAAAATG 184
QY 46 GlyIYAlaCyGlyYrGlyYasnLeuYrSerGlnGlyYrGlyYThrAsnThrValAla 65
DB 185 GGTGGTCTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 244
QY 66 LeuSerThrAlaLeuPheAsnAsnGlyLeuSerCyGlyAlaCyPheGluMetThrCys 85
DB 245 CTAGCAGACGCTCTCTTCAACATGACTGACTGCTGCTTCTTCAAGATGATGATGATG 304
QY 86 ThrAsnAspProLyserTrpCysLeuProGlyThrIleArgValThrAlaThrAsnPheCys 105
DB 305 GAAACGATGTAATAGGTGTTTACCTGCTCAATCGTTGTAAACCGCTTCAAACTTCTGC 364
QY 106 ProProAsnPheAlaLeuProAsnAsnAsnGlyYrTrpCysAsnProProLeuGlnHis 125
DB 365 CCGCCAAATPACGCGTTAGCCGAATAATAGCGGTGGTGTGAATCTCTCTTGAACAC 424
QY 126 PheAspMetAlaGluProAlaPheLeuGlnIleAlaGlnYrArgAlaGlyIleValPro 145
DB 425 TTGACCTTGTCTACACCTGTTTTCACAGCATTGCTCACTAGTACAGCTGGAATCTCCT 484
QY 146 ValSerPheArgValProCyMetIysGlyGlyValArgPheThrIleAsnGly 165
DB 485 GTTCCCTACAGAAAGGTTCTCTTGCAGAGAAAGAGAAATTAAGATTACGATAACGGC 544
QY 166 HisSerYrPheAsnLeuValLeuIleThrAsnValGlyGlyAlaGlyAspValHisSer 185
DB 545 CACTCATCTTCAACCTGTGTGATCAACAACTGGGTGGTGGTGGTGGTGGTGGTGGTGGT 604
QY 186 ValSerIleYrGlySerArgThrGlyYrPGLInserMetSerArgAsnTrpGlyGlnAsn 205

```
Db      605 GCGCGCATCAAGGCTTCAAGAACAGTGTGGCAAGCTATGTCACAGAACTGGGGGCAAAAT 664
Qy      206 TrpInserAsnaenTyrLeuAnGlyGlnGlyLeuSerPheGlnValThrLeuSerAsp 225
        665 TGGCAAAAGCACTTACCTTACCTCAACGCTCAAGCACTTTCTTAAGCTCACCACACGCGAC 724
Qy      226 GlyArgThrLeuThrAlaTyrAsnLeuValProSerAsnTyrGlnPheGlyGlnThrTyr 245
        725 GGGCGCACAGTGTCTCTCTTCAACGCGCTCTCGCGCTGTGCTTATAGGCGACACTTTT 784
Qy      246 GluGlyProGlnPhe 250
Db      785 GCGGTGACAGTTC 799

RESULT 10
AAC50633
ID AAC50633 standard; DNA; 1233 BP.
XX
AC      AAC50633;
XX
DT      18-OCT-2000 (first entry)
XX
DE      Arabidopsis thaliana DNA fragment SEQ ID NO: 65567.
XX
KW      Hybridisation assay; genetic mapping; gene expression control;
KM      protein identification; signal transduction pathway;
XX      metabolic pathway; promoter; termination sequence; ss.
OS      Arabidopsis thaliana.
XX
PN      EP1033405-A2.
XX
PD      06-SEP-2000.
XX
PF      25-FEB-2000; 2000EP-0301439.
XX
PR      25-FEB-1999; 99US-0121825.
PR      05-MAR-1999; 99US-0123180.
PR      09-MAR-1999; 99US-0123548.
PR      23-MAR-1999; 99US-0125788.
PR      25-MAR-1999; 99US-0126264.
PR      29-MAR-1999; 99US-0126785.
PR      01-APR-1999; 99US-0127462.
PR      06-APR-1999; 99US-0128234.
PR      08-APR-1999; 99US-0128714.
PR      16-APR-1999; 99US-0129845.
PR      19-APR-1999; 99US-0130077.
PR      21-APR-1999; 99US-0130449.
PR      23-APR-1999; 99US-0130510.
PR      28-APR-1999; 99US-0130891.
PR      30-APR-1999; 99US-0131449.
PR      30-APR-1999; 99US-0132048.
PR      30-APR-1999; 99US-0132407.
PR      04-MAY-1999; 99US-0132484.
PR      05-MAY-1999; 99US-0132485.
PR      06-MAY-1999; 99US-0132486.
PR      06-MAY-1999; 99US-0132487.
PR      07-MAY-1999; 99US-0132863.
PR      11-MAY-1999; 99US-0134256.
PR      14-MAY-1999; 99US-0134218.
PR      14-MAY-1999; 99US-0134219.
PR      14-MAY-1999; 99US-0134221.
PR      14-MAY-1999; 99US-0134370.
PR      18-MAY-1999; 99US-0134768.
PR      19-MAY-1999; 99US-0134941.
PR      20-MAY-1999; 99US-0135124.
PR      21-MAY-1999; 99US-0135353.
PR      24-MAY-1999; 99US-0135629.
PR      25-MAY-1999; 99US-0136021.
PR      27-MAY-1999; 99US-0136392.
PR      28-MAY-1999; 99US-0136782.
PR      01-JUN-1999; 99US-0137222.
PR      03-JUN-1999; 99US-0137528.
PR      04-JUN-1999; 99US-0137502.
PR      07-JUN-1999; 99US-0137724.
PR      08-JUN-1999; 99US-0138094.
PR      10-JUN-1999; 99US-0138540.
PR      10-JUN-1999; 99US-0138847.
PR      14-JUN-1999; 99US-0139119.
PR      16-JUN-1999; 99US-0139452.
PR      16-JUN-1999; 99US-0139453.
PR      17-JUN-1999; 99US-0139492.
PR      18-JUN-1999; 99US-0139454.
PR      18-JUN-1999; 99US-0139455.
PR      18-JUN-1999; 99US-0139456.
PR      18-JUN-1999; 99US-0139457.
PR      18-JUN-1999; 99US-0139458.
PR      18-JUN-1999; 99US-0139459.
PR      18-JUN-1999; 99US-0139460.
PR      18-JUN-1999; 99US-0139461.
PR      18-JUN-1999; 99US-0139462.
PR      18-JUN-1999; 99US-0139463.
PR      18-JUN-1999; 99US-0139750.
PR      18-JUN-1999; 99US-0139763.
PR      21-JUN-1999; 99US-0139817.
PR      22-JUN-1999; 99US-0139899.
PR      23-JUN-1999; 99US-0140353.
PR      24-JUN-1999; 99US-0140354.
PR      24-JUN-1999; 99US-0140695.
PR      28-JUN-1999; 99US-0140823.
PR      29-JUN-1999; 99US-0140991.
PR      30-JUN-1999; 99US-0141287.
PR      01-JUL-1999; 99US-0141842.
PR      02-JUL-1999; 99US-0142154.
PR      06-JUL-1999; 99US-0142390.
PR      08-JUL-1999; 99US-0142803.
PR      09-JUL-1999; 99US-0142920.
PR      12-JUL-1999; 99US-0142977.
PR      13-JUL-1999; 99US-0143542.
PR      14-JUL-1999; 99US-0143624.
PR      15-JUL-1999; 99US-0144005.
PR      16-JUL-1999; 99US-0144085.
PR      16-JUL-1999; 99US-0144086.
PR      19-JUL-1999; 99US-0144325.
PR      19-JUL-1999; 99US-0144331.
PR      19-JUL-1999; 99US-0144332.
PR      19-JUL-1999; 99US-0144333.
PR      19-JUL-1999; 99US-0144334.
PR      19-JUL-1999; 99US-0144335.
PR      20-JUL-1999; 99US-0144632.
PR      20-JUL-1999; 99US-0144684.
PR      21-JUL-1999; 99US-0144814.
PR      21-JUL-1999; 99US-0145086.
PR      21-JUL-1999; 99US-0145088.
PR      22-JUL-1999; 99US-0145085.
PR      22-JUL-1999; 99US-0145087.
PR      22-JUL-1999; 99US-0145089.
PR      22-JUL-1999; 99US-0145192.
PR      23-JUL-1999; 99US-0145145.
PR      23-JUL-1999; 99US-0145218.
PR      23-JUL-1999; 99US-0145224.
PR      26-JUL-1999; 99US-0145276.
PR      27-JUL-1999; 99US-0145913.
PR      27-JUL-1999; 99US-0145918.
PR      27-JUL-1999; 99US-0145919.
PR      28-JUL-1999; 99US-0145951.
PR      02-AUG-1999; 99US-0146386.
PR      02-AUG-1999; 99US-0146388.
PR      02-AUG-1999; 99US-0146389.
PR      03-AUG-1999; 99US-0147038.
PR      04-AUG-1999; 99US-0147204.
PR      04-AUG-1999; 99US-0147302.
PR      05-AUG-1999; 99US-0147192.
PR      05-AUG-1999; 99US-0147260.
```

```

PR 06-AUG-1999: 99US-0147303.
PR 06-AUG-1999: 99US-0147416.
PR 09-AUG-1999: 99US-0147493.
PR 09-AUG-1999: 99US-0147935.
PR 10-AUG-1999: 99US-0148171.
PR 11-AUG-1999: 99US-0148319.
PR 12-AUG-1999: 99US-0148341.
PR 13-AUG-1999: 99US-0148654.
PR 13-AUG-1999: 99US-0148684.
PR 16-AUG-1999: 99US-0149368.
PR 17-AUG-1999: 99US-0149175.
PR 18-AUG-1999: 99US-0149426.
PR 20-AUG-1999: 99US-0149722.
PR 20-AUG-1999: 99US-0149723.
PR 20-AUG-1999: 99US-0149929.
PR 23-AUG-1999: 99US-0149902.
PR 23-AUG-1999: 99US-0149930.
PR 25-AUG-1999: 99US-0150566.
PR 26-AUG-1999: 99US-0150884.
PR 27-AUG-1999: 99US-0151065.
PR 27-AUG-1999: 99US-0151066.
PR 27-AUG-1999: 99US-0151080.
PR 30-AUG-1999: 99US-0151303.
PR 31-AUG-1999: 99US-0151438.
PR 01-SEP-1999: 99US-0151930.
PR 07-SEP-1999: 99US-0152363.
PR 10-SEP-1999: 99US-0153070.
PR 13-SEP-1999: 99US-0153758.
PR 15-SEP-1999: 99US-0154018.
PR 16-SEP-1999: 99US-0154039.
PR 20-SEP-1999: 99US-0154779.
PR 22-SEP-1999: 99US-0155139.
PR 23-SEP-1999: 99US-0155486.
PR 24-SEP-1999: 99US-0155659.
PR 28-SEP-1999: 99US-0156458.
PR 29-SEP-1999: 99US-0156596.
PR 04-OCT-1999: 99US-0157117.
PR 05-OCT-1999: 99US-0157753.
PR 06-OCT-1999: 99US-0157865.
PR 07-OCT-1999: 99US-0158029.
PR 08-OCT-1999: 99US-0158232.
PR 12-OCT-1999: 99US-0158369.
PR 13-OCT-1999: 99US-0159293.
PR 13-OCT-1999: 99US-0159294.
PR 13-OCT-1999: 99US-0159295.
PR 14-OCT-1999: 99US-0159320.
PR 14-OCT-1999: 99US-0159330.
PR 14-OCT-1999: 99US-0159331.
PR 14-OCT-1999: 99US-0159637.
PR 14-OCT-1999: 99US-0159638.
PR 18-OCT-1999: 99US-0159584.
PR 21-OCT-1999: 99US-0160741.
PR 21-OCT-1999: 99US-0160767.
PR 21-OCT-1999: 99US-0160768.
PR 21-OCT-1999: 99US-0160770.
PR 21-OCT-1999: 99US-0160814.
PR 21-OCT-1999: 99US-0160815.
PR 22-OCT-1999: 99US-0160980.
PR 22-OCT-1999: 99US-0160981.
PR 22-OCT-1999: 99US-0160989.
PR 25-OCT-1999: 99US-0161404.
PR 25-OCT-1999: 99US-0161405.
PR 25-OCT-1999: 99US-0161406.
PR 26-OCT-1999: 99US-0161359.
PR 26-OCT-1999: 99US-0161360.
PR 26-OCT-1999: 99US-0161361.
PR 28-OCT-1999: 99US-0161920.
PR 28-OCT-1999: 99US-0161922.
PR 28-OCT-1999: 99US-0161932.
PR 29-OCT-1999: 99US-0162142.

```

Alignment Scores:
Pred. No.: 2.13e-100

Length: 1233

```

Score: 1041.00 Matches: 179
Percent Similarity: 89.78%
Best Local Similarity: 79.56%
Query Match: 74.68%
DB: 21 Gaps: 0

US-09-383-579c-10 (1-250) x AAC50633 (1-1233)

QY 26 GYGLYTPGINSERGLHIALATHRPHERYGLYGLYASPLASERGLYTHMET 45
DB 163 GCGCGTGGATCAACGCTCACCCCACTTTTAAAGGTGGTGGATGCTTCCGCAATG 222
QY 46 GYGLYALACYSGLTYRGLYASMLEUYRSENGLYTYRGLYTHASANTHRVALA 65
DB 223 GGTGGTCTGTGGATATGATATATATATATATATATATATATATATATATATAT 282
QY 66 LEUSERTHRALALEUPHESANANGLYSEUSERCYSGLYALACYPHEGLUMETTHCY 85
DB 283 CTAAACACAGCTCTCTTCAACATGACTGACTGCTGCTGCTGCTGCTGCTGCTGCT 342
QY 86 THRANAPPROLYETPCYLEUDPROGLYTHRIEATGVALTHRALATHRANPHECY 105
DB 343 GAAACGATGATTAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 402
QY 106 PROPROPANPHEALALEUPROPSANANGLYGLYTPCYASNPPOPROLEUGINHIS 125
DB 403 CCGCCAAATACGCTTACGACAAATATATATATATATATATATATATATATATATAT 462
QY 126 PHEAPMEALAGLUPROALAPHELEUGINILEAGINTYRARGALAGLYLEVALPRO 145
DB 463 TTTGACCTTGCACACCTGTTTTCACGCAATGCTGACGATGACGATGACGATGAC 522
QY 146 VALSERPHEARGARVALPROCYSEMETLYSGLYGLYVALARGPHETHRILEANGLY 165
DB 523 GTTTCCTACAGAGGTTCTCTTGCAGAGAGAGAGATTAAGATTACGATTAACCGC 582
QY 166 HISERTYRPHASLEUVALLEUITLEHRASVALGLYVALAGLYASPVALHISER 185
DB 583 CACTACTACTTACCTTGTCTGATCAACAACGTCGGGGTGGTGGTGGTGGTGGTGGT 642
QY 186 VALSERILEYGLYSERARTHRGLYTPGINSEMETSERARGASNTIPGLYGLNAN 205
DB 643 GCGCGCATTAAGGTTCAAGAACAGTGTGCAAGCTATGTCAAGAACCTGGGGCAAAAT 702
QY 206 TRPGINSEARASNTYRLEUANGLYGLNGLYSEUSERPHEGLVALTHREUSERARP 225
DB 703 TGGCAAGCACTTACTTCAACGCTCAAGCACTTCTTAAAGTCAACCAACGCGAC 762
QY 226 GLYARGTHRLEUTHRALATYRANLEUVALPROSERANTTPGINPHEGLYGLNTHRY 245
DB 763 GCGCGACAGTGTCTCTTCAACGCGCTCTGCGGCTGTCTTATGACCACTTTT 822
QY 246 GLUGLYPROGLNPH 250
DB 823 GCGGTTGACAGTTTC 837

RESULT 11
AB212286
ID AB212286 standard; DNA; 753 BP.
XX
AC AB212286;
XX
DT 21-JAN-2003 (first entry)
XX
DE Arabidopsis thaliana stress regulated gene SEQ. ID NO 91.
XX
KW Arabidopsis thaliana; plant; gene; stress; transgenic; ds.
XX
OS Arabidopsis thaliana.
XX
PN WO200216655-A2.
XX
PD 28-FEB-2002.

```


[illegible]

DB 222 ACAATGGGAGGAGCTTGTGGCTACGGGAACCTCTACAGTCAAGGTTACGGGACCAACAG 261
QY 64 VALAIAleuSerThraIaleuPheAsnAnglyLeuSerCyGlyAlaCysPhegluwtc 83
DB 282 GCGGCGTTGAGCAGCTGCTGTTCAACAACGGCTTACCTGGCGGCTGTTTGAGATC 341
QY 84 ThrCysThraAsnAspProlySerTrpCysLeuProGlyThrlIeArgAlaThrIleAsn 103
DB 342 AAGTGCAGAGCAGCGCGCGTGTGTCTTACCTGGCTATCATTTCTACAGCCACCAAT 401
QY 104 PheCysProPAsnAsnAlaLeuProAsnAsnAnglyGlyTrpCysAsnProPoleu 123
DB 402 TTCTGTCCCTCCACCAACGCTCTCCCAATACGCGGTGGTGGTGAACCTCCGCTT 461
QY 124 GlnHsPheAspMetAlaGluProAlaPheLeuGlnIleAlaGlnTrpArgAlaGlyIle 143
DB 462 CATCATTTGCATCTCTCAGCCTGTTTCAACGCAATTCAGTACAAAGCTGGTGT 521
QY 144 ValProValSerPheArgArgValProCysMetIyGlyGlyValArgPheThrIle 163
DB 522 GTCCCTGTTCCACAGAGGGTCCGTGTATGAGAGAGAGATATAGATTCCACATC 581
QY 164 AenglyHsSerTyxPheAsnLeuValIleuIleThraAsnValGlyGlyAlaGlyAspVal 183
DB 582 AAGCGTCACTTACTTCAACCTGTGCTTGTCGACCAATGTTGTGTCTGGAGATGTT 641
QY 184 HsSerValSerIleGlySerArgThrglyTrpGlnSerMetSerArgAsnTrpGly 203
DB 642 CATTCGGTTCGGTTAAGGTTCTAGAACAGGTGGCAACAAATGCAGAAATCGGGA 701
QY 204 GlnAsnTrpGlnSerAsnAsnTrpLeuAsnGlyGlnGlyLeuSerPheGlnAlaThrIle 223
DB 702 CAGAACGGCAAGCAACAATCTCTTAACGGCAACGATGTCATTAAAGTGACTGCT 761
QY 224 SerAspGlyArgThrlleuThraIleAlaTyraAsnLeuValProSerAsnTrpGlnPheGlyGln 243
DB 762 AATGATGTCGTACCGTCTGCTCTACAAACATTGCTCCAGCTGAGTGTGCTTGGACAA 821
QY 244 ThrTyxGlnGlyProGlnPhe 250
DB 822 ACCTTCACCGCGCGTCAATTC 842

RESULT 14
AAC40169
ID AAC40169 standard; DNA; 1326 BP.
XX
AC AAC40169;
XX
DT 17-OCT-2000 (first entry)
XX
DE Arabidopsis thaliana DNA fragment SEQ ID NO: 27308.
XX
KW Hybridisation assay; genetic mapping; gene expression control;
KW protein identification; signal transduction pathway;
KW metabolic pathway; promoter; termination sequence; ss.
XX
OS Arabidopsis thaliana.
XX
PN EP1033405-A2.
XX
PD 06-SEP-2000.
XX
PF 25-FEB-2000; 2000EP-0301439.
XX
PR 25-FEB-1999; 99US-0121825.
PR 05-MAR-1999; 99US-0123180.
PR 23-MAR-1999; 99US-0123548.
PR 25-MAR-1999; 99US-0126264.
PR 29-MAR-1999; 99US-0126785.
PR 01-APR-1999; 99US-0127462.
PR 06-APR-1999; 99US-0128234.

PR 08-APR-1999; 99US-0128714.
PR 16-APR-1999; 99US-0129845.
PR 19-APR-1999; 99US-0130077.
PR 21-APR-1999; 99US-0130449.
PR 23-APR-1999; 99US-0130510.
PR 28-APR-1999; 99US-0130891.
PR 30-APR-1999; 99US-0131449.
PR 30-APR-1999; 99US-0132048.
PR 04-MAY-1999; 99US-0132407.
PR 05-MAY-1999; 99US-0132484.
PR 06-MAY-1999; 99US-0132485.
PR 07-MAY-1999; 99US-0132486.
PR 11-MAY-1999; 99US-0132487.
PR 14-MAY-1999; 99US-0132487.
PR 14-MAY-1999; 99US-0134221.
PR 14-MAY-1999; 99US-0134221.
PR 14-MAY-1999; 99US-0134370.
PR 18-MAY-1999; 99US-0134370.
PR 19-MAY-1999; 99US-0134768.
PR 20-MAY-1999; 99US-0134941.
PR 21-MAY-1999; 99US-0135124.
PR 21-MAY-1999; 99US-0135353.
PR 24-MAY-1999; 99US-0135629.
PR 25-MAY-1999; 99US-0136021.
PR 27-MAY-1999; 99US-0136392.
PR 28-MAY-1999; 99US-0136782.
PR 01-JUN-1999; 99US-0137222.
PR 03-JUN-1999; 99US-0137528.
PR 04-JUN-1999; 99US-0137528.
PR 07-JUN-1999; 99US-0137724.
PR 08-JUN-1999; 99US-0138094.
PR 10-JUN-1999; 99US-0138540.
PR 10-JUN-1999; 99US-0138847.
PR 14-JUN-1999; 99US-0139119.
PR 16-JUN-1999; 99US-0139452.
PR 16-JUN-1999; 99US-0139453.
PR 17-JUN-1999; 99US-0139492.
PR 18-JUN-1999; 99US-0139454.
PR 18-JUN-1999; 99US-0139455.
PR 18-JUN-1999; 99US-0139456.
PR 18-JUN-1999; 99US-0139457.
PR 18-JUN-1999; 99US-0139457.
PR 18-JUN-1999; 99US-0139458.
PR 18-JUN-1999; 99US-0139459.
PR 18-JUN-1999; 99US-0139459.
PR 18-JUN-1999; 99US-0139460.
PR 18-JUN-1999; 99US-0139461.
PR 18-JUN-1999; 99US-0139461.
PR 18-JUN-1999; 99US-0139462.
PR 18-JUN-1999; 99US-0139463.
PR 18-JUN-1999; 99US-0139750.
PR 18-JUN-1999; 99US-0139763.
PR 21-JUN-1999; 99US-0139817.
PR 22-JUN-1999; 99US-0139899.
PR 23-JUN-1999; 99US-0140353.
PR 23-JUN-1999; 99US-0140354.
PR 24-JUN-1999; 99US-0140695.
PR 28-JUN-1999; 99US-0140823.
PR 29-JUN-1999; 99US-0140991.
PR 30-JUN-1999; 99US-0141287.
PR 01-JUL-1999; 99US-0141842.
PR 01-JUL-1999; 99US-0142154.
PR 02-JUL-1999; 99US-0142055.
PR 06-JUL-1999; 99US-0142390.
PR 08-JUL-1999; 99US-0142803.
PR 09-JUL-1999; 99US-0142920.
PR 12-JUL-1999; 99US-0142977.
PR 13-JUL-1999; 99US-0143542.
PR 14-JUL-1999; 99US-0143624.
PR 15-JUL-1999; 99US-0144005.
PR 16-JUL-1999; 99US-0144085.
PR 16-JUL-1999; 99US-0144086.
PR 19-JUL-1999; 99US-0144325.
PR 19-JUL-1999; 99US-0144331.
PR 19-JUL-1999; 99US-0144332.


```

PR 19-JUL-1999; 99US-0144333.
PR 19-JUL-1999; 99US-0144334.
PR 19-JUL-1999; 99US-0144335.
PR 20-JUL-1999; 99US-0144332.
PR 20-JUL-1999; 99US-0144332.
PR 20-JUL-1999; 99US-0144884.
PR 21-JUL-1999; 99US-0144814.
PR 21-JUL-1999; 99US-0145086.
PR 21-JUL-1999; 99US-0145088.
PR 22-JUL-1999; 99US-0145085.
PR 22-JUL-1999; 99US-0145087.
PR 22-JUL-1999; 99US-0145089.
PR 22-JUL-1999; 99US-0145192.
PR 23-JUL-1999; 99US-0145145.
PR 23-JUL-1999; 99US-0145218.
PR 23-JUL-1999; 99US-0145224.
PR 25-JUL-1999; 99US-0145276.
PR 27-JUL-1999; 99US-0145913.
PR 27-JUL-1999; 99US-0145918.
PR 28-JUL-1999; 99US-0145919.
PR 02-AUG-1999; 99US-0146386.
PR 02-AUG-1999; 99US-0146388.
PR 02-AUG-1999; 99US-0146389.
PR 03-AUG-1999; 99US-0147038.
PR 04-AUG-1999; 99US-0147204.
PR 04-AUG-1999; 99US-0147302.
PR 05-AUG-1999; 99US-0147182.
PR 05-AUG-1999; 99US-0147260.
PR 06-AUG-1999; 99US-0147303.
PR 06-AUG-1999; 99US-0147416.
PR 09-AUG-1999; 99US-0147493.
PR 09-AUG-1999; 99US-0147935.
PR 10-AUG-1999; 99US-0148171.
PR 11-AUG-1999; 99US-0148319.
PR 12-AUG-1999; 99US-0148341.
PR 13-AUG-1999; 99US-0148565.
PR 16-AUG-1999; 99US-0148684.
PR 17-AUG-1999; 99US-0149368.
PR 17-AUG-1999; 99US-0149175.
PR 18-AUG-1999; 99US-0149426.
PR 20-AUG-1999; 99US-0149722.
PR 20-AUG-1999; 99US-0149723.
PR 20-AUG-1999; 99US-0149929.
PR 23-AUG-1999; 99US-0149902.
PR 23-AUG-1999; 99US-0149910.
PR 25-AUG-1999; 99US-0150566.
PR 26-AUG-1999; 99US-0150884.
PR 27-AUG-1999; 99US-0151065.
PR 27-AUG-1999; 99US-0151066.
PR 27-AUG-1999; 99US-0151080.
PR 30-AUG-1999; 99US-0151303.
PR 31-AUG-1999; 99US-0151438.
PR 01-SEP-1999; 99US-0151930.
PR 07-SEP-1999; 99US-0152363.
PR 10-SEP-1999; 99US-0153070.
PR 13-SEP-1999; 99US-0153758.
PR 15-SEP-1999; 99US-0154018.
PR 16-SEP-1999; 99US-0154039.
PR 20-SEP-1999; 99US-0154779.
PR 22-SEP-1999; 99US-0155139.
PR 23-SEP-1999; 99US-0155486.
PR 24-SEP-1999; 99US-0155659.
PR 28-SEP-1999; 99US-0156458.
PR 29-SEP-1999; 99US-0156596.
PR 04-OCT-1999; 99US-0157117.
PR 05-OCT-1999; 99US-0157753.
PR 06-OCT-1999; 99US-0157865.
PR 07-OCT-1999; 99US-0158029.
PR 08-OCT-1999; 99US-0158232.
PR 12-OCT-1999; 99US-0158369.
PR 13-OCT-1999; 99US-0159293.
PR 13-OCT-1999; 99US-0159294.

```

```

PR 13-OCT-1999; 99US-0159295.
PR 14-OCT-1999; 99US-0159329.
PR 14-OCT-1999; 99US-0159330.
PR 14-OCT-1999; 99US-0159331.
PR 14-OCT-1999; 99US-0159337.
PR 14-OCT-1999; 99US-0159637.
PR 18-OCT-1999; 99US-0159538.
PR 21-OCT-1999; 99US-0159584.
PR 21-OCT-1999; 99US-0160741.
PR 21-OCT-1999; 99US-0160767.
PR 21-OCT-1999; 99US-0160768.
PR 21-OCT-1999; 99US-0160770.
PR 21-OCT-1999; 99US-0160814.
PR 21-OCT-1999; 99US-0160815.
PR 22-OCT-1999; 99US-0160980.
PR 22-OCT-1999; 99US-0160981.
PR 22-OCT-1999; 99US-0160989.
PR 25-OCT-1999; 99US-0161404.
PR 25-OCT-1999; 99US-0161405.
PR 25-OCT-1999; 99US-0161406.
PR 26-OCT-1999; 99US-0161359.
PR 26-OCT-1999; 99US-0161360.
PR 26-OCT-1999; 99US-0161361.
PR 28-OCT-1999; 99US-0161920.
PR 28-OCT-1999; 99US-0161992.
PR 28-OCT-1999; 99US-0161993.
PR 29-OCT-1999; 99US-0162142.

Alignment Scores:
Pred. No.: 1,32e-98
Score: 1024.50
Percent Similarity: 79.78%
Best Local Similarity: 69.29%
Query Match: 73.49%
DB: 21
Gaps: 4

US-09-383-579c-10 (1-250) x AAC40169 (1-1326)

QY 3 PheSerTySerPro-----PheSerSer-----LeuPheLeu----- 13
DB 44 TTCTCTCACTCTCTCTCCATTAAAGCTCTGCACCTTCTTCAAGAGAAATGTTCAAGGGCTAAG 103
QY 14 -----LeuProPhePhePheValPheThrPheAlaSerTyGly 26
DB 104 ATGGGCTTTTGGGAATGCTGTTGTGTTTGGTGCATGAGTGGCTGTGTTACAGA 163
QY 27 -----GlyTrpGlnSerGlyHisAlaThrPheTyGlyGlyAlaSerGly 43
DB 164 TATGACGCTGAGTGGGTCAATGCTCATGCTTCTATGTGGAAGTGAATGCTTCAGCA 223
QY 44 ThMetGlyGlyAlaCysGlyTyrglyAenLeuTySerGlnGlyTyrglyThrAsnThr 63
DB 224 ACAATGGGTGAGCTGTTGGCTACGGGAACCTTACAGTAAAGTTACGGGACCAACAGC 283
QY 64 ValAlaLeuSerThrAlaLeuPheAsnAsnGlyLeuSerCysGlyAlaCysPheGluMet 83
DB 284 GCGGCGTTGAGCACTGCTCTTCAACACGCTTACAGTTCAGTCCGGGCGCTTTTGAGATC 343
QY 84 ThrCysThrAsnAspProlystTyrglyLeuProGlyThrIleArgValThrAlaThrAsn 103
DB 344 AAGTGTACAGCAGCAGCGCGGTGCTTTTACCTGCTTCATTCGACAGCACCACAT 403
QY 104 PheCysProProAsnAlaLeuProAsnAsnGlyGlyTyrglyCysAsnProProLeu 123
DB 404 TTCTGTCTCTCTTACCAACGCTCTTCCAAATACGCTGGTGGTGAACCTCCGCTT 463
QY 124 GlnHisPheAspMetAlaGluProAlaPheLeuGlnIleAlaGlnTyrglyArgAlaGlyIle 143
DB 464 CATCATTTGATGATCTCTACGCTGTTTTCACACGATTCCTCAGTACAAAGCTGGTGT 523
QY 144 ValProValSerPheArgArgValProCysMetLeuGlyGlyGlyValIleArgPheThrIle 163
DB 524 GTCCCTGTTTCTTACAGAAAGGTTCCGTGTATAGAGAAGAGATATTAAGATTACACATC 583

```

QY 164 AaenGIyHieSerTyRphesnleuValleuIleThraSnValGIyAlaGIyAlaSpVal 183
 Db 584 AACGGTCACTCTTACTTCAACCTTGCTTGGAACCAAGTGTGTGTGAGATGTT 643
 QY 184 HieSerValSerIleIySGIySerArGThrGIyTrpGlnSerMetSerArGAnTTrpGIy 203
 Db 644 CATTCGTTGCGGTTAAAGTTCTAGACAAAGTGGCAAAATGTCAGAACTGGGA 703
 QY 204 GlnAenTrpGlnSerArGAnTTrpGlnAenGIyGlnGIyLeuSerPheGlnValThrLeu 223
 Db 704 CAGAACTGGCAAGCAACATCTTAAACGGTCAAGCATTTGCAATTAAAGTACTGCT 763
 QY 224 SerArSGIyArGThrLeuThraIaTyraSnleuValProSerArGAnTTrpGlnPheGIyGln 243
 Db 764 AGTGAATGTCGTAACCTGCTCTTAACAACATTCCTCAAGTGTGTGCTTTGACAA 823
 QY 244 ThrTyGluGIyProGlnPhe 250
 Db 824 ACCTTCACCGCGCTCAATTTC 844
 RESULT 15
 AB213264
 ID AB213264 standard; DNA; 747 BP.
 XX
 AC AB213264;
 XX
 DT 21-JAN-2003 (first entry)
 XX
 DB Arabidopsis thaliana stress regulated gene SEQ ID NO 1069.
 XX
 KW Arabidopsis thaliana; plant; gene; stress; transgenic; ds.
 XX
 OS Arabidopsis thaliana.
 XX
 PN WO200216655-A2.
 XX
 PD 28-FEB-2002.
 XX
 PF 24-AUG-2001; 2001WO-US26685.
 XX
 PR 24-AUG-2000; 2000US-227866P.
 XX
 PR 26-JAN-2001; 2001US-264647P.
 XX
 PR 22-JUN-2001; 2001US-300111P.
 XX
 PA (SCRI) SCRIPPS RES INST
 XX
 PA (SYGN) SYNGENTA PARTICIPATIONS AG.
 XX
 PI Harper JF, Kreps J, Wang X, Zhu T;
 XX
 DR WPI; 2002-304127/34.
 XX
 PT Identifying a stress condition to which a plant cell has been exposed
 XX
 PT and producing plants with increased tolerance to these abiotic stresses
 XX
 PS Claim 144; SEQ ID NO 1069; 577bp + Sequence Listing; English.
 XX
 CC The invention relates to identifying a stress condition to which a plant
 XX
 CC cell has been exposed, comprising:
 XX
 CC (a) contacting nucleic acid representative of expressed polynucleotides
 XX
 CC in the plant cell with an array or probes representative of the plant
 XX
 CC cell genome; and
 XX
 CC (b) detecting a profile of expressed polynucleotides in the plant cell
 XX
 CC characteristic of a stress response. The method is useful in the
 XX
 CC production of transgenic plants, cells and seeds and in producing plants
 XX
 CC with increased tolerance to abiotic stress. The present sequence is that
 XX
 CC of an Arabidopsis thaliana stress regulated gene (AB212196-AB217574) used
 XX
 CC in methods of the invention.
 XX
 CC Note: The sequence data for this patent is not represented in the printed
 XX
 CC specification but is based on sequence information supplied to Derwent by
 XX
 CC the European Patent Office.
 XX
 SQ Sequence 747 BP; 166 A; 169 C; 192 G; 220 T; 0 other;

Alignment Scores:
 Pred. No.: 6,63e-99 Length: 747
 Score: 1024.00 Matches: 175
 Percent Similarity: 88.39% Conservative: 23
 Best Local Similarity: 78.12% Mismatches: 26
 Query Match: 73.46% Indels: 0
 DB: 24 Gaps: 0
 US-09-383-579c-10 (1-250) x AB213264 (1-747)
 QY 27 GIYTrpGlnSerGIyHieSerValIleThraPheTyRGIyGIyAlaSpValSerGIyThrMetGIy 46
 Db 70 GGATGGTCAATGCTCATCTCTTCTATGTGGAAGATGCTTACGAACATGGGT 129
 QY 47 GIyAlaCySGIyTyRGIyAenleuTySerGlnGIyTyRGIyThraSnThraValleu 66
 Db 130 GGAGCTTGTGGCTACGGGAACCTTAAGTCAGTCAAGGTAACGGAACACCGCGGCTTG 189
 QY 67 SerThraIleuPheAenGIyLeuSerCySGIyAlaCyPheGlnMetThrCySerThr 86
 Db 190 AGCACTGCTCTGTAAACAACGCTCTTAGCTGGGCGCTTGTGAGATCAAGTCTAG 249
 QY 87 AenAapProLyTrpCyLeuPProGIyThrIleArGValThraIleThraSnPheCySerPro 106
 Db 250 AGCGACGGCGGCTGTGTCTTACTGTGTCTATCATCTTCAACGCCACCAATTTCTGTCT 309
 QY 107 ProAenPheAlaIleuProAenAenAenGIyGIyTyRGIyAenPProLeuGlnIlePhe 126
 Db 310 CCTAACCAACGCTCTTCCCAATTAACCGTGTGTGTGTAAACCTCCGCTCATCATTC 369
 QY 127 AapMetAlaIleuProAlaPheLeuGlnIleAenGIyTyRGIyAlaGIyAlaValProVal 146
 Db 370 GATCTCTCAGCTGTGTCTTTCACGCAATGCTCTGACAAAGCTGTGTGTGTCTCTGT 429
 QY 147 SerPheArGIyValProCySerMetLySGIyGIyValArGThrIleAenGIyHie 166
 Db 430 TCCTACAGAAAGGTTCCGTTATGAGAGAGAGATTAAGTTACATCAACGCTGC 489
 QY 167 SerTyRphesnleuValleuIleThraSnValGIyAlaGIyAlaSpValHieSerVal 186
 Db 490 TCTTACTTCAACCTTGTCTTGTGTGACCAATGTGTGTGTGTGTGTGTGTGTGTGT 549
 QY 187 SerIleIySGIySerArGThrGIyTrpGlnSerMetSerArGAnTTrpGlnAenTTrp 206
 Db 550 GCGGTTAAAGTCTTAAGCAAGTGGCAAAATGTCAAGAACTGGGACAGAACTGG 609
 QY 207 GlnSerAenAenTyRleuAenGIyGlnGIyLeuSerPheGlnValThrLeuSerArGIy 226
 Db 610 CAAAGCAACATCTCTTAAACGCTCAAGCATTTGCTAATTAAGTACTGTCTAGTGT 669
 QY 227 ArgThrLeuThraIleThraSnleuValProSerArGAnTTrpGlnPheGIyGlnThrTyGlu 246
 Db 670 CGTACCGTCTCTTAACCAACATGCTCAGCTAGTGTGTCTTGTGACAAACCTTACC 729
 QY 247 GIYTrpGlnPhe 250
 Db 730 GGCGGCTCAATTTC 741
 Search completed: December 18, 2003, 23:41:27
 Job time : 263 sec

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: December 18, 2003, 23:29:07 ; Search time 78 Seconds
(without alignments)
1414.690 Million cell updates/sec

Title: US-09-383-579C-10

Perfect score: 1394
Sequence: 1 MAFSYSPFSSFLPLFFFEV.....AYNLVPSNMQFGQTEGPGQF 250

Scoring table:

BLOSUM62	
Xgapop 10.0 , Xgapext 0.5	
Ygapop 10.0 , Ygapext 0.5	
Fgapop 6.0 , Fgapext 7.0	
Delop 6.0 , Delext 7.0	

Searched: 569978 seqs, 220691566 residues

Total number of hits satisfying chosen parameters: 1139956

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODE=frame+ p2n.model -DEV=xlp
-Q=/cgn2_1/USFTO.spool/p/US09383579/runat_18122003_171927_28806/app_query.fasta_1.391
-DB=Issued_Patents_NA -OPMT=faetap -SUFFIX=tni -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blomsum62 -TRANS=human40.cdi
-LIST=45 -DOCLIGN=200 -THR SCORE=PCT -THR MAX=100 -THR MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USR=US09383579 @CGN 1.1 103 @runat_18122003_171927_28806 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEOUTRY -NEG_SCORES=0 -WAIT -DSPBLCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=5 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

Issued Patents NA:*
1: /cgn2_6/ptodata/2/ina/5A.COMB.seq:*
2: /cgn2_6/ptodata/2/ina/5B.COMB.seq:*
3: /cgn2_6/ptodata/2/ina/6A.COMB.seq:*
4: /cgn2_6/ptodata/2/ina/6B.COMB.seq:*
5: /cgn2_6/ptodata/2/ina/PTUS.COMB.seq:*
6: /cgn2_6/ptodata/2/ina/backfile1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1275	91.5	681	2	US-08-440-517A-1
2	1275	91.5	681	3	US-09-092-160-1
3	919.5	66.0	2415	1	US-07-885-970A-26
4	919.5	66.0	2415	1	US-08-298-687A-26
5	919.5	66.0	2415	1	US-08-298-829-26
6	841.5	60.4	702	4	US-09-362-642-1
7	839.5	60.2	702	2	US-08-845-539-5
8	797	57.2	537	4	US-08-845-539-5
9	797	57.2	537	4	US-08-362-642-5
10	732	52.5	501	2	US-08-845-539-3
11	732	52.5	501	4	US-09-362-642-3
12	706	50.6	727	1	US-07-885-970A-6

13	706	50.6	727	1	US-08-298-687A-6	Sequence 6, Appli
14	706	50.6	727	1	US-08-530-797-5	Sequence 5, Appli
15	706	50.6	727	1	US-08-298-829-6	Sequence 6, Appli
16	706	50.6	727	2	US-08-787-335-5	Sequence 5, Appli
17	324.5	23.3	279	4	US-09-313-294A-1276	Sequence 1276, Ap
18	249.5	17.9	1072	1	US-07-971-096-1	Sequence 1, Appli
19	249.5	17.9	1072	1	US-08-175-096-1	Sequence 1, Appli
20	249.5	17.9	1072	1	US-08-441-507-20	Sequence 20, Appli
21	236	16.9	759	3	US-07-969-875A-20	Sequence 20, Appli
22	233	16.7	810	3	US-08-413-874-5	Sequence 5, Appli
23	233	16.7	810	3	US-08-434-418-5	Sequence 5, Appli
24	233	16.7	810	3	US-08-433-288-5	Sequence 5, Appli
25	233	16.7	810	3	US-08-174-739A-5	Sequence 5, Appli
26	233	16.7	810	3	US-08-434-256-5	Sequence 5, Appli
27	233	16.7	1123	1	US-07-971-096-3	Sequence 3, Appli
28	233	16.7	1123	1	US-08-175-096-3	Sequence 3, Appli
29	173	12.4	775	4	US-08-441-507-3	Sequence 3, Appli
30	173	12.4	775	4	US-07-969-875A-3	Sequence 3, Appli
31	173	12.4	802	3	US-08-441-507-18	Sequence 18, Appli
32	173	12.4	802	4	US-07-969-875A-18	Sequence 18, Appli
33	173	12.4	832	3	US-08-441-507-19	Sequence 19, Appli
34	173	12.4	832	4	US-07-969-875A-19	Sequence 19, Appli
35	150.5	10.8	1645	4	US-09-112-988A-1	Sequence 1, Appli
36	145	10.4	2614	4	US-09-004-056-1	Sequence 1, Appli
37	142.5	10.2	368	3	US-08-441-507-22	Sequence 22, Appli
38	142.5	10.2	368	4	US-07-969-875A-22	Sequence 22, Appli
39	119.5	8.6	756	3	US-08-413-874-3	Sequence 3, Appli
40	119.5	8.6	756	3	US-08-434-418-3	Sequence 3, Appli
41	119.5	8.6	756	3	US-08-433-288-3	Sequence 3, Appli
42	119.5	8.6	756	3	US-08-174-739A-3	Sequence 3, Appli
43	119.5	8.6	756	3	US-08-434-256-3	Sequence 3, Appli
44	103.5	7.4	4403765	3	US-09-103-840A-2	Sequence 2, Appli
45	103.5	7.4	4411529	3	US-09-103-840A-1	Sequence 1, Appli

ALIGNMENTS

RESULT 1
US-08-440-517A-1
Sequence 1, Application US/08440517A
Patent No. 5959082
GENERAL INFORMATION:
APPLICANT: COSGROVE, DANIEL J.;
APPLICANT: GUILTYMAN, MARK;
APPLICANT: SHCHERBAN, TATYANA;
APPLICANT: SHI, JUN
TITLE OF INVENTION: PURIFIED EXPANSIN PROTEINS
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: INTELLECTUAL PROPERTY OFFICE, THE
STREET: 113 TECHNOLOGY CENTER
CITY: UNIVERSITY PARK
STATE: PENNSYLVANIA
COUNTRY: UNITED STATES OF AMERICA
ZIP: 16802-7000
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: NEC 286
OPERATING SYSTEM: DOS
SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/440,517A
FILING DATE:
CLASSIFICATION: 530
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 681
TYPE: NUCLEIC ACID
STRANDEDNESS: SINGLE
TOPOLOGY: UNKNOWN
US-08-440-517A-1

Alignment Scores:

Pred. No.: 9,54e-137 Length: 681
 Score: 1275.00 Matches: 227
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 91.46% Indels: 0
 DB: 2 Gaps: 0

US-09-383-579C-10 (1-250) x US-08-440-517A-1 (1-681)

```

OY 24 AAPPYRGYGLYTRPGINSErGlyhIsAlaThrPheTYrGlyGlyAspAlaSerGly 43
DB 1 GACTACGGTGGCTGGAGAGCGGCCACGCCACTTTATGCGTGTGATGCGATGTGGC 60
OY 44 ThrMetGlyGlyAlaCyGlyTYrGlyAsnLeuTYrSerGlnGlyTYrGlyThrAsnThr 63
DB 61 ACCATGGGTGGAGCTGTGGGTATGGGAATTTATACAGCCAAAGGGATGGCAGAACACG 120
OY 64 ValAlaLeuSerThrAlaLeuPheAsnAnglyLeuSerCyGlyAlaCySpheGlnMet 83
DB 121 GTGGCGCTGAGCACTGGCTATTTCACATGATTAAGTTGTTGCTTGTCTTGGAAATG 180
OY 84 ThrCyThrAsnAspProlySTrPcySleuProGlyThrIlleArgValThrAlaThrAsn 103
DB 181 ACTTGACAAAGCAACCTTAATGTGTCTTCGGGAACTATTAGGTCTACTGCGACCAAC 240
OY 104 PheCyProProAsnPheAlaLeuProAsnAsnAnglyGlyTYrPcyAsnProProLeu 123
DB 241 TTTTGCCCTCTCACTTCTCTCTCTCTCAACAAATGATGGATGGCAACCTCTCTC 300
OY 124 GlnHisPheAspMetAlaGluProAlaPheLeuGlnIlleAlaGlnTYrArgAlaGlyIle 143
DB 301 CAACACTTGACATGGCTAGCTAGCTGCTCTTCAATATGCTCAATACGAGCTGGATATC 360
OY 144 ValProValSerPheArgArgValProCyMetIleGlyGlyValArgPheThrIle 163
DB 361 GTCCCGCTCTCTTCTGTGAGGATGACATGATGATGATGATGATGATGATGATGATG 420
OY 164 AsnGlyHisSerTYrPheAsnLeuValLeuIlleThrAsnValGlyValArgPheThrIle 183
DB 421 AATGGCCACTCACTTCACTCAACCTGTTGATGATCAAAAGCTGGGCGACGCGATC 480
OY 184 HisSerValSerIleLeuGlySerArgThrGlyTYrGlnSerMetSerArgAsnTrpGly 203
DB 481 CACTCTGTGTGATTAAGGGGTCTCGACATGGATGGCAATCCATGCTGAATTTGGGCG 540
OY 204 GlnAsnTrpGlnSerAsnAsnTYrLeuAsnGlyGlnGlyLeuSerPheGlnValThrLeu 223
DB 541 CAAACTGGCAAAAGCAACAATCTCATATGGCCAAAGGCTTCTTCAAGTCACTCTT 600
OY 224 SerAspGlyArgThrLeuThrAlaTYrAsnLeuValProSerAsnTrpGlnPheGlyGln 243
DB 601 AGTGATGGTGGCACTGCTCACTGCTTAATCTGTTCTTCCAAATGGCAATTTGGCCAA 660
OY 244 ThrTYrGluGlyProGlnPhe 250
DB 661 ACCTATGAAGGCCCTCAATTC 681

```

RESULT 2
 US-09-092-160-1
 Sequence 1, Application US/09092160C

Patent No. 6255466
 GENERAL INFORMATION:
 APPLICANT: Cosgrove, Daniel J
 APPLICANT: McQueen-Mason, Simon
 APPLICANT: Guiltinan, Mark J
 APPLICANT: Shcherban, Tatyana
 APPLICANT: Shi, Jun
 TITLE OF INVENTION: PURIFIED EXPANSIN PROTEINS
 FILE REFERENCE: 1194/1C11AUS3
 CURRENT APPLICATION NUMBER: US/09/092,160C
 CURRENT FILING DATE: 1998-06-05
 EARLIER APPLICATION NUMBER: 08/440,517

EARLIER FILING DATE: 1995-05-12
 EARLIER APPLICATION NUMBER: 08/242,090
 EARLIER FILING DATE: 1994-05-12
 EARLIER APPLICATION NUMBER: 08/060,944
 EARLIER FILING DATE: 1993-05-12
 NUMBER OF SEQ ID NOS: 7
 SOFTWARE: PatentIn Ver. 2.1
 SEQ ID NO 1
 LENGTH: 681
 TYPE: DNA
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: Description of Artificial Sequence: cDNA cucumber
 US-09-092-160-1

Alignment Scores:

Pred. No.: 9,54e-137 Length: 681
 Score: 1275.00 Matches: 227
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 91.46% Indels: 0
 DB: 3 Gaps: 0

US-09-383-579C-10 (1-250) x US-09-092-160-1 (1-681)

```

OY 24 AAPPYRGYGLYTRPGINSErGlyhIsAlaThrPheTYrGlyGlyAspAlaSerGly 43
DB 1 GACTACGGTGGCTGGAGAGCGGCCACGCCACTTTATGCGTGTGATGCGATGTGGC 60
OY 44 ThrMetGlyGlyAlaCyGlyTYrGlyAsnLeuTYrSerGlnGlyTYrGlyThrAsnThr 63
DB 61 ACCATGGGTGGAGCTGTGGGTATGGGAATTTATACAGCCAAAGGGATGGCAGAACACG 120
OY 64 ValAlaLeuSerThrAlaLeuPheAsnAnglyLeuSerCyGlyAlaCySpheGlnMet 83
DB 121 GTGGCGCTGAGCACTGGCTATTTCACATGATTAAGTTGTTGCTTGTCTTGGAAATG 180
OY 84 ThrCyThrAsnAspProlySTrPcySleuProGlyThrIlleArgValThrAlaThrAsn 103
DB 181 ACTTGACAAAGCAACCTTAATGTGTCTTCGGGAACTATTAGGTCTACTGCGACCAAC 240
OY 104 PheCyProProAsnPheAlaLeuProAsnAsnAnglyGlyTYrPcyAsnProProLeu 123
DB 241 TTTTGCCCTCTCACTTCTCTCTCTCTCAACAAATGATGGATGGCAACCTCTCTC 300
OY 124 GlnHisPheAspMetAlaGluProAlaPheLeuGlnIlleAlaGlnTYrArgAlaGlyIle 143
DB 301 CAACACTTGACATGGCTAGCTAGCTGCTCTTCAATATGCTCAATACGAGCTGGATATC 360
OY 144 ValProValSerPheArgArgValProCyMetIleGlyGlyValArgPheThrIle 163
DB 361 GTCCCGCTCTCTTCTGTGAGGATGACATGATGATGATGATGATGATGATGATGATG 420
OY 164 AsnGlyHisSerTYrPheAsnLeuValLeuIlleThrAsnValGlyValArgPheThrIle 183
DB 421 AATGGCCACTCACTTCACTCAACCTGTTGATGATCAAAAGCTGGGCGACGCGATC 480
OY 184 HisSerValSerIleLeuGlySerArgThrGlyTYrGlnSerMetSerArgAsnTrpGly 203
DB 481 CACTCTGTGTGATTAAGGGGTCTCGACATGGATGGCAATCCATGCTGAATTTGGGCG 540
OY 204 GlnAsnTrpGlnSerAsnAsnTYrLeuAsnGlyGlnGlyLeuSerPheGlnValThrLeu 223
DB 541 CAAACTGGCAAAAGCAACAATCTCATATGGCCAAAGGCTTCTTCAAGTCACTCTT 600
OY 224 SerAspGlyArgThrLeuThrAlaTYrAsnLeuValProSerAsnTrpGlnPheGlyGln 243
DB 601 AGTGATGGTGGCACTGCTCACTGCTTAATCTGTTCTTCCAAATGGCAATTTGGCCAA 660
OY 244 ThrTYrGluGlyProGlnPhe 250
DB 661 ACCTATGAAGGCCCTCAATTC 681

```

```

RESULT 3
US-07-885-970A-26
: Sequence 26, Application US/07885970A
: Patent No. 5495070
: GENERAL INFORMATION:
: APPLICANT: John, Malyakal E.
: TITLE OF INVENTION: GENETICALLY ENGINEERING COTTON
: NUMBER OF SEQUENCES: 33
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Nicholas J. Seay, Quarles & Brady
: STREET: P.O. Box 2113, First Wisconsin Plaza
: CITY: Madison
: STATE: Wisconsin
: COUNTRY: USA
: ZIP: 53701
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Microsoft Word
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/07/885,970A
: FILING DATE: 19920518
: CLASSIFICATION: 435
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 07/617,239
: FILING DATE: 21-NOV-1990
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 07/255,243
: FILING DATE: 04-OCT-1988
: ATTORNEY/AGENT INFORMATION:
: NAME: Seay, Nicholas J.
: REGISTRATION NUMBER: 27,386
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (608) 283-2478
: TELEFAX: (608) 251-5139
: INFORMATION FOR SEQ ID NO: 26:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 2415 base pairs
: TYPE: NUCLEIC ACID
: STRANDEDNESS: double
: TOPOLOGY: linear
: MOLECULE TYPE: DNA (genomic)
: HYPOTHEetical: NO
: ANTI-SENSE: NO
: ORIGINAL SOURCE:
: ORGANISM: Gossypium barbadense
: STRAIN: Sea Island
: IMMEDIATE SOURCE:
: LIBRARY: EMBL 51
: CLONE: SIB12
: US-07-885-970A-26

Alignment Scores:
Pred. No.: 3,13e-95 Length: 2415
Score: 919.50 Matches: 184
Percent Similarity: 70.43% Conservative: 28
Best Local Similarity: 61.13% Mismatches: 36
Query Match: 65.96% Indels: 56
DB: 1 Gaps: 2

US-09-383-579C-10 (1-250) x US-07-885-970A-26 (1-2415)

QY 3 PhseSerTySerProPheSerIeuPheLeuLeuProPhePheValPheThrPhe 22
Db 784 TTTCACCTTCTCTCTTTGTTGAGGTATGCACTCATTTTCTTGCTCTAATGGA- 842
QY 23 AAlAsPTyGtGtYTrpGInserGtYhIsAlAtnPhetYgYgYgYVAspAlAsr 42
Db 843 GATGACAAATGATGTGTG-CAAAATGCCCATGC-ACCTTCTACGAGTGTGATGTTACC 900
QY 43 GtYThrMet----- 45

```

```

Db      901 GGCAATGGGTGAGTTTCAAACCTTTGAACCATTAACCTAATAAAATCTTAGCCTAT   960
        |||||
Qy      46 -----GlyglyalaCyeglytyrilyanleutyrsargl   57
Db      961 GTTCTTAATTGATGATGTTTCTTAATAGGGGAGCGCTTGTTATGAAACCTGTACAGTCA   1020
Qy      57 nglytyrglythrasmnhrvalaleuserrhrhalaleuphasnbnnglyleusercy   77
Db      1021 AGGTTATGGAACGAGCACACAGCTGTTGAGCACACTTTTCAAACAATGGCTTGACCTG   1080
Qy      77 sglvala-CyspheglnmetThrCysethrasnapprolystprCyaleuprogllythri   97
Db      1081 CGGCGACCTGCTACGAGCTCCGGTGCAACAATGATCTCTCAATGTGCATTAAGTGAACCA   1140
Qy      97 learyalThrhalathrasnpheCyepbrofproasnpehalaleuproasnasnanglyg   117
Db      1141 TPAACCGTAGACGCCAACCACTTTGTGTCCCTCAACTATGCTTTATCTATGAGACAAATGGCG   1200
Qy      117 lytprCyaaenProProLeuglnhiAphaspmetAlagluProAlaphelenglnlea   137
Db      1201 GGTGTGTCCAATCCCCCGACGAAACACTTATATYTTGGCGGAACCGGCATTCTTGACATCG   1260
Qy      137 lagintyrarqalaglIlevalProvalserphearg-----   149
Db      1261 CGGAATTCAGAGCTGGAATGCTCCCTGTTATGTTCAAGAGTGSTGATATAAACTCAATT   1320
Qy      150 -----ArgVal   151
Db      1321 CAATCATCAACACTTTAAGTATGTTAAACTGTTGGGTGTTAACTTTTGACAGGSGT   1380
Qy      152 ProCyemetylsylsglyglyValangphetheThlleanglyhisertyrPheAsnleu   171
Db      1381 TCATGTGTGAAGAAGAGGACATCAGGTATACCATGATATGACATTCGTACTTCACATG   1440
Qy      172 ValleunlethrnsnvalelglyValaglyAspvAlhiservalseerlleybglySer   191
Db      1441 GTGTGTATTAACCAACGTTGGAGGGGCGAGGGGATATTAAGTCAGGTGCATCAAGTGTCC   1500
Qy      192 ArgThrslgltprglinsermetseryArgasntrpglyglnasntrpglnseerAsnaentyr   211
Db      1501 AAAACAGAGTGGCTACTACTATGTCAGAAATTGGGGCCAAAATCGCGACAGCAATGCTTAC   1560
Qy      212 LeuannglynglyleuserPheglnValThrleuserAspglyargThrleuthra   231
Db      1561 CTTAACGGCCAAAGCCTCTCTTCAAGTAGACTGCCAGCATGGCAGAGCTATCAACAAC   1620
Qy      232 TyrAsnleuValproserAsntrpglnPheglynhrthyrgluglyProglnPhe   250
Db      1621 TACAATGTAGTGCCTGCTGTTGGCAATTGGAACCACTTTGAAAGAGGCCAGTTT   1677

RESULT 4
US-08-298-687A-26
Sequence 26 Application US/08298687A
Patent No. 5521078
GENERAL INFORMATION:
APPLICANT: John, Malyiakal E.
TITLE OF INVENTION: GENERALLY ENGINEERING COTTON
TITLE OF INVENTION: PLANTS FOR ALTERED FIBER
NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS:
ADDRESSEE: Nicholas J. Seay, Quarles & Brady
STREET: P.O. Box 2113, First Wisconsin Plaza
CITY: Madison
STATE: Wisconsin
COUNTRY: USA
ZIP: 53701
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Microsoft word
CURRENT APPLICATION DATA:
```

```

Oy      137  lagInGTYrARgAAGlAGlYlleVAlProVAlSerPheArG----- 149
Db      1261 CGGATATCGAGCTGGAATGCTCTGTATGTTTCAGAGAGTGCTGAATAAACTCAATT 1320
Oy      150  -----ArgVal 151
Db      1321 CAATTCATCACTCTTAAGTATGTTAAACTGTGGGTGTTTAACCTTTGCAGGGTG 1380
Oy      152  ProCyMeUcYlYsGlyGlyValArgPheThrIleAnGlyHisSerTYrPheAnleu 171
Db      1381 TCATGTGTGAAGAAGAGGAGCATCAGGTACACCATGATGACATTTGTACTTCAACATG 1440
Oy      172  ValIeuIleThrAnValAGlyGlyValGlyAspValHisSerValSerIleUcGlySer 191
Db      1441 GTGTGTATACCAACGCGGAGGGGCGAGGAGATATTAAGTCATGTCATCAAGTGTTC 1500
Oy      192  ArgThrGlyTYrPGInSerMetSerArgAsnTrpGlyInAnSerTPGInSerAsnAsnTYr 211
Db      1501 AAAACAGAGATGCTACTATATCTCCAGAAATTGGGGCCAAAATCGCAGAGCAATGCTTAC 1560
Oy      212  LeuAnGlyInGlyInLeuSerPheGlnValThrLeuSerAspGlyArgTYrLeuThrAla 231
Db      1561 CTTAACGGCCAAAGCCTCTCTTCAAGTAGCTCCAGCATGCGACGACTATACAAAC 1620
Oy      232  TyrAnLeuValProSerAsnTrpGlnPheGlyGlnThrTYrGlyGlyProGlnPhe 250
Db      1621 TACATGTAGTGCCTGCTGTTGGCAATTGCGAACAACTTTGAAGAGGCCAGTTT 1677

RESULT 5
US-08-298-829-26
; Sequence 26, Application US/08298829
; Patent No. 5620882
; GENERAL INFORMATION:
; APPLICANT: John, Maliyakal E.
; TITLE OF INVENTION: GENETICALLY ENGINEERING COTTON
; TITLE OF INVENTION: PLANTS FOR ALTERED FIBER
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Nicholas J. Seay, Quarles & Brady
; STREET: P.O. Box 2113, First Wisconsin Plaza
; CITY: Madison
; STATE: Wisconsin
; COUNTRY: USA
; ZIP: 53701
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Microsoft word
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/298,829
; FILING DATE: 19-OCT-1994
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/885,970
; FILING DATE: 18-MAY-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/617,239
; FILING DATE: 21-NOV-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/253,243
; FILING DATE: 04-OCT-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Seay, Nicholas J.
; REGISTRATION NUMBER: 27,386
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (608) 283-2478
; TELEFAX: (608) 251-5139
; INFORMATION FOR SEQ ID NO: 26:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2415 base pairs
; TYPE: nucleic acid
;

```

```

STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Gossypium barbadense
STRAIN: Sea Island
IMMEDIATE SOURCE:
LIBRARY: EMBL-SI
CLONE: SIB12
US-08-298-829-26

Alignment Scores:
Pred. No.: 3,13e-95 Length: 2415
Score: 919.50 Matches: 184
Percent Similarity: 70.43% Conservative: 28
Best Local Similarity: 61.13% Mismatches: 36
Query Match: 65.96% Indels: 56
DB: 1 Gaps: 2

US-09-383-579c-10 (1-250) x US-08-298-829-26 (1-2415)
QY 3 PheserTySerProPheSerSerLeuPheLeuPhePhePheValPheThrPhe 22
DB 784 TTTCACCTTTCTCTTTGTTGTCAGTGTGCACTCCATTCTTGCGTAAATGCA- 842
QY 23 AlaAspTyTrpGlyTyrPgiInserGlyHisAlaThrPheTyTrpGlyValAspAlaSer 42
DB 843 GATGACATAGTGTGTG-CAAACTGCCCATGC-ACCTTTCAGGTGTGTGATGCTAAC 900
QY 43 GlyThrMet----- 45
DB 901 GGACCATGGGTGATTTCAAACTTCAACCATTAACATAAAATCTCAGCTAT 960
QY 46 -----GlyGlyAlaCyGlyTyrGlyAsnLeuTyrSerGly 57
DB 961 GTTCTTAATTTGATGATTTCTATAGGGGGAGCTTGATGAAACCTGTACACTCA 1020
QY 57 nglyTyTrpGlyThrAsnThrValAlaLeuSerThrAlaLeuPheAsnnglyLeuSerGly 77
DB 1021 AGGCTATGACAGCAGCAGACAGCTTGTAGACACTTTCACCATGCTTGAGCTG 1080
QY 77 sglYAla-CysPheGluMetThrCysThrAsnAspProLysTyrCysLeuProGlyThrI 97
DB 1081 CGGTGACCTGCTAGACGCTCCGGTCAACATATGCTCATGCTGATTAAGTGAACA 1140
QY 97 leaArgValThrAlaThrAsnPheCysProProAsnPheAlaLeuProAsnAsnnglyG 117
DB 1141 TAACCGTGAAGCAGCAGCAACTTTGTGCTTACTTATCTTAAGTGAACAATGGCG 1200
QY 117 lyTyTrpCysAsnProProLeuGlnHisPheAspMetAlaGluProAlaPheLeuGlnIleA 137
DB 1201 GGTGTGTCAATCCCGCAGAAACACTTGTATTTGGCGAAACCGCACTTCTTGACATCG 1260
QY 137 laGlnTyTrpArgAlaGlyIleValProValSerPheArg----- 149
DB 1261 CGGAATTCAGCTGGAATGCTCCCTGTATGTTCAAGAAGTGTGATTAATAACTCAAT 1320
QY 150 -----ArgVal 151
DB 1321 CAATCATCACACTCTTAAGTATGTTAAACGTGTGGTGTTAACCTTTTGACAGGTG 1380
QY 152 ProCysMetLysLysGlyValArgPheThrIleAsnGlyHisSerTyrrPheAsnLeu 171
DB 1381 TCATGTGTGAAGAAAGAGGAGCATCGTACCACTGATGACATTTGCTCTTCAACATG 1440
QY 172 ValLeuIleThrAsnValGlyValGlyValAspValHisSerValSerIleLysGlySer 191
DB 1441 GTGTGTATTAACAACGTCGAGGGGAGGGGATTAACGTCAGTGTCTCATCAAGTCTCC 1500
QY 192 ArgThrGlyTyrPgiInserMetSerArgAsnTyrPgiValAsnTyrPgiInserAsnAsnTyr 211

```

```

DB 1501 AAAACAGATGCTTACCTATGTCAGAAATTGGGGCCAAAACCTGCAGACCAATGCTTAC 1560
QY 212 leuAsnGlyInglLeuSerPheGlnValThrLeuSerAspGlyArgThrLeuThrAla 231
DB 1561 CTTAAGGCCCAAGAGCTCTCTTTCAAAGTATGCTCCAGCATGCGAGCATATATACAAAC 1620
QY 232 TyrAsnLeuValProSerAsnTyrPgiInPheGlyGlnThrTyTrpGlyInglProGlnPhe 250
DB 1621 TACATGTATGCTGCTGTGTTGCAATTCGACAACTTTGAAAGAGCGCAAGTTT 1677

RESULT 6
US-09-362-642-1
Sequence 1, Application US/09362642
Patent No. 6350935
GENERAL INFORMATION:
APPLICANT: Bennett, Alan B.
APPLICANT: Rose, Jocelyn K.C.
TITLE OF INVENTION: The Regents of the University of California
TITLE OF INVENTION: Fruit-Specific and Ripening Regulation Expansin Genes
FILE REFERENCE: 023070-078210US
CURRENT FILING DATE: 1999-07-27
NUMBER OF SEQ ID NOS: 8
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 1
LENGTH: 702
TYPE: DNA
ORGANISM: Lycopersicon esculentum cv. 75
FEATURE:
NAME/KEY: CDS
LOCATION: (28)..(702)
OTHER INFORMATION: tomato expansin (Lbex1)
US-09-362-642-1

Alignment Scores:
Pred. No.: 4.09e-87 Length: 702
Score: 841.50 Matches: 149
Percent Similarity: 77.48% Conservative: 23
Best Local Similarity: 67.12% Mismatches: 31
Query Match: 60.37% Indels: 19
DB: 4 Gaps: 3

US-09-383-579c-10 (1-250) x US-09-362-642-1 (1-702)
QY 13 leuLeuProPhePhePheValPheThrPheAlaAspTyr----- 25
DB 34 ATCATATTTTCATCTCTGTTCTTCTTGTAGACTCATGTTCAACATTGTTGAAGA 93
QY 26 -----GlyGlyTyrPgiInserGlyHisAlaThrPheTyTrpGly 37
DB 94 AGAATCCCTGCTGTTTACTGCTGTGCTGATGGAACCTGACATGTTTACGCG 153
QY 38 GlyGlyAspAlaSerGlyThrMetGlyGlyAlaCyGlyTyrGlyAsnLeuTyrSerGln 57
DB 154 GGAAGTATGCTCTTGTGAACAATGGGGCGGTGTGTTATGAATTTATACAGCA 213
QY 58 GlyTyTrpGlyThrAsnThrValAlaLeuSerThrAlaLeuPheAsnnglyLeuSerCys 77
DB 214 GGATACGAGGAGTTAACACAGCAGCACTGAGTACGCTTGTTTAAACATGATTAAGTTGT 273
QY 78 GlyAlaCysPheGluMetThrCysThrAsnAspPro-----LysTyrPysLeuProGly 95
DB 274 GAGGCTGTTTGAACCTTAATATGACAAATCTCTTAATTGAAATGGTGTCTTCTGGA 333
QY 96 -----ThrIleArgValThrAlaThrAsnPheCysProProAsnPheAlaLeuProAsn 113
DB 334 AACCTTCATTTTATATACAGCTACCAATTTCTGCCACCAATTAACGCTTGCCAAAT 393
QY 114 AsnAsnGlyGlyTyrPysAsnProProLeuGlnHisPheAspMetAlaGluProAlaPhe 133
DB 394 GACAAATGTGTGCTGTGTAAACCTCTCGCCCTCACTTGAACCTGCTATGCTATGTTT 453

```

```

QY      134 LeuGlnIleAlaGlyThrArgAlaGlyIleValProValSerPheArgArgValProCys 153
      |||.....|
Db      454 CTCAAACTGCTCAGACCGCGCTGCGATGTTCTCGTACTATTCGACGAGATCCCATGC 513
QY      154 MetLysLysGlyGlyValArgPheThrIleAsnGlyHisSerLysPheAsnLeuValIleu 173
      |||.....|
Db      514 CGAAGCAGAGAGATCAGATTCATTCATCATGATTCCTGTTACTTCAACTTAGCTTG 573
QY      174 IleThrAsnValGlyGlyValAlaGlyAspValHisSerValSerIleLysGlySerArgThr 193
      |||.....|
Db      574 ATCAGCAATGTAGCAGGTCCAGCGGATATTATTAAAGTTGGGTAAAGCAACAAGACA 633
QY      194 GlyTPGlnSerMetSerArgPheThrPglYlnAsnTrpGlnSerAsnValIleuAsn 213
      |||.....|
Db      634 AATTGATTGCATTGAGCCGTAATTGGGACAAATTTGCAATCAATGCGGTTTAACT 693
QY      214 GlyGln 215
      |||
Db      694 GGTCAA 699

RESULT 7
US-08-845-539-1
; Sequence 1, Application US//08845539
; Patent No. 5929303
; GENERAL INFORMATION:
; APPLICANT: Benmett, Alan B.
; APPLICANT: Rose, Jocelyn K.C.
; TITLE OF INVENTION: Fruit-Specific and Ripening-Regulation
; TITLE OF INVENTION: Expansin Genes to Control Fruit Texture and Softening
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/845, 539
; FILING DATE: 25-APR-1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Bastian, Kevin L.
; REGISTRATION NUMBER: 34,774
; REFERENCE/DOCKET NUMBER: 023070-078200US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0360
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 702 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 28..702
; OTHER INFORMATION: /product= "tomato leEx1"
US-08-845-539-1

Alignment Scores:
Pred. No.: 6,93e-87 Length: 702
Score: 839.50 Matches: 149
Percent Similarity: 77.03% Conservative: 22
Best Local Similarity: 67.12% Mismatches: 32
Query Match: 60.22% Indels: 19
DB: 2 Gaps: 3

```

```

US-09-383-579c-10 (1-250) x US-08-845-539-1 (1-702)
QY      13 LeuLeuProPhePhePheValPheThrPheAlaSerTYr----- 25
      |||.....|
Db      34 ATCATTAATTTTCATCTTGTCTTCTTTTGGAGCTCATGTTTCACATTTGTGAAGA 93
QY      26 -----GlyGlyTPGlnSerGlyHisAlaThrPheTYrGly 37
      |||.....|
Db      94 AGAATCCCTGGTGTACTCTGTGTTCAAGGAACTGCACATGCATCATTTTAAAGCG 153
QY      38 GlyLysAspAlaSerGlyThrMetGlyAlaCysGlyTYrGlyAsnLeuTYrSerGln 57
      |||.....|
Db      154 GGAAGTATGCTCTTCGAAACAAATGGCCGCTGTGTATGAAATTTATACAGCCA 213
QY      58 GlyTYrGlyThrAsnThrValAlaLeuSerThrAlaLeuPheAsnGlyLeuSerCys 77
      |||.....|
Db      214 GGATACGGAGTTAATACAGACAGCACTGAGTACTGTTTGTTAACATGATTAAGTTGT 273
QY      78 GlyAlaCysPheGluMetThrCysThrAsnAspPro-----LysTrpCysLeuProGly 95
      |||.....|
Db      274 GGAGCCTGTTTGAACCTTAATGTAACAATCTCTTAATTGGAAATGGTGTTCTTGA 333
QY      96 -----ThrIleArgValThrAlaThrAsnPheCysProProAsnPheAlaLeuProAsn 113
      |||.....|
Db      334 AACCTTCATTTTATATACACACTACCAATTTCTCCACCAAAATTAAGCGTTCGAAT 393
QY      114 AsnAsnGlyGlyTYrCysAsnProProLeuGlnHisPheAspMetAlaGluProAlaPhe 133
      |||.....|
Db      394 GACATGGTGGCTGTGTAACTTCCCTCGCCCTCACTTGAACCTGCTATGCTGT 453
QY      134 LeuGlnIleAlaGlnTYrArgAlaGlyIleValProValSerPheArgArgValProCys 153
      |||.....|
Db      454 CTCAAACTGCTCAGACCGCGCTGCGATGTTCTCGTACTATTCGACGAGATCCCATGC 513
QY      154 MetLysLysGlyGlyValArgPheThrIleAsnGlyHisSerLysPheAsnLeuValIleu 173
      |||.....|
Db      514 CGAAGCAGAGAGATCAGATTCATTCATCATGATTCCTGTTACTTCAACTTAGCTTG 573
QY      174 IleThrAsnValGlyGlyValAlaGlyAspValHisSerValSerIleLysGlySerArgThr 193
      |||.....|
Db      574 ATCAGCAATGTAGCAGGTCCAGCGGATATTATTAAAGTTGGGTAAAGCAACAAGACA 633
QY      194 GlyTPGlnSerMetSerArgPheThrPglYlnAsnTrpGlnSerAsnValIleuAsn 213
      |||.....|
Db      634 AATTGATTGCATTGAGCCGTAATTGGGACAAATTTGCAATCAATGCGGTTTAACT 693
QY      214 GlyGln 215
      |||
Db      694 GGTCAA 699

RESULT 8
US-08-845-539-5
; Sequence 5, Application US//08845539
; Patent No. 5929303
; GENERAL INFORMATION:
; APPLICANT: Benmett, Alan B.
; APPLICANT: Rose, Jocelyn K.C.
; TITLE OF INVENTION: Fruit-Specific and Ripening-Regulation
; TITLE OF INVENTION: Expansin Genes to Control Fruit Texture and Softening
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30

```



```

CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/845,539
; FILING DATE: 25-APR-1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Baetian, Kevin L.
; REGISTRATION NUMBER: 34,774
; REFERENCE/DOCKET NUMBER: 023070-078200US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 537 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..537
; OTHER INFORMATION: /product= "melon CmEx1"
US-08-845-539-5

Alignment Scores:
Pred. No.: 3,38e-82 Length: 537
Score: 797.00 Matches: 140
Percent Similarity: 86.44% Conservative: 13
Best Local Similarity: 79.10% Mismatches: 22
Query Match: 57.17% Indels: 2
DB: Gaps: 1

US-09-383-579C-10 (1-250) x US-08-845-539-5 (1-537)
QY 33 AlAThPherYrGlyGlyGlyAAspAlaSerGlyThrMetGlyGlyAlaCyGlyYTyrgly 52
DB 7 GCCACGTTTATGAGGACGAGCGATGCTCCGGAACATGGGTGGTGGTATGAGGC 66
QY 53 AsnLeuTySerGlnGlyYrGlyYrThsAnThrValAlaLeuSerThrAlaLeuPheAsn 72
DB 67 AATCTCTACAGCCAGGCGCTATGGCGTCAACACAGCTCTTATGACTGCTTCTTCAAC 126
QY 73 AsnGlyLeuSerCyGlyAlaCySphGluMetThrCySthrsAnAapProLySTrPCys 92
DB 127 AATGGCCTCAGCTGTGGTCTGCTTGAAGATCAAGTGTCTATGACCTCGATGTC 186
QY 93 LeuProGlyThr-----lIeArgValThrAlaThrsAnPheCySProProAsnPheAla 110
DB 187 CATCTGTGATGACCTTGTATCTTCAATACCGCTACCAATTTTGTCCCTTAATTGCT 246
QY 111 LeuProAsnAsnAnGlyGlyYrTPCyAsnProProLeuGlnHisPheAapMetAlaGlu 130
DB 247 CTTCCTATATACATAGCGGTGTGTGTGATMACCTTCTCGCACTCATTTTCGACTGCTATG 306
QY 131 ProAlaPheLeuGlnIleAlaGlnTyFArGAlaGlyIleValProValSerPheArg 150
DB 307 CCTATGTCCTCAAGATCGCTGAGTACCGCGCTGGAATCGGACTGTCTTACCGCGCG 366
QY 151 ValProCyMetLeuLySgLyGlyValArgPheThrIleAnGlyHisSerTyPheAsn 170
DB 367 GTTCCATGTAGAAACAAGAGAGAAATCAGGTTCAATCAACGGTTCCGTTACTTCAAT 426
QY 171 LeuValLeuIleThrsAnValGlyGlyAlaGlyAspValHisSerValSerIleLyGly 190
DB 427 TTGGTGTATATCAACCAAGTCGCGGGGACAGGGGATATCTGAGGGGTCAACGTAAGA 486
QY 191 SerArgThrGlyYrPGLInserMetSerArgAsnTrpGlyGlnAsnTrpGln 207
DB 487 TCAAAACCCGGTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 537

```

```

Patent No. 6350935
; GENERAL INFORMATION:
; APPLICANT: Bennett, Alan B.
; APPLICANT: Rose, Jocelyn K.C.
; TITLE OF INVENTION: The Regents of the University of California
; TITLE OF INVENTION: Fruit-Specific and Ripening Regulation Expansin Genes
; FILE REFERENCE: 023070-078210US
; CURRENT APPLICATION NUMBER: US/09/362,642
; CURRENT FILING DATE: 1999-07-27
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 537
; TYPE: DNA
; ORGANISM: Cucumis melo
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(537)
; OTHER INFORMATION: melon expansin (CmEx1) partial cDNA clone
US-09-362-642-5

Alignment Scores:
Pred. No.: 3.38e-82 Length: 537
Score: 797.00 Matches: 140
Percent Similarity: 86.44% Conservative: 13
Best Local Similarity: 79.10% Mismatches: 22
Query Match: 57.17% Indels: 2
DB: Gaps: 1

US-09-383-579C-10 (1-250) x US-09-362-642-5 (1-537)
QY 33 AlAThPherYrGlyGlyGlyAAspAlaSerGlyThrMetGlyGlyAlaCyGlyYTyrgly 52
DB 7 GCCACGTTTATGAGGACGAGCGATGCTCCGGAACATGGGTGGTGGTATGAGGC 66
QY 53 AsnLeuTySerGlnGlyYrGlyYrThsAnThrValAlaLeuSerThrAlaLeuPheAsn 72
DB 67 AATCTCTACAGCCAGGCGCTATGGCGTCAACACAGCTCTTATGACTGCTTCTTCAAC 126
QY 73 AsnGlyLeuSerCyGlyAlaCySphGluMetThrCySthrsAnAapProLySTrPCys 92
DB 127 AATGGCCTCAGCTGTGGTCTGCTTGAAGATCAAGTGTCTATGACCTCGATGTC 186
QY 93 LeuProGlyThr-----lIeArgValThrAlaThrsAnPheCySProProAsnPheAla 110
DB 187 CATCTGTGATGACCTTGTATCTTCAATACCGCTACCAATTTTGTCCCTTAATTGCT 246
QY 111 LeuProAsnAsnAnGlyGlyYrTPCyAsnProProLeuGlnHisPheAapMetAlaGlu 130
DB 247 CTTCCTATATACATAGCGGTGTGTGTGATMACCTTCTCGCACTCATTTTCGACTGCTATG 306
QY 131 ProAlaPheLeuGlnIleAlaGlnTyFArGAlaGlyIleValProValSerPheArg 150
DB 307 CCTATGTCCTCAAGATCGCTGAGTACCGCGCTGGAATCGGACTGTCTTACCGCGCG 366
QY 151 ValProCyMetLeuLySgLyGlyValArgPheThrIleAnGlyHisSerTyPheAsn 170
DB 367 GTTCCATGTAGAAACAAGAGAGAAATCAGGTTCAATCAACGGTTCCGTTACTTCAAT 426
QY 171 LeuValLeuIleThrsAnValGlyGlyAlaGlyAspValHisSerValSerIleLyGly 190
DB 427 TTGGTGTATATCAACCAAGTCGCGGGGACAGGGGATATCTGAGGGGTCAACGTAAGA 486
QY 191 SerArgThrGlyYrPGLInserMetSerArgAsnTrpGlyGlnAsnTrpGln 207
DB 487 TCAAAACCCGGTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 537

```

```

RESULT 9
US-09-362-642-5
; Sequence 5, Application US/09362642

```

```

RESULT 10
US-08-845-539-3
; Sequence 3, Application US/08845539
; Patent No. 5929303
; GENERAL INFORMATION:

```

APPLICANT: Bennett, Alan B.
 APPLICANT: Rose, Jocelyn K.C.
 TITLE OF INVENTION: Fruit-Specific and Ripening-Regulation
 TITLE OF INVENTION: Expansin Genes to Control Fruit Texture and Softening
 NUMBER OF SEQUENCES: 8
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Townsend and Townsend and Crew LLP
 STREET: Two Embarcadero Center, Eighth Floor
 CITY: San Francisco
 STATE: California
 COUNTRY: USA
 ZIP: 94111-3834
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/845,539
 FILING DATE: 25-APR-1997
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: Bastian, Kevin L.
 REGISTRATION NUMBER: 34,774
 REFERENCE/DOCKET NUMBER: 023070-078200US
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (415) 576-0200
 TELEFAX: (415) 576-0300
 INFORMATION FOR SEQ ID NO: 3:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 501 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: DNA (genomic)
 FEATURE:
 NAME/KEY: CDS
 LOCATION: 1..501
 OTHER INFORMATION: /product= "strawberry FaEx1"
 US-08-845-539-3

Alignment Scores:
 Pred. No.: 8,376-75 Length: 501
 Score: 732.00 Matches: 127
 Percent Similarity: 85.63% Conservative: 16
 Best Local Similarity: 76.05% Mismatches: 22
 Query Match: 52.51% Indels: 2
 DB: 2 Gaps: 1

US-09-383-579c-10 (1-250) x US-08-845-539-3 (1-501)

QY 43 GYTHrMetGlyGlyAlaCyseGlyTyrgIyaenLeuTyrsenGlnIyTyrgIyThraan 62
 DB 1 GGAACCATGGGGGGGCTGTGGATATGGAACCTCTACAGCCAGGGCTACGGAGTCAAC 60
 QY 63 ThrValAlaLeuSerThrAlaLeuPheAsnaengIyLeuSerCyseGlyAlaCysePheGlu 82
 DB 61 ACTGCTGCCTAGCAGCGGCTCTGTTCACCAATGGCTTAGCGGCGCTTGTCTCGAG 120
 QY 83 MetThrCyseThraAsnaPProLySTrCyseLeuProGly-----ThrIleArgValThr 100
 DB 121 ATCAAGTGGGGGAGCAGCACCAGAGTGTGTCACCTGCCGGAAGCCCTTCATTTCGTCAAC 180
 QY 101 AlaThrAsnaPheCyseProPheAsnaPheAlaLeuProAsnaAsnaGlyGlyTyPcyAsna 120
 DB 181 GCCACCACTTCTGCGCTCCCACTTCGCTCAGCCAGCAGCAATGGCGGTGTGTCAAC 240
 QY 121 ProProLeuGlnHisPheAsnaPheAlaGluProAlaPheLeuGlnIleAlaGlnTyArg 140
 DB 241 CTTCCCGGAGCCACTTGACCTTCGCCATGCCCATGTTCTCAAGATGCCCGGATCAAA 300
 QY 141 AlagIyIleValProValSerPheArgValProCyseMetIyysGlyGlyValArg 160

DB 301 GCCGGAATGTCCTCCGCTCTTACCGCGGGGTCCCATGGTAAAGAGGTGATCAG 360
 QY 161 PheThrIleAengIyHiserTyPheAsnaLeuValIleThrAsnaValGlyAla 180
 DB 361 TTCACAACTCAAGGGCAGCAAGACTTCACTGCTTGTATACCAACGTGGCGGCGCA 420
 QY 181 GYAAPValHiserValserIleIyysGlyserArgThyGlyTrpIlnserMetSerArg 200
 DB 421 GGGATATGTGAGCGTGAAGCTGAAGGACCAACACCGGGTGAATGCATAGACCA 480
 QY 201 AantTPGlyGlnAsnTPGln 207
 DB 481 AATGGGTCAAACTGGCAG 501
 RESULT 11
 US-09-362-642-3
 ; Sequence 3, Application US/09362642
 ; Patent No. 6350935
 ; GENERAL INFORMATION:
 ; APPLICANT: Bennett, Alan B.
 ; APPLICANT: Rose, Jocelyn K.C.
 ; TITLE OF INVENTION: The Regents of the University of California
 ; TITLE OF INVENTION: Fruit-Specific and Ripening Regulation Expansin Genes
 ; TITLE OF INVENTION: to Control Fruit Texture and Softening
 ; FILE REFERENCE: 023070-078210US
 ; CURRENT APPLICATION NUMBER: US/09/362,642
 ; NUMBER OF SEQ ID NOS: 8
 ; SOFTWARE: Patent Ver. 2.1
 ; SEQ ID NO 3
 ; LENGTH: 501
 ; TYPE: DNA
 ; ORGANISM: Fragaria x ananassa
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: (1)..(501)
 ; OTHER INFORMATION: strawberry expansin (FaEx1) partial cDNA clone
 US-09-362-642-3

Alignment Scores:
 Pred. No.: 8,376-75 Length: 501
 Score: 732.00 Matches: 127
 Percent Similarity: 85.63% Conservative: 16
 Best Local Similarity: 76.05% Mismatches: 22
 Query Match: 52.51% Indels: 2
 DB: 4 Gaps: 1

US-09-383-579c-10 (1-250) x US-09-362-642-3 (1-501)

QY 43 GYTHrMetGlyGlyAlaCyseGlyTyrgIyaenLeuTyrsenGlnIyTyrgIyThraan 62
 DB 1 GGAACCATGGGGGGGCTGTGGATATGGAACCTCTACAGCCAGGGCTACGGAGTCAAC 60
 QY 63 ThrValAlaLeuSerThrAlaLeuPheAsnaengIyLeuSerCyseGlyAlaCysePheGlu 82
 DB 61 ACTGCTGCCTAGCAGCGGCTCTGTTCACCAATGGCTTAGCGGCGCTTGTCTCGAG 120
 QY 83 MetThrCyseThraAsnaPProLySTrCyseLeuProGly-----ThrIleArgValThr 100
 DB 121 ATCAAGTGGGGGAGCAGCACCAGAGTGTGTCACCTGCCGGAAGCCCTTCATTTCGTCAAC 180
 QY 101 AlaThrAsnaPheCyseProPheAsnaPheAlaLeuProAsnaAsnaGlyGlyTyPcyAsna 120
 DB 181 GCCACCACTTCTGCGCTCCCACTTCGCTCAGCCAGCAGCAATGGCGGTGTGTCAAC 240
 QY 121 ProProLeuGlnHisPheAsnaPheAlaGluProAlaPheLeuGlnIleAlaGlnTyArg 140
 DB 241 CTTCCCGGAGCCACTTGACCTTCGCCATGCCCATGTTCTCAAGATGCCCGGATCAAA 300
 QY 141 AlagIyIleValProValSerPheArgValProCyseMetIyysGlyGlyValArg 160
 DB 301 GCCGGAATGTCCTCCGCTCTTACCGCGGGGTCCCATGGTAAAGAGGTGATCAG 360

QY 161 PheThrIleanglyHisSerTyrPheAsnLeuValleuIleThrAsnValGlyGlyAla 180
DB 361 TTCACATCAACGCCACAGTAAGTCTGATGATCAACCAAGTGGCGGCGCA 420
QY 181 GlyAspValHisSerValSerIleGlySerArgThrGlyTyrGlnSerMetSerArg 200
DB 421 GGGGATATCTGTGAGCGTGAAGGACCAACACCGGTGATGCCAATGAGCGCA 480
QY 201 AsnTyrGlyGlnAsnTyrGln 207
DB 481 AATTGGGTCAAACTGGCAG 501
RESULT 12
US-07-885-970A-6
; Sequence 6, Application US/07885970A
; Patent No. 5495070
; GENERAL INFORMATION:
; APPLICANT: John, Maliyakal E.
; TITLE OF INVENTION: GENETICALLY ENGINEERING COTTON
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Nicholas J. Seay, Charles & Brady
; STREET: P.O. Box 2113, First Wisconsin Plaza
; CITY: Madison
; STATE: Wisconsin
; COUNTRY: USA
; ZIP: 53701
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Microsoft Word
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/885,970A
; FILING DATE: 19920518
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/617,239
; FILING DATE: 21-NOV-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/253,243
; FILING DATE: 04-OCT-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Seay, Nicholas J.
; REGISTRATION NUMBER: 27,386
; TELEPHONE: (608) 283-2478
; TELEFAX: (608) 251-5139
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 727 base pairs
; TYPE: NUCLEIC ACID
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Gossypium hirsutum
; STRAIN: Coker 312
; DEVELOPMENTAL STAGE: 10 day old fiber cells
; TISSUE TYPE: fiber cells
; IMMEDIATE SOURCE:
; LIBRARY: CKB10
; CLONE: B12
; US-07-885-970A-6
Alignment Scores:
Pred. No.: 1,39e-71 Length: 727
Score: 706.00 Matches: 123
Percent Similarity: 91.56% Conservative: 18
Best Local Similarity: 79.87% Mismatches: 13
Query Match: 50.65% Indels: 0

DB: 1 Gaps: 0
US-09-383-579c-10 (1-250) x US-07-885-970A-6 (1-727)
QY 97 IleArgValThrAlaThrAsnPheCysProProAsnPheAlaLeuProAsnAsnGly 116
DB 1 ATAAACGTGACACGCCACCAACTTTTGCCACTTAATCATCTTATCTAGTACAAATGCG 60
QY 117 GlyTyrCysAsnProProLeuGlnIleAspAsnMetAlaLeuProAlaPheLeuGlnIle 136
DB 61 GGGGTGTGACATCCCCACGAGAACACTTGTATTTGGCCAAACCGGATCTTGGCGATA 120
QY 137 AlaGlnTyrArgAlaGlyIleValProValSerPheArgArgValProCysMetLeuGly 156
DB 121 GCAGATATGACACTGGAATCGTCCCTGTTATGTTCAAGAGGTGATGATGAGAA 180
QY 157 GlyGlyValArgPheThrIleAsnGlyHisSerTyrPheAsnLeuValleuIleThrAsn 176
DB 181 GGAGGATCATGATGACACCAATGATGACATTCCTACTTCAACATGTGTGATTAACGAA 240
QY 177 ValGlyGlyValaGlyAspValHisSerValSerIleGlySerArgThrGlyTyrGln 196
DB 241 GTGGAGGGGACAGGAGATATACGTGATGTCATCAAGGCTTCAGAACAGAGTGGCTA 300
QY 197 SerMetSerArgAsnTyrGlyGlnAsnTyrGlnSerAsnAsnTyrLeuAsnGlyGlnGly 216
DB 301 CCTATGTCAGAAATTTGGGCGCAAACTGGCAGACGATCTTACCTTAACGACAAAGC 360
QY 217 LeuSerPheGlnValThrLeuSerAspGlyArgThrLeuThrAlaTyrAsnLeuValPro 236
DB 361 CTCTCTTTTAAAGTACGTCGCCAGATGCGAGAGATATACACCTTCAATGATGTCCT 420
QY 237 SerAsnTyrGlnPheGlyGlnThrTyrGlyGlyProGlnPhe 250
DB 421 GCTGTGGCAATTGCGACAACTTTTGAAGGCGCAGTTT 462
RESULT 13
US-08-298-687A-6
; Sequence 6, Application US/08298687A
; Patent No. 5521078
; GENERAL INFORMATION:
; APPLICANT: John, Maliyakal E.
; TITLE OF INVENTION: GENETICALLY ENGINEERING COTTON
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Nicholas J. Seay, Charles & Brady
; STREET: P.O. Box 2113, First Wisconsin Plaza
; CITY: Madison
; STATE: Wisconsin
; COUNTRY: USA
; ZIP: 53701
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Microsoft Word
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/298,687A
; FILING DATE:
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/617,239
; FILING DATE: 21-NOV-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/253,243
; FILING DATE: 04-OCT-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Seay, Nicholas J.
; REGISTRATION NUMBER: 27,386
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (608) 283-2478
; TELEFAX: (608) 251-5139

```

; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 727 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Gossypium hirsutum
; STRAIN: Coker 312
; DEVELOPMENTAL STAGE: 10 day old fiber cells
; TISSUE TYPE: fiber cells
; IMMEDIATE SOURCE:
; LIBRARY: CKEFB10
; CLONE: B12
; US-08-298-687A-6

Alignment Scores:
Pred. No.: 1,39e-71 Length: 727
Score: 706.00 Matches: 123
Percent Similarity: 91.56% Conservative: 18
Best Local Similarity: 79.87% Mismatches: 13
Query Match: 50.65% Indels: 0
DB: 1 Gaps: 0

US-09-383-579C-10 (1-250) x US-08-298-687A-6 (1-727)
QY 97 IleaGValaThraAlaThraPheCysProProaPheAlaLeuProaAnaAngly 116
DB 1 ATACCGTACACGCCCACTTTTGTCCACTTAAGTCTTAACTGATGACAAATGCC 60
QY 117 GIYTPCyAsnProProLeuGlnHisPheAspMetAlaGluProAlaPheLeuGlnle 136
DB 61 GGGTGGTGAATCCGCCCAAGAGAACACTTGTATTTGGCCGAACGGCAATTTCTGGCGATA 120
QY 137 AlaGlnTYrArgAlaGlyIleValProValSerPheArgValaProCysMetIyslys 156
DB 121 GCAGAAATACGAGCTGGAATCGCCCTGTATGTTGAGAGAGGTGCATGTGTGAGAGAA 180
QY 157 GIYGIYValArgPheThrIleAsnGlyHisSerTYrPheAsnLeuValLeuIleThraAn 176
DB 181 GAGGCGATCAGGTACACCATGANTGACATTCTTCACTTAACATGAGTGTGATACGAAC 240
QY 177 ValGIYGIYAlaGlyAspValHisSerValSerIleIysGlySerArgThrglyTyrGln 196
DB 241 GTGGAGGGGGCAGGGGATATTAACGTCACTGTCATCAAGGGTTCAGAAACAGAGATGGCTA 300
QY 197 SerMetSerArgAsnTyrPglYlnAntTyrGlnAntTyrGlnSerAsnAsnTyrIleuAsnGlyGlnGly 216
DB 301 CCTATGTCAGAAATTTGGGGCCAAACCTGGCAGAGCAATGCTTAACTTAACGACAAAC 360
QY 217 LeuSerPheGlnValaThrLeuSerAspGlyArgThrLeuThraAlaTyrAsnLeuValPro 236
DB 361 CTCTCTTTAAAGTACCTCCAGCCATGGCAGACATATACACACCTTAACATGATGCTCT 420
QY 237 SerAsnTyrGlnPheGlyIleThrTYrGlnGlyProGlnPhe 250
DB 421 GCTGGTGGCAATTCGACCAAACTTTTGAAGAGGGCCAGTTT 462

RESULT 14
US-08-530-797-5
; Sequence 5, Application US/08530797
; Patent No. 5597718
; GENERAL INFORMATION:
; APPLICANT: John, Maliyakal E.
; APPLICANT: Umbeck, Paul F.
; APPLICANT: Brill, Winston J.
; TITLE OF INVENTION: GENETICALLY ENGINEERED COTTON PLANTS
; TITLE OF INVENTION: FOR ALTERED FIBER
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:

```

```

; ADDRESSEE: Quarles and Brady
; STREET: P O BOX 2113
; CITY: MADISON
; STATE: WISCONSIN
; COUNTRY: U.S.A.
; ZIP: 53701
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette - 3.50 inch, 800Kb storage
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh
; SOFTWARE: Microsoft Word 4.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/530,797
; FILING DATE: 20-SEP-1995
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/617,239
; FILING DATE: 21-NOV-90
; APPLICATION NUMBER: US 07/253,243
; FILING DATE: 04-OCT-88
; ATTORNEY/AGENT INFORMATION:
; NAME: Nicholas J. Seay
; REGISTRATION NUMBER: 27,386
; REFERENCE/DOCKET NUMBER: 1122990245
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 727 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA to mRNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Gossypium hirsutum
; STRAIN: Coker 312
; TISSUE TYPE: fiber cells
; IMMEDIATE SOURCE:
; LIBRARY: CKEFB10
; CLONE: B12
; US-08-530-797-5

Alignment Scores:
Pred. No.: 1,39e-71 Length: 727
Score: 706.00 Matches: 123
Percent Similarity: 91.56% Conservative: 18
Best Local Similarity: 79.87% Mismatches: 13
Query Match: 50.65% Indels: 0
DB: 1 Gaps: 0

US-09-383-579C-10 (1-250) x US-08-530-797-5 (1-727)
QY 97 IleaGValaThraAlaThraPheCysProProaPheAlaLeuProaAnaAngly 116
DB 1 ATACCGTACACGCCCACTTTTGTCCACTTAAGTCTTAACTGATGACAAATGCC 60
QY 117 GIYTPCyAsnProProLeuGlnHisPheAspMetAlaGluProAlaPheLeuGlnle 136
DB 61 GGGTGGTGAATCCGCCCAAGAGAACACTTGTATTTGGCCGAACGGCAATTTCTGGCGATA 120
QY 137 AlaGlnTYrArgAlaGlyIleValProValSerPheArgValaProCysMetIyslys 156
DB 121 GCAGAAATACGAGCTGGAATCGCCCTGTATGTTGAGAGAGGTGCATGTGTGAGAGAA 180
QY 157 GIYGIYValArgPheThrIleAsnGlyHisSerTYrPheAsnLeuValLeuIleThraAn 176
DB 181 GAGGCGATCAGGTACACCATGANTGACATTCTTCACTTAACATGAGTGTGATACGAAC 240
QY 177 ValGIYGIYAlaGlyAspValHisSerValSerIleIysGlySerArgThrglyTyrGln 196
DB 241 GTGGAGGGGGCAGGGGATATTAACGTCACTGTCATCAAGGGTTCAGAAACAGAGATGGCTA 300

```

QY 197 SerwteSerAArganTTPGlyGlnAsnTPGlnSerAsnAsnTYrLeuAsnGlyGlnGly 216
 Db 301 CCTATGTCAGAAATTGGGGCCAAACTGGCAGAGCATGCTTACCTTAACGACCAAGC 360
 QY 217 LeuSerPheGlnValThrLeuSerAspGlyArgThrLeuThrAlaTYrAsnLeuValPro 236
 Db 361 CTCCTTTTAAAGTGAAGTCCAGCGATGCGAGACTATCACAGCCTTACCAATGTAGTGCT 420

QY 237 SerAsnTPGlnPheGlyGlnThrTYrGlyGlyProGlnPhe 250
 Db 421 GCTGCTTGCAATTGGACAACTTTTGAAGAGGCCAGTTT 462

RESULT 15
 US-08-298-829-6
 Sequence 6, Application US/08298829
 Patent No. 5620882

GENERAL INFORMATION:
 APPLICANT: John, Maliyaka E.
 TITLE OF INVENTION: GENETICALLY ENGINEERING COTTON
 TITLE OF INVENTION: PLANTS FOR ALTERED FIBER
 NUMBER OF SEQUENCES: 33
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Nicholas J. Seay, Charles & Brady
 STREET: P.O. Box 2113, First Wisconsin Plaza
 CITY: Madison
 STATE: Wisconsin
 COUNTRY: USA
 ZIP: 53701

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Microsoft Word
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/298,829
 FILING DATE: 19-OCT-1994
 CLASSIFICATION: 800
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/885,970
 FILING DATE: 18-MAY-1992
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/617,239
 FILING DATE: 21-NOV-1990
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/253,243
 FILING DATE: 04-OCT-1988
 ATTORNEY/AGENT INFORMATION:
 NAME: Seay, Nicholas J.
 REGISTRATION NUMBER: 27,386
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (608) 283-2478
 TELEFAX: (608) 251-5139
 INFORMATION FOR SEQ ID NO: 6:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 727 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: double
 TOPOLOGY: linear
 MOLECULE TYPE: cDNA
 HYPOTHETICAL: NO
 ANTI-SENSE: NO
 ORIGINAL SOURCE:
 ORGANISM: Gossypium hirsutum
 STRAIN: Coker 312
 DEVELOPMENTAL STAGE: 10 day old fiber cells
 TISSUE TYPE: fiber cells
 IMMEDIATE SOURCE:
 LIBRARY: CKFB10
 CLONE: B12
 US-08-298-829-6

Alignment Scores:

Pred. No.: 1.39e-71 Length: 727
 Score: 706.00 Matches: 123
 Percent Similarity: 91.56% Conservative: 18
 Best Local Similarity: 79.87% Mismatches: 13
 Query Match: 50.65% Indels: 0
 DB: 1 Gaps: 0

US-09-383-579c-10 (1-250) x US-08-298-829-6 (1-727)

QY 97 IleArgValThrAlaThrAsnPheCysProProAsnPheAlaLeuProAsnAsnGly 116
 Db 1 ATACCGTGAAGCAGACCACTTTTGTCCACTTAACATGCTTATCTAGAGCAATGGC 60

QY 117 GlyTTPCyAsnProProLeuGlnHisPheAspMetAlaGluProAlaPheLeuGlnIle 136
 Db 61 GGGTGGTGCATCCCCACAGAAACCTTTGATTTGGCCGACCGCATTTCTTGGGATA 120

QY 137 AlaGlnTYrArgAlaGlyIleValProValSerPheArgValProCysMetLeuLys 156
 Db 121 GCAGATATCGAGCTGGAAATCGTCCCTTATATGTCAGAAAGGTGCATGTGTGAGAAA 180

QY 157 GlyGlyValArgPheThrIleAsnGlyHisSerTYrPheAsnLeuValIleThrAsn 176
 Db 181 GGAGGCATCGAGTACACCAATGACATTCGACTTCAACATGTGTGATTAACGAAAC 240

QY 177 ValGlyValAlaGlyAspValHisSerValSerIleLeuGlySerArgThrGlyTrpGln 196
 Db 241 GTGGAGGGGACAGGGGATTAACGCTCGATGCCATCAAGGCTTCACAGACGAGTGGCTA 300

QY 197 SerwteSerAArganTTPGlyGlnAsnTPGlnSerAsnAsnTYrLeuAsnGlyGlnGly 216
 Db 301 CCTATGTCAGAAATTGGGGCCAAACTGGCAGAGCATGCTTACCTTAACGACCAAGC 360

QY 217 LeuSerPheGlnValThrLeuSerAspGlyArgThrLeuThrAlaTYrAsnLeuValPro 236
 Db 361 CTCCTTTTAAAGTGAAGTCCAGCGATGCGAGACTATCACAGCCTTACCAATGTAGTGCT 420

QY 237 SerAsnTPGlnPheGlyGlnThrTYrGlyGlyProGlnPhe 250
 Db 421 GCTGCTTGCAATTGGACAACTTTTGAAGAGGCCAGTTT 462

Search completed: December 19, 2003, 01:04:20
 Job time : 88 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: December 19, 2003, 00:28:28 ; Search time 292 Seconds
(without alignments)
2852.914 Million cell updates/sec

Title: US-09-383-579C-10
Perfect score: 1394
Sequence: 1 MAFSVPFSSFLPLPFVVF.....AYNLVPSNMQFGQYEGPGP 250

Scoring table: BLOSUM62
Xgapop 10.0, Xgapext 0.5
Ygapop 10.0, Ygapext 0.5
Fgapop 6.0, Fgapext 7.0
Delop 6.0, Delext 7.0

Searched: 2211978 seqs, 1666101734 residues
Total number of hits satisfying chosen parameters: 4423956

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
-MODE=frame+ p2n.model -DEV=xip
-Q=/cgn2_1/USFTO.spool/p/US0933579/runat_18122003_171929_28889/app.query.fasta_1.391
-DB=Published Applications NA -QFMT=fastap -SUFFIX=trmb -MINMATCH=0.1
-LOOPC=0 -LOOPEXT=0 -UNITS=bites -START=1 -END=-1 -MATRIX=blomsum62
-TRANS=human40.cdd -LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100
-THR MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pico -NORM=ext -HEAPSIZE=500 -MINLEN=0
-MAXLEN=2000000000 -USER=US0933579 @CGN_1.1.107 @runat_18122003_171929_28889
-NCPU=6 -ICPU=3 -NO MMAP -LARGQUERY -NEG SCORES=0 -WAIT -DSBLOCK=100
-LONGLOG -DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5
-FGAPOP=6 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Published Applications NA:*

1:	/cgn2_6/prodata/1/pubpna/US07_PUBCOMB.seq:*
2:	/cgn2_6/prodata/1/pubpna/PCT_NEW_PUB.seq:*
3:	/cgn2_6/prodata/1/pubpna/US06_NEW_PUB.seq:*
4:	/cgn2_6/prodata/1/pubpna/US06_PUBCOMB.seq:*
5:	/cgn2_6/prodata/1/pubpna/US07_NEW_PUB.seq:*
6:	/cgn2_6/prodata/1/pubpna/PCTUS_PUBCOMB.seq:*
7:	/cgn2_6/prodata/1/pubpna/US08_NEW_PUB.seq:*
8:	/cgn2_6/prodata/1/pubpna/US08_PUBCOMB.seq:*
9:	/cgn2_6/prodata/1/pubpna/US09_PUBCOMB.seq:*
10:	/cgn2_6/prodata/1/pubpna/US09B_PUBCOMB.seq:*
11:	/cgn2_6/prodata/1/pubpna/US09C_PUBCOMB.seq:*
12:	/cgn2_6/prodata/1/pubpna/US09_NEW_PUB.seq:*
13:	/cgn2_6/prodata/1/pubpna/US09A_PUBCOMB.seq:*
14:	/cgn2_6/prodata/1/pubpna/US10_NEW_PUB.seq:*
15:	/cgn2_6/prodata/1/pubpna/US10B_PUBCOMB.seq:*
16:	/cgn2_6/prodata/1/pubpna/US10_NEW_PUB.seq:*
17:	/cgn2_6/prodata/1/pubpna/US60_NEW_PUB.seq:*
18:	/cgn2_6/prodata/1/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB ID	Description
------------	-------	-------	--------	-------	-------------

1	1275	91.5	601	10	US-09-896-301-1	Sequence 1, Appl1
2	1085	77.8	762	10	US-09-938-842A-1088	Sequence 1088, Ap
3	1044	74.9	1153	13	US-10-150-559-3	Sequence 3, Appl1
4	1036.5	74.4	753	10	US-09-938-842A-91	Sequence 91, Appl1
5	1027	73.7	759	13	US-10-409-701-8	Sequence 8, Appl1
6	1024	73.5	747	10	US-09-938-842A-1069	Sequence 1069, Ap
7	993	71.2	774	10	US-09-938-842A-89	Sequence 89, Appl1
8	938	67.4	774	10	US-09-938-842A-842	Sequence 842, App
9	938	67.3	768	9	US-09-770-445-491	Sequence 491, App
10	838.5	60.2	788	10	US-09-938-842A-1046	Sequence 1046, Ap
11	676	48.5	410	10	US-09-878-574-3973	Sequence 3973, Ap
12	643	46.1	351	10	US-09-878-574-62	Sequence 62, Appl1
13	506	36.3	366	9	US-09-770-791-430	Sequence 430, App
14	491.5	35.3	373	10	US-09-878-574-3468	Sequence 3468, Ap
15	389.5	27.9	391	10	US-09-878-574-1206	Sequence 1206, Ap
16	294	21.1	1273	15	US-10-125-001-3	Sequence 3, Appl1
17	288.5	20.7	1293	9	US-09-924-0938-2002	Sequence 2002, Ap
18	276	19.8	1147	13	US-10-259-165-614	Sequence 614, App
19	271	19.4	810	13	US-10-259-165-776	Sequence 776, App
20	267.5	19.2	340	10	US-09-878-574-2728	Sequence 2728, Ap
21	266.5	19.1	1273	15	US-10-125-001-1	Sequence 1, Appl1
22	266.5	19.1	1428	13	US-10-102-349-1	Sequence 15, Appl1
23	262.5	18.8	735	15	US-10-125-001-15	Sequence 10, Appl1
24	246	17.6	849	13	US-10-409-701-10	Sequence 1496, A
25	240	17.2	262	10	US-09-878-574-14926	Sequence 1, Appl1
26	236.5	17.0	720	9	US-09-949-888-1	Sequence 13697, A
27	230	16.5	285	10	US-09-878-574-13697	Sequence 391, App
28	223	16.0	666	13	US-10-259-165-391	Sequence 43, App
29	223	16.0	669	13	US-10-259-165-43	Sequence 275, App
30	222.5	16.0	718	13	US-10-259-165-275	Sequence 1951, Ap
31	206	14.8	798	10	US-09-938-842A-1951	Sequence 12313, A
32	196	14.1	259	10	US-09-878-574-12313	Sequence 461, App
33	180.5	12.9	339	10	US-09-924-035A-461	Sequence 4389, Ap
34	170.5	12.2	238	9	US-09-294-0938-4389	Sequence 3, Appl1
35	154.5	11.1	2536	13	US-10-102-349-3	Sequence 183, App
36	140	10.0	380	9	US-09-770-791-183	Sequence 176, Ap
37	139.5	10.0	229	9	US-09-294-0938-1776	Sequence 6865, Ap
38	126.5	9.1	277	10	US-09-878-574-8765	Sequence 5784, Ap
39	125.5	9.0	244	10	US-09-878-574-6584	Sequence 6801, Ap
40	122.5	8.8	275	10	US-09-878-574-6801	Sequence 7975, Ap
41	121	8.7	252	10	US-09-878-574-7975	Sequence 84, Appl1
42	119.5	8.6	1503	13	US-09-846-903-84	Sequence 5917, Ap
43	118	8.5	264	10	US-09-878-574-5917	Sequence 1, Appl1
44	113	8.1	1952	15	US-10-197-294A-1	Sequence 652, App
45	103	7.4	852	13	US-10-259-165-652	

ALIGNMENTS

RESULT 1
US-09-896-301-1
Sequence 1, Application US/09896301
Patent No. US2002010335A1
GENERAL INFORMATION:
APPLICANT: Cosgrove, Daniel J
APPLICANT: McQueen-Mason, Simon
APPLICANT: Gultinan, Mark J
APPLICANT: Sheerban, Tatyana
APPLICANT: Shi, Jun
TITLE OF INVENTION: PURIFIED EXPANSIN PROTEINS
FILE REFERENCE: 1194/1C11AUS3
CURRENT APPLICATION NUMBER: US/09/896,301
CURRENT FILING DATE: 2001-06-29
PRIOR APPLICATION NUMBER: 09/092,160
PRIOR FILING DATE: 1998-06-05
PRIOR APPLICATION NUMBER: 08/440,517
PRIOR FILING DATE: 1995-05-12
PRIOR APPLICATION NUMBER: 08/242,090
PRIOR FILING DATE: 1994-05-12
PRIOR APPLICATION NUMBER: 08/060,944
PRIOR FILING DATE: 1993-05-12
NUMBER OF SEQ ID NOS: 7
SOFTWARE: PatentIn Ver. 2.1

```

; SEQ ID NO 1
; LENGTH: 681
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: cDNA cucumber
US-09-896-301-1

```

Alignment Scores:

Pred. No.:	1,92e-149	Length:	681
Score:	1275.00	Matches:	227
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	91.46%	Indels:	0
DB:	10	Gaps:	0

US-09-383-579c-10 (1-250) x US-09-896-301-1 (1-681)

```

QY 24 AAPPYRGLYGLYTRPGINSEGLYHISALATHRPHELYGLYGLYVAPALASERGLY 43
DB 1 GACTACGGTGGCTGGAGAGCGGCCACGACCTTTATGAGTGAGCGCATCTGGC 60
QY 44 ThrMetGLYGLYALCYseGLYTYrGLYAsnLeuTYrSeGLYGLYTYrGLYThraSerThr 63
DB 61 ACCATGGGTGGAGCTTGAGGTATGGAAATTATACAGCCAAAGGATAGCGAAGCAGC 120
QY 64 VALAlaleuSerThrAlaleuPheAsnAsnGLYLeuSerCYseGLYVALaCYsPheGluMet 83
DB 121 GGGGGCGTACGACATCGCGTATTTAACATGATTAAGTTGGTGCTTGCTTCGAAAG 180
QY 84 ThrCYseThrAsnAsnProLYrTYrCYsLeuProGLYThrILeArGLYThraAlaThrAsn 103
DB 181 ACTTGACAAAGACACCTTAATAGTGCGCTTCGCGGAACATAATAGGCTCACGCAACAA 240
QY 104 PheCYsProProAsnPheAlaleuProAsnAsnAsnGLYGLYTYrCYsAsnProProLeu 123
DB 241 TTTTGGCCCTTACTTCTCTCTCCCTTAACAACAATGGAGTGGCAACCTCTCTCTC 300
QY 124 GlnHisPheAspMetAlaGluProAlaPheLeuGlnILeAlaGlnTYrArGLYAlaGlyIle 143
DB 301 CAACACTTGACATGCGTACAGCTGCGCTTCCTTCAATAGCTCAATACCGAGCTGTATC 360
QY 144 ValProValSerPheArGLYrGLYProCYseMetLYseGLYGLYValArGpHeThrIle 163
DB 361 GTCCCGCTCTCTTCTGTAAGGGTACCATGTATGAAAGAGTGGAGTGTATCAATC 420
QY 164 AsnGLYHisSerTYrPheAsnLeuValLeuILeThrAsnValGLYGLYValaGlyAspVal 183
DB 421 AATGGCCACTCAACTTCAACCTCGTTTGATCAACAACGTCGGTGGCCAGGCGACGTC 480
QY 184 HisSerValSerILEYseGLYSerArGLYrGLYTrPGINSerMetSerArGLYrGLY 203
DB 481 CACTCTGCTCGATTAAGGGGTCTCGAATCGATGCGATTCATGCTTGAATTTGGGGC 540
QY 204 GlnAsnTrPGINSerAsnAsnTYrLeuAsnGLYGLYLeuSerPheGlnValThrLeu 223
DB 541 CAAACTGGCAAGCAACAATATCTCAATGCGCAAGGCTTCCTTCAAGTCACTCTT 600
QY 224 SerAsnGLYArGLYThrLeuThrAlaTYrAsnLeuValProSerArGLYrGLYrGLY 243
DB 601 AGTGAAGTGGCACTCTCACTGCTTAATCTCGTTCCTTCAATTGGCAATTGGCCAA 660
QY 244 ThrTYrGLYGLYProGlnPhe 250
DB 661 ACCTATGAAGGCCCTTCAATTC 681

```

```

RESULT 2
US-09-938-842A-1088
; Sequence 1088, Application US/09938842A
; Patent No. US20020160378A1
; GENERAL INFORMATION:
; APPLICANT: Harper, Jeff

```

```

; APPLICANT: Kreps, Joel
; APPLICANT: Wang, Xun
; APPLICANT: Zhu, Tong
; TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
; TITLE OF INVENTION: SAME, AND METHODS OF USE
; FILE REFERENCE: S001300-3
; CURRENT APPLICATION NUMBER: US/09/938,842A
; CURRENT FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: US 60/227,866
; PRIOR FILING DATE: 2000-08-24
; PRIOR APPLICATION NUMBER: US 60/264,647
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/300,111
; PRIOR FILING DATE: 2001-06-22
; NUMBER OF SEQ ID NOS: 5379
; SEQ ID NO 1088
; LENGTH: 762
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-938-842A-1088

```

Alignment Scores:

Pred. No.:	1.25e-125	Length:	762
Score:	1085.00	Matches:	194
Percent Similarity:	86.75%	Conservative:	22
Best Local Similarity:	77.91%	Mismatches:	31
Query Match:	77.83%	Indels:	2
DB:	10	Gaps:	2

US-09-383-579c-10 (1-250) x US-09-938-842A-1088 (1-762)

```

QY 4 SerLYSerProPheSerSerLeuPheLeuProPhePheVal---PheThrPhe 22
DB 13 TCATCTTAATAATATTCAATATCTCAATTAATCCGATTAATCTCTCAAGAACTCAT 72
QY 23 AlaAspTYrGLYGLYTrPGINSEGLYHISALATHRPHELYGLYGLYVAPALASER 42
DB 73 GGAGCAGCAGGAGTGGAGTGGATGCGCACGCTTTTACGGCGCGCAAGATGCTTCC 132
QY 43 GLYThrMetGLYGLYALCYseGLYTYrGLYAsnLeuTYrSeGLYGLYTYrGLYThraSer 62
DB 133 GGCACACATGGGGGAGGCTTGCTGCTATGGAATTTGTATGGCCAAAGTTACGGAGCAGAAC 192
QY 63 ThrValAlaleuSerThrAlaleuPheAsnAsnGLYLeuSerCYseGLYVALaCYsPheGlu 82
DB 193 ACGGGCGCTTTAAGTACGCTCTATTCAACAACGACCTCACGTGGCGCGGTATGAG 252
QY 83 MetThrCYseThrAsnAsnProLYrTYrCYsLeuProGLYThrILeArGLYThraAlaThr 102
DB 253 ATGAAGTGTACGATGACCGAGGTGGTGTCTCGGCTCAACCATCAACGCTCACAGCTACA 312
QY 103 AsnPheCYsProProAsnPheAlaleuProAsnAsnAsnGLYGLYTYrCYsAsnProPro 122
DB 313 AACTTTGGCCACCTTAACCTCGCTTCCAACGATTAAGAGTGGTGGCAATCTCTCT 372
QY 123 LeuGlnHisPheAspMetAlaGluProAlaPheLeuGlnILeAlaGlnTYrArGLYAlaGly 142
DB 373 CTTCAGCAATTCGACCTCGCCAGGACAGCTTTCTTCAGATGCTCAGATGCTCGCGC 432
QY 143 IleValProValSerPheArGLYrGLYProCYseMetLYseGLYGLYValArGpHeThr 162
DB 433 ATTTGCTCTCTCTTCCGAAGATGACATGATGAAGAAAGGAGAAATGAGTTTACG 492
QY 163 IleAsnGLYHisSerTYrPheAsnLeuValLeuILeThrAsnValGLYGLYValaGlyAsp 182
DB 493 ATCAACGACATCTACTTCACTCTGCTCGATCTCCAAGTGAAGGAGACAGGAGAGC 552
QY 183 ValHisSerValSerILEYseGLYSerArGLYrGLYTrPGINSerMetSerArGLYrGLY 201
DB 553 GTACACGCGCTCTCATCAAGCTCAAAACACACAGTGTGGCAAGCGATGCTGAGAAC 612
QY 202 TrPGINAsnTrPGINSerAsnAsnTYrLeuAsnGLYGLYLeuSerPheGlnVal 221

```


Pred. No.:	5.07e-118	Length:	747
Score:	1024.00	Matches:	175
Percent Similarity:	88.39%	Conservative:	23
Best Local Similarity:	78.12%	Mismatches:	26
Query Match:	73.46%	Indels:	0
DB:	10	Gaps:	0

US-09-383-579C-10 (1-250) x US-09-938-842A-1069 (1-747)

Qy	27	GlyTyrGlnSerIshAlaThrPheTyrGlyGlyValAspAlaSerGlyThrMetGly	46
Db	70	GGATGGGTCAATGCTCATGCTACTACTTCTATGGTGGAAAGTACGTTTCAGAAACATAGGT	125
Qy	47	GlyValAspGlyTyrGlyValenLeuTyrSerGlnGlyTyrGlyYThrAsnThrValAlaLeu	66
Db	130	GGAGCTTGGGCTTACGGGAACCTCTACATCAAGGTTCAGGGACCAACACGGCGCGTTG	189
Qy	67	SerThrAlaLeuPheAsnGlnGlyLeuSerCysGlyValaCysPheGluMetThrCysThr	86
Db	190	AGCACTGCTCTGTTCACCAACCGCTCTTACTCTGGGGCTTGTTTGAATACAAAGTGCAG	249
Qy	87	AsnAspProLysTyrCysLeuProGlyYThrIleArgValThraIaThrAsnPheCysPro	106
Db	250	AGGACCGCGCGTGGGGTGTATTACTGCTGCTATCATGTTCACAGCCACCAATTTCTGTCCT	309
Qy	107	ProAsnPheAlaLeuProAsnAsnGlnGlyTyrCysAsnProProLeuGlnHisPhe	126
Db	310	CTTACACACGCTCTTCCCATTAACGCTGGTGGTGGTGTATGACCCCTCCGCTCATCATTC	369
Qy	127	AspMetAlaGluProAlaPheLeuGlnIlealGlnTyrArgAlaGlyLeuAlaProVal	146
Db	370	GATCTCTCTACGCTGTGTTTTTTCACCATTCGCTCAGTCAAGAGCTGGTGTGTCCTGTT	427
Qy	147	SerPheArgArgAlaProCysMetLysLysGlyValAlaArgPheThrIleAsnGlyHis	166
Db	430	TCTTACAGAAAGGCTTCGTTATGAAGAAAGAGGATTAAGTTATCATCAATCAACGGTAC	489
Qy	167	SerTyrPheAsnLeuValLeuIleThrAsnValGlyValAlaGlyAspValHisSerVal	186
Db	490	TCTTACTTCAACTGTGCTTGGTGGACCAATGTGGTGGTGGTGGAGATGTTCAATTCGGTT	549
Qy	187	SerIleLysGlySerArgThrGlyTyrGlnInsMetSerArgAsnTyrGlyIleAsnTyr	206
Db	550	GCGGTTAAAGTTCCTAGAAACAAGTGGCAACAAATGTCAGAAATCGGGGACAAAGCTGG	609
Qy	207	GlnSerAsnAsnTyrLeuAsnGlnGlyGlnGlyLeuSerPheGlnValThrLeuSerAspGly	226
Db	610	CAAGCAACATCTTTAAACGGTCAAGCATGTGCTATTAAAGTACGCTAGAGTGGT	669
Qy	227	ArgThrLeuThrAlaTyrAsnLeuValProSerAsnTyrGlnPheGlyGlnThrTyrGlu	246
Db	670	CGTACCGTGCCTCTAAACAACATGCTCCAGCTAGTGGTCTCTTGGACAAACCTTCACC	729
Qy	247	GlyProGlnPhe	250
Db	730	GGCGCTCAATTC	741

RESULT 7
 US-09-938-842A-89
 ; Sequence 89, Application US/09938842A
 ; Patent No. US20020160378A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Harper, Jeff
 ; APPLICANT: Kreps, Joel
 ; APPLICANT: Wang, Xun
 ; APPLICANT: Zhu, Tong
 ; TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
 ; TITLE OF INVENTION: SAME, AND METHODS OF USE
 ; FILE REFERENCE: SCRIPI300-3
 ; CURRENT APPLICATION NUMBER: US/09/938, 842A
 ; CURRENT FILING DATE: 2001-08-24
 ; PRIOR APPLICATION NUMBER: US 60/227, 866
 ; PRIOR FILING DATE: 2000-08-24

```

? PRIOR APPLICATION NUMBER: US 60/264,647
? PRIOR FILING DATE: 2001-01-16
? PRIOR APPLICATION NUMBER: US 60/300,111
? PRIOR FILING DATE: 2001-06-22
? NUMBER OF SEQ ID NOS: 5379
? SEQ ID NO 89
? LENGTH: 774
? TYPE: DNA
? ORGANISM: Arabidopsis thaliana
US-09-938-842A-89

Alignment Scores:
Pred. No.: 3,99e-114
Score: 993.00
Percent Similarity: 81.53%
Best local Similarity: 71.89%
Query Match: 71.23%
DB: 10
Gap:

```

US-09-383-579C-10 (1-250) X US-09-938-842A-89 (1-774)

Qy	12	PheLeuLeuProPhePhePheValPheThrPheAlaSerTyr-----	25
Db	20	TTCTATTTCACACA-TTTGTTCTTTTATGAGCTCGGACGCTAGAAATCCCGGATTATTC	78
Qy	26	-----GlyGlyTTPGlnSerGlyHisAlaThrPheTyrGlyGlyAspAlaSerGly	43
Db	79	TCCGGGGGGCGCATGGCAAAACGACACCCCACTTTTTCGGGTGGACGACGCTCCGGC	138
Qy	44	ThMetGlyValAlaCysGlyTyrGlyIleuLeuTyrSerGlnGlyTyrGlyTThrAsnThr	63
Db	139	ACAAATGGAGAGAGCTTGTTGGTTACGGTAACCTATACACCAAGGGATACGGGACCAACACG	196
Qy	64	ValAlaLeuSerThrAlaLeuPheAsnGlnGlyLeuSerCysGlyValAlaCysPheGlnMet	83
Db	199	GCCTCTTGAATACGGCGCGCTTTTAAACAATGATAGATTGTGAGCTCGCTTTGACCTA	256
Qy	84	ThrCysThrAsnAspProLeuTyrCysLeuProGly-----ThrIleArgValThrAla	101
Db	259	AAATGGCCCAACGACCCCTCAATGATGTGTCACCTAGAGTACTCTTGACCTCATCACGCA	318
Qy	102	ThAsnPheCysProProAsnPheAlaLeuProAsnAsnGlnGlyTyrCysAsnPro	122
Db	319	ACCAATTTCTGCCACACAAACTTGCTCAGCTACGCTACGCAACGAGAGTGTGTCAACCA	378
Qy	122	ProLeuGlnHisPheAspMetAlaGluProAlaPheLeuGlnIleAlaGlnTyrArgAla	141
Db	379	CCACGTGAACACTTGACCTAGCCACCATGCTGTCTTTAAGATGGCTCAATATACGGCC	438
Qy	142	GlyIleValProValSerPheArgTyrValProCysMetCysGlyGlyValArgPhe	161
Db	439	GGCATTTGTCCTCGTCTCAACCGGACGGGTGCATGTAAAGAGAGAGCGATAGGTTTC	498
Qy	162	ThrIleAsnGlyHisSerTyrPheAsnLeuValLeuIleThrAsnValGlyValAlaGly	181
Db	499	ACAAATCAACGGTCACCGTTACTTCAACTGGTTCTGATCACTAACGTGCTGAGCAGAGA	558
Qy	182	AspValHisSerValSerIleLeuGlySerArgThrGlyTyrTPGlnSerMetSerArgAsn	201
Db	559	GAACTGTGAGGGCTAGTGTGAAGAGATCACGGATGGTGTGATGAGTTTGAAGAGAAAC	618
Qy	202	TyrGlyGlnAsnTyrGlnSerAsnAsnTyrLeuAsnGlnGlyGlnGlyLeuSerPheGlnVal	221
Db	619	TGGGGACAAAATCGGCATCTAATCTGTGTTTGGTTGGTCAAGCACTCTTTCCGTC	678
Qy	222	ThrLeuSerAspGlyValArgThrLeuThrAlaTyrArgIleuValProSerAsnTyrGlnPhe	241
Db	679	ACAGGCAAGACCGGTAGAAACATCTACTCTTCGAAACATGATCTCTTCAACTGCAAGTTT	738
Qy	242	GlyGlnThrTyrGlnGlyProGlnPhe	250
Db	739	GGTCAAACTTTGTGGGAGAAATTTTC	765

```

RESULT 8
US-09-938-842A-842
; Sequence 842, Application US/0938842A
; Patent No. US20020160378A1
; GENERAL INFORMATION:
; APPLICANT: Harper, Jeff
; APPLICANT: Kreps, Joel
; APPLICANT: Wang, Xun
; APPLICANT: Zhu Tong
; TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
; TITLE OF INVENTION: SAME, AND METHODS OF USE
; FILE REFERENCE: SCRIPI300-3
; CURRENT APPLICATION NUMBER: US/09/938,842A
; PRIOR FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: US 60/227,866
; PRIOR FILING DATE: 2000-08-24
; PRIOR APPLICATION NUMBER: US 60/264,647
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/300,111
; PRIOR FILING DATE: 2001-06-22
; NUMBER OF SEQ ID NOS: 5379
; SEQ ID NO 842
; LENGTH: 774
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-938-842A-842

Alignment Scores:
Pred. No.: 2,23e-107 Length: 774
Score: 939.00 Matches: 161
Percent Similarity: 83.70% Conservative: 29
Best Local Similarity: 70.93% Mismatches: 35
Query Match: 67.36% Indels: 2
DB: 10 Gaps: 1

US-09-383-579c-10 (1-250) x US-09-938-842A-842 (1-774)
QY 26 G1G1YTPGInserGc1YH1sAlaThrPheTYrG1Yg1YAspAlaSerG1YThrMet 45
DB 85 GGTGGTGGGAACGCTCAACCGCACCTTCTACGGGGCTCTGATGCTTCTGGAACAAG 144
QY 46 G1G1YAlaCYeG1YTYrG1YAsnLeuTYrSerG1YTYrG1YThraThrValAla 65
DB 145 GGAGAGGCTTGTTGGTTATGTAATTATACGCCAAGGCTATGCTGAACGCGGCT 204
QY 66 LeuSerThraLeuPheAsnG1YLeuSerCYeG1YAlaCYePheGluThrCys 85
DB 205 TTAAAGCAGCGCTCTGTTCAACAATGGTTTACGCTGGTGTGCTTTTGAGCTCAATGT 264
QY 86 ThrAsnAPrOlySTrPcYsLeuPrcG1Y-----ThrIleArgValThraIleThra 103
DB 265 GCTAGGATCCAAATAGTGCCATCTGTGTAAGCTCTTCAATCTTCATCACTGGACTAAT 324
QY 104 PheCYsPrOProAsnPheAlaLeuProAsnAsnG1YG1YTYrCYsAsnProProl 123
DB 325 TTCTGTCCTCCGAACCTTCTCAGCCTAGTACAAAGTGTTGGTGAACCTCTCTAGA 384
QY 124 G1nH1sPheAspMetAlaGluProAlaPheLeuG1nIleAlaG1nTYrAlaG1YIle 143
DB 385 CCTCACTTGAATCTGCTGATGCTTATGTTCTCAATATCGTGAATGCTGCGGGAATC 444
QY 144 ValProValSerPheArgArgValProCYsMetLeuYg1Yg1YValArgPheThrIle 163
DB 445 GTCCCGGTCTCTTCCGCGAGTGCATCCGGAAGAGGAATTAAGTTCAACAATC 504
QY 164 Aeng1YH1sSerTYrPheAsnLeuValLeuIleThraAsnValG1Yg1YAlaG1YAspVal 183
DB 505 AACGGTTTCCGTTATTTTAACTTGCTTACGTCACTAAGCTGCGCCCGGAACAATA 564
QY 184 H1sSerValSerIleLeuG1YSerArgThnG1YTYrG1nSerIleSerArgThnTYrG1Y 203
DB 565 GTGCGGCTAGTGTAAGGAACAACATACCTTGTGATGATGATGATGATGATGATGATG 624

```

```

QY 204 G1nAsnTrpG1nSerAsnAsnTYrLeuBeng1Yg1Yg1YLeuSerPheG1nValThrLeu 223
DB 625 CAAAACGCGAATCTTACTCACTTTTGTTGGTGTGATGCTACTTCTTTTAAAGTCAACG 684
QY 224 SerAspG1YArgThrLeuThraIleTYrAsnLeuValProSerAsnTrpG1nG1Yg1n 243
DB 685 AGTGACCGTAGAAGCTCAACGCTGGAACATTTGCTCCGCGCAATTTGGAAGTTGTGTAG 744
QY 244 ThyrTYrG1nG1YProG1nPhe 250
DB 745 ACTTTCATGGAAGAAGACTTC 765

RESULT 9
US-09-770-445-491/C
; Sequence 491, Application US/09770445
; Patent No. US20020023281A1
; GENERAL INFORMATION:
; APPLICANT: Goriach, Jörn
; APPLICANT: An, Yong-Qiang
; APPLICANT: Hamilton, Carol M.
; APPLICANT: Price, Jennifer L.
; APPLICANT: Raines, Tracy M.
; APPLICANT: Yu, Yang
; APPLICANT: Rameaka, Joshua G.
; APPLICANT: Page, Amy
; APPLICANT: Matthew, Abraham V.
; APPLICANT: Ledford, Brooke L.
; APPLICANT: Woessner, Jeffrey P.
; APPLICANT: Haas, William David
; APPLICANT: Garcia, Carlos A.
; APPLICANT: Kriker, Meja
; APPLICANT: Slader, Ted
; APPLICANT: Davis, Keith R.
; APPLICANT: Allen, Keith
; APPLICANT: Hoffman, Neil
; APPLICANT: Hurban, Patrick
; TITLE OF INVENTION: Expressed Sequences of Arabidopsis
; TITLE OF INVENTION: thaliana
; FILE REFERENCE: 2023US (PARA-012PRV)
; CURRENT APPLICATION NUMBER: US/09/770,445
; PRIOR FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: US 60/178,472
; PRIOR FILING DATE: 2000-01-27
; NUMBER OF SEQ ID NOS: 999
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 491
; LENGTH: 893
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(893)
; OTHER INFORMATION: n = A,T,C or G
US-09-770-445-491

Alignment Scores:
Pred. No.: 3.67e-107 Length: 893
Score: 938.00 Matches: 161
Percent Similarity: 83.70% Conservative: 29
Best Local Similarity: 70.93% Mismatches: 35
Query Match: 67.29% Indels: 2
DB: 9 Gaps: 1

US-09-383-579c-10 (1-250) x US-09-770-445-491 (1-893)
QY 26 G1G1YTPGInserGc1YH1sAlaThrPheTYrG1Yg1YAspAlaSerG1YThrMet 45
DB 774 GGTGGTGGGAACGCTCAACCGCACCTTCTACGGGGCTCTGATGCTTCTGGAACAAG 715
QY 46 G1G1YAlaCYeG1YTYrG1YAsnLeuTYrSerG1YTYrG1YThraThrValAla 65
DB 714 GGAGAGGCTTGTTGGTTATGTAATTATACGCCAAGGCTATGCTGAACACGCGGCT 655

```

Qy	66	leuserfrralaleuphasnangllyeusercygylacyspneglumethrCys	85
Db	654	TTAAGCAGCGCTCTGTTCAACAATGCTTTAGCTGTGCTTTTGAAGCTCAAAATGT	595
Qy	86	ThrsanapProlystPysaleupProgly-----ThrleargValThrAlathrasn	103
Db	594	GCTAGTATCCAAATATGGTGCATCTGTGATGCTTCAATCTTCATCAGTCCGACATAT	535
Qy	104	PheCyProProAenPheAlaleuProAasnAnanglylyTPCyAsnProleu	123
Db	534	TTCTGCTCTCGAAGCTTGTCTCAGCTATGACATGGTGGTGTAACTCCCTTAGA	475
Qy	124	GlnHisPheapmetAlagluProAlaphelenglnleAlaglnlTyrragAlaglyle	143
Db	474	CCTCACTTGAATCTTGCTATGCTATGTTTCTCAAGATCGCTGAGTATCGGCCGATC	415
Qy	144	ValProValSerPheargArgValProCySmethylsrglygylValAargPheThrle	163
Db	414	GTCCCGGCTCTTTCCGCCGAGTGCAGCCCGAAGAGGAGAAATRAAGTTTACATAC	355
Qy	164	AenGlyHisSerTyrrPheAsnleuValleuIleThrAnValglylyAlaglyAspVal	183
Db	354	AACGGTTTCCCTTATTTTAACTTGCTTACTACTAAAGTNNNGCGCCGGAACATA	295
Qy	184	HisSerValserIlelyserArgThrlylrrpGlnserMetserArgAsnTrgly	203
Db	294	GTGGCGCTAGGTGTGAAGAACACATATCTTCGGAGATGACATGAGTCTGATCGGGA	235
Qy	204	GlnAsnTrpGlnSerAsnAsnTyrrleuAnsglyGlnlyleuserPheGlnValThrleu	223
Db	234	CAAACTGGCATCTACTACGTGTTGGTGGTCAAGTCACTTTTTTAGAGTCAACAAC	175
Qy	224	SerAepGlyArgThrleuThrAlaTyrrAsnleuValProSerAsnTrpGlnPheglyln	243
Db	174	AGTACCGCTAGAAAGCTCGACGTCGTGGAACATGCTCGCGGATTTGGAAGTTGTCTAG	115
Qy	244	ThrTyrrGlnGlyProGlnPhe	250
Db	114	ACTTTCATGGGAAGAACTTC	94

RESULT 10
US-09-938-842A-1046
Sequence 1046, Application US/09938842A
Patent No. US20020160378A1
GENERAL INFORMATION:
APPLICANT: Harper, Jeff
APPLICANT: Kreps, Joel
APPLICANT: Wang, Xun
APPLICANT: Zhu, Tong
TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
FILE REFERENCE: SAME, AND METHODS OF USE
CURRENT APPLICATION NUMBER: US/09/938, 842A
CURRENT FILING DATE: 2001-08-24
PRIORITY APPLICATION NUMBER: US 60/227, 866
PRIORITY FILING DATE: 2000-08-24
PRIORITY APPLICATION NUMBER: US 60/264, 647
PRIORITY FILING DATE: 2001-01-16
PRIORITY APPLICATION NUMBER: US 60/300, 111
PRIORITY FILING DATE: 2001-06-22
NUMBER OF SEQ ID NOS: 5379
SEQ ID NO 1046
LENGTH: 768
TYPE: DNA
ORGANISM: Arabidopsis thaliana
US-09-938-842A-1046

Alignment Scores:
Pred. No.: 7.98e-95 Length: 768
Score: 838.50 Matches: 152
Percent Similarity: 76.83% Conservative: 37
Best Local Similarity: 61.79% Mismatches: 50
Query Match: 60.15% Indels: 7

LENGTH: 410
TYPE: DNA
ORGANISM: Glycine max
OTHER INFORMATION: Clone ID: LIB028-003-Q1-B1-D9
US-09-878-574-3973

Alignment Scores:

Pred. No.:	6,44e-75	Length:	410
Score:	676.00	Matches:	120
Percent Similarity:	96.30%	Conservative:	10
Best Local Similarity:	88.89%	Mismatches:	5
Query Match:	48.49%	Indels:	0
DB:	10	Gaps:	0

US-09-383-579c-10 (1-250) x US-09-878-574-3973 (1-410)

QY 113 AaenAaenGlyGlyTTPCyAsnProPLeuGlnHsPheaspMetAlaGluProAla 132
DB 5 AACAAACATGGTGGCGGCGCAACCTCTTGCAACACTTTCATCTGCTGAGCTGCT 64
QY 133 PheleuGlnHsAlaGlnTyrArgAlaGlylleValProValSerPheArgValPro 152
DB 65 TTCTTGCAATGGCTCAATACAAAGCTGGAATGTTCCAGTTCTTCCAGAGAGCTCC 124
QY 153 CysMetLeuGlyGlyValArgPheThrIleAsnGlyHisSerTyrPheAsnLeuVal 172
DB 125 TGTGTGAAGAAAGAGGAGATCAGGTCACATCAATGTCACCTTCACTTCACTTGGTT 184
QY 173 LeuIleThrAsnValGlyValArgPheValHisSerValSerIleLeuGlySerArg 192
DB 185 CTCATACAAATGTTGCTGAGCTGAGATGTTTCATCTGTCCTCAAAAGGCTTAA 244
QY 193 ThrGlyTTPGlnSerMetSerArgAsnTTPGlyGlnAsnTTPGlnSerAsnTyrIleu 212
DB 245 ACTGGGTGGCAACCATGTCTAGAACTGGGGGCAAGATGGTAAAGCAACTCTACCTG 304
QY 213 AaenGlyGlnGlyLeuSerPheGlnValThrLeuSerAspGlyArgPheThrAlaTyr 232
DB 305 AATGGCAAGCCCTCTCTTTTCAGGTCACCTACCAAGAGGAGGAGCTCTCACTAGCAAC 364
QY 233 AaenLeuValProSerAsnTTPGlnPheGlyGlnThrTyrGlyGly 247
DB 365 AACATTGCTGCTGCTAAGCTGCAATTGGACAAACATTGGAAGG 409

RESULT 12

US-09-878-574-62
Sequence 62, Application US/09878574
Patent No. US20020110548A1

GENERAL INFORMATION:

APPLICANT: Byrum, Joseph R.
APPLICANT: La Rosa, Thomas J.
APPLICANT: Thompson, Michael D.
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
FILE REFERENCE: 38-21(15401) B
CURRENT APPLICATION NUMBER: US/09/878,574
CURRENT FILING DATE: 2001-12-21
PRIOR APPLICATION NUMBER: 09/333,535
PRIOR FILING DATE: 1999-06-14
NUMBER OF SEQ ID NOS: 15775
SEQ ID NO 62

LENGTH: 391

TYPE: DNA

ORGANISM: Glycine max

FEATURE:

NAME/KEY: unsure

LOCATION: (1)...(391)

OTHER INFORMATION: unsure at all n locations

OTHER INFORMATION: Clone ID: LIB028-056-Q1-B1-E10

US-09-878-574-62

Alignment Scores:

Pred. No.: 7.99e-71

Length:

391

Score:	643.00	Matches:	112
Percent Similarity:	96.15%	Conservative:	13
Best Local Similarity:	86.15%	Mismatches:	5
Query Match:	46.13%	Indels:	0
DB:	10	Gaps:	0

US-09-383-579c-10 (1-250) x US-09-878-574-62 (1-391)

QY 116 GlyGlyTTPCyAsnProPLeuGlnHsPheaspMetAlaGluProAlaPheLeuGln 135
DB 1 GGTGGTGGTGAACCTCTCTTGCAACACTTGTATAGGCTGCAACCTGCTCTTCA 60
QY 136 IleAlaGlnTyrArgAlaGlylleValProValSerPheArgValProCysMetLeu 155
DB 61 ATTGCTGATATAGAGCTGGAATGCTGCTGAGGCTTCAAGAGGCTTCTGTGTGAA 120
QY 156 LysGlyGlyValArgPheThrIleAsnGlyHisSerTyrPheAsnLeuValLeuIleThr 175
DB 121 AAGGAGGATATAGATTCATCAATCAATGCGCACTTCTTCAACTGATTTGATCAC 180
QY 176 AaenValGlyGlyAlaGlyAspValHisSerValSerIleLeuGlySerArgThrGlyTyr 195
DB 181 AATGGCTGAGAGCTGTGATGTGAATTCAGTGTCCATTTAAAGGCTCCAAAGCTGGTGG 240
QY 196 GlnSerMetSerArgAsnTTPGlyGlnAsnTTPGlnSerAsnTyrLeuAsnGlyGln 215
DB 241 CAGCCCATGTCAAGAACTGGGGGCAAACTGGAGCAACTCATACCTCAATGACAA 300
QY 216 GlyLeuSerPheGlnValThrLeuSerAspGlyArgThrLeuThrAlaTyrAsnLeuVal 235
DB 301 TNCCTCTCTTTCAAGTCAACCAACGATGATGCAAACTGTGACAAAGCTGCAATGTGGCA 360
QY 236 ProSerAsnTTPGlnPheGlyGlnThrTyr 245
DB 361 CCAGCAATTTGGCAATTTGGCCAGACCTTC 390

RESULT 13

US-09-770-791-430
Sequence 430, Application US/09770791
Patent No. US2002062014A1

GENERAL INFORMATION:

APPLICANT: Goriach, Jörn
APPLICANT: An, Yong-Qiang
APPLICANT: Hamilton, Carol M.
APPLICANT: Price, Jennifer L.
APPLICANT: Raines, Tracy M.
APPLICANT: Yu, Yang
APPLICANT: Rameaka, Joshua G.
APPLICANT: Page, Amy
APPLICANT: Matthew, Abraham V.
APPLICANT: Ledford, Brooke L.
APPLICANT: Woessner, Jeffrey P.
APPLICANT: Haas, William David
APPLICANT: Garcia, Carlos A.
APPLICANT: Kricker, Maja
APPLICANT: Slader, Ted
APPLICANT: Davis, Keith R.
APPLICANT: Allen, Keith
APPLICANT: Hoffman, Neil
APPLICANT: Hubban, Patrick
TITLE OF INVENTION: Expressed Sequences of Arabidopsis
FILE REFERENCE: 2029 (PARA-018PRV)
CURRENT APPLICATION NUMBER: US/09/770,791
CURRENT FILING DATE: 2001-01-26
PRIOR APPLICATION NUMBER: 60/178,480
PRIOR FILING DATE: 2000-01-27
NUMBER OF SEQ ID NOS: 999
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 430

LENGTH: 366

TYPE: DNA

ORGANISM: Arabidopsis thaliana

US-09-770-791-430

Alignment Scores:

Pred. No.:	9.54e-54	Length:	366
Score:	506.00	Matches:	85
Percent Similarity:	87.27%	Conservative:	11
Best Local Similarity:	77.27%	Mismatches:	12
Query Match:	36.30%	Indels:	2
DB:	9	Gaps:	1

US-09-383-579c-10 (1-250) x US-09-770-791-430 (1-366)

QY 26 GlyGlyTrpGlnSerGlyHsaIaThrPheTyrGlyGlyGlyAspAlaSerGlyThrMet 45
DB 36 GGACCGGCGGAGATGACACAGCCACTTCTACGGTGGCAGTAGCGCTCCGGCACATG 95
QY 46 GlyGlyAlaCysGlyTyrGlyAsnLeuTyrSerGlnGlyTyrGlyThrAsnThrValAla 65
DB 96 GGGCGCGCGTGGTGGTACGGGAACTTGTACAGCCAGCAAGATACGGTGTGAACACGGCGCG 155
QY 66 LeuSerThrAlaLeuPheAsnAsnGlyLeuSerCysGlyAlaCysPheGlnMetThrCys 85
DB 156 TTGAGCATGCTGTTTTCACACAGCATTCACGCTGTGTGCTGTTGAGATTAACTGT 215
QY 86 ThrAsnAspProIleTyrCysLeuProGly-----ThrIleArgValThrAlaThrAsn 103
DB 216 ACTGATGATCCGAGATGCTGTGTTCCGGAAATCATCTATTCTTGAGCGGACGAC 275
QY 104 PheCysProProAsnPheAlaLeuProAsnAsnAsnGlyGlyTyrCysAsnProProLeu 123
DB 276 TTTTGTCGCCGGAATTTGCTCAGCCGAGTGCACAGCAGAGGTGTGCAATCCGCCCGC 335
QY 124 GlnHisPheAspMetAlaGluProAlaPhe 133
DB 336 GAGCATTTTATCTCCGCAATGCTTATGTTTC 365

RESULT 14

US-09-878-574-3468
; Sequence 3468, Application US/09878574
; Patent No. US20020110548A1

; GENERAL INFORMATION:
; APPLICANT: Byrum, Joseph R.
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Thompson, Michael D.
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
; FILE REFERENCE: 38-21(15401)B
; CURRENT APPLICATION NUMBER: US/09/878,574
; PRIOR FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: 09/333,535
; NUMBER OF SEQ ID NOS: 15775
; SEQ ID NO 3468
; LENGTH: 373
; TYPE: DNA
; ORGANISM: Glycine max
; OTHER INFORMATION: Clone ID: LIB3028-010-Q1-B1-E9

US-09-878-574-3468

Alignment Scores:

Pred. No.:	6.36e-52	Length:	373
Score:	491.50	Matches:	85
Percent Similarity:	78.40%	Conservative:	13
Best Local Similarity:	68.00%	Mismatches:	16
Query Match:	35.26%	Indels:	11
DB:	10	Gaps:	2

US-09-383-579c-10 (1-250) x US-09-878-574-3468 (1-373)

QY 12 PheLeuLeuProPhePhePheValPheThrPheAla-----AspTyrGlyGlyTyr 28
DB 21 TTTCTCTGGAGCTTTTCTACATGATCTCACATGTCAAGGGTATGTGTTTGGAGGTGG 80

QY 29 GlnSerGlyHsaIaThrPheTyrGlyGlyGlyAspAlaSerGlyThrMetGlyAla 48
DB 81 ACCAATGACATGCGACCTTCTATGAGGGGGTATGCTTCTGGACCAATGGGGGCT 140

QY 49 CysGlyTyrGlyAsnLeuTyrSerGlnGlyTyrGlyThrAsnThrValAlaLeuSerThr 68
DB 141 TGTGGTATGGAATCTGTATAGCCAAAGTTATGGAATCATACACAGCATGAGCACT 200

QY 69 AlaLeuPheAsnAsnGlyLeuSerCysGlyAlaCysPheGlnMetThrCysThrAsnAsp 88
DB 201 GCACTGTTCAACAATGCTTACCTGTGTGCTGCTTCAATTAATGTCGAAATGAC 260

QY 89 ProIleTyrCysLeuProGlyThrIleArgValThrAlaThrAsnPheCysProProAsn 108
DB 261 CCAAAATGGTCCCTTCCTGCTCCATCATATGATGACCCCAAAATTTCTGTCCACT 317

QY 109 PheAlaLeuProAsnAsnAsnGlyGlyTyrCysAsnProProLeuGlnHisPheAspMet 128
DB 318 -----GGTGGTGGTGTGACCTTCCAAATCACCACTTTGATCCT 356

QY 129 AlaGluProAlaPhe 133
DB 357 TCCCAATGCTGTTTC 371

RESULT 15

US-09-878-574-1206
; Sequence 1206, Application US/09878574
; Patent No. US20020110548A1

; GENERAL INFORMATION:
; APPLICANT: Byrum, Joseph R.
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Thompson, Michael D.
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
; FILE REFERENCE: 38-21(15401)B
; CURRENT APPLICATION NUMBER: US/09/878,574
; PRIOR FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: 09/333,535
; NUMBER OF SEQ ID NOS: 15775
; SEQ ID NO 1206
; LENGTH: 391
; TYPE: DNA
; ORGANISM: Glycine max
; OTHER INFORMATION: Clone ID: LIB3028-040-Q1-B1-G6

US-09-878-574-1206

Alignment Scores:

Pred. No.:	3.79e-39	Length:	391
Score:	389.50	Matches:	75
Percent Similarity:	78.70%	Conservative:	10
Best Local Similarity:	69.44%	Mismatches:	16
Query Match:	27.94%	Indels:	7
DB:	10	Gaps:	3

US-09-383-579c-10 (1-250) x US-09-878-574-1206 (1-391)

QY 1 MetAlaPheSerTyrSerProPheSer---SerLeuPheLeuLeuProPhePheVal 19
DB 67 CTTAGATGGACACCAAGAAATTTTCATTGCTAGTCACTCTCATTTCTTTGTC 126

QY 20 PheThr-----PheAlaAspTyr---GlyGlyTrpGlnSerGlyHsaIa 33
DB 127 AACACGAACTCCAAAGTGCACGCTGACTATGTGTGTGGCAGAGTCTCATGCC 186

QY 34 ThrPheTyrGlyGlyAlaAspAlaSerGlyThrMetGlyGlyAlaCysGlyTyrGlyAsn 53
DB 187 ACTTTTATGTTGGGTGTATGCTTCTGACAAATGGGTGACCAATGTGGTATGGAAT 246

QY 54 LeuTyrSerGlnGlyTyrGlyThrAsnThrValAlaLeuSerThrAlaLeuPheAsnAsn 73
DB 247 TTTGTATAGCGACGAGTATGGAAGTACACTGTGGCTCTTAAGCACTGTTTCAACAT 306

QY 74 GYIleuSeSeCYGIALAacySpmegumetThCYeThhAsnaapProlvstPPCYsleu 93
DB 307 GCGTTAACTGTGGATCTCTCTTAAGAAATGAGATGTGATGATACCCAAATGTGTCAA 366
QY 94 PCCGlyThIleargValThrala 101
DB 367 CCGGCTCAATTAACCTCACTGCT 390

Search completed: December 19, 2003, 02:03:22
Job time : 296 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: December 18, 2003, 17:46:53 ; Search time 20 Seconds

(without alignments)
1202.109 Million cell updates/sec

Title: US-09-383-579C-10

Perfect score: 1394

Sequence: 1 MAFSYSPFSSLPFLPFVFFV.....AYNLVPSNMQFGQTEGPQF 250

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 9616862 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1394	100.0	250	T10079	expansin S1 precursor
2	1092	78.3	232	T09821	expansin (clone pp
3	1087	78.0	232	T09818	expansin (clone pp
4	1085	77.8	232	T09826	expansin (clone pp
5	1085	77.8	253	F84831	probable expansin
6	1077	77.3	232	T09825	expansin (clone pp
7	1051	77.4	258	T09786	expansin - upland
8	1043	74.8	251	T03298	expansin 2 - rice
9	1038	74.5	246	T04175	expansin - rice
10	1032	74.0	237	T50654	expansin EXP1 (imp
11	1030	73.9	255	T50656	expansin EXP2 (imp
12	1024	73.5	248	C84444	probable expansin
13	993	71.2	257	D84820	probable expansin
14	979	70.2	260	T47689	expansin
15	949.5	68.1	261	T07630	expansin 1 - tomato
16	945	67.8	257	T50658	expansin 9 (import
17	944	67.7	262	T02530	probable expansin
18	941.5	67.5	255	T06573	expansin 18 - toma
19	939	67.4	257	T02727	expansin
20	939	67.4	259	T50653	probable expansin
21	937	67.2	258	S53082	pollen allergen ho
22	935	67.1	264	T50659	alpha-expansin OsE
23	934	67.0	258	T48247	expansin-like prot
24	934	67.0	260	T08016	probable expansin
25	924.5	66.3	262	T50660	alpha-expansin 2
26	905	64.9	258	T10083	expansin S2 precursor
27	889.5	63.8	255	T50655	expansin EXP5 (imp
28	865.5	62.1	252	F86335	hypothetical prote
29	854.5	61.3	261	T03737	expansin - rice

30	838.5	60.2	255	2	T02010	expansin homolog T
31	825.5	59.2	255	2	T03299	expansin 3 - rice
32	730	52.4	160	2	T09871	expansin - upland
33	692	49.6	257	2	G96554	hypothetical prote
34	684	49.1	257	2	F86259	protein T12C24.10
35	604	43.3	256	2	T05648	expansin homolog F
36	328	23.5	102	2	T09815	expansin (clone pp
37	322.5	23.1	77	2	T09815	expansin (clone pp
38	289.5	20.8	81	2	T09830	expansin (clone pp
39	281	20.2	277	2	S48032	ctm1 protein - soy
40	279	20.0	259	2	T50657	beta-expansin (imp
41	279	20.0	271	2	H84592	beta-expansin (imp
42	273	19.6	259	2	E84886	probable beta-expa
43	271.5	19.5	261	2	T04301	beta-expansin - ri
44	270.5	19.4	491	2	F96681	protein F1E32.6
45	246.5	17.7	262	2	S38520	allergen Phl pi

ALIGNMENTS

RESULT 1

T10079
expansin S1 precursor - cucumber
C/Species: Cucumis sativus (cucumber)
C/Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #ext_change 21-Jul-2000
C/Accession: T10079
R/Schierban, T.Y.; Shi, J.; Duracko, D.M.; Gultinan, M.J.; McQueen-Mason, S.J.; Shieh
Proc. Natl. Acad. Sci. U.S.A. 92, 9245-9249, 1995
A/Title: Molecular cloning and sequence analysis of expansins--a highly conserved, mult
A/Reference number: Z14894; PMID:96016146; PMID:7568110
A/Accession: T10079
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 1-250 <SHC>
A/Cross-references: EMBL:U30382; NID:G1040874; PIDN:AAB37746.1; PID:G1040875
A/Experimental source: cultivar Burpee Pickler
C/Genetics:
A/Gene: EXP1
C/Function:
A/Description: mediates cell wall extension
C/Superfamily: expansin
F/1-23/Domain: signal sequence
F/24-250/Product: expansin #status predicted <SIG>

Query Match	100.0%; Score 1394; DB 2; Length 250;
Best Local Similarity	100.0%; Pred. No. 1.1e-110;
Matches	250; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY	1 MAFSYSPFSSLPFLPFVFTPADYGMOSGHATFYGGGDASGTMGAGSYGNLYSQYV 60
DB	1 MAFSYSPFSSLPFLPFVFTPADYGMOSGHATFYGGGDASGTMGAGSYGNLYSQYV 60
QY	61 TTNVALSTALFNNGSGCAFEWTCNDPKMCLPGTIRVATNFCPPNFALPNNNGMWN 120
DB	61 TTNVALSTALFNNGSGCAFEWTCNDPKMCLPGTIRVATNFCPPNFALPNNNGMWN 120
QY	121 PPIQHTDABPAFLQIAQIRAGIVPSFRVPCMKKGVRFTTNGSYFNVLITVNGA 180
DB	121 PPIQHTDABPAFLQIAQIRAGIVPSFRVPCMKKGVRFTTNGSYFNVLITVNGA 180
QY	181 GDVHSVIRKSRGWSMRNMGNNNNYLNQGLSFQVTLSDRRTTAVNLVPSNMQ 240
DB	181 GDVHSVIRKSRGWSMRNMGNNNNYLNQGLSFQVTLSDRRTTAVNLVPSNMQ 240
QY	241 FGQTEGPQF 250
DB	241 FGQTEGPQF 250
RESULT 2	
T09821	
expansin (clone pTexp3) - loblolly pine (fragment)	

```
C:Species: Pinus taeda (loblolly pine)
C>Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 26-May-2000
C:Accession: T09821
R:Hutchinson, K.W.; Singer, P.B.; Diaz-Sala, C.; Greenwood, M.S.
submitted to the EMBL Data Library, July 1996
A:Description: Expansins are conserved in conifers and expressed in response to exogenous
A:Reference number: Z16866
A:Accession: T09821
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-232 <HUT>
A:Cross-references: EMBL:U64891; NID:g1778100; PID:g1778101
A:Experimental source: clone pPexp3
C:Superfamily: expansin

Query Match
Best Local Similarity 82.7%; Score 1092; DB 2; Length 232;
Matches 186; Conservative 22; Mismatches 17; Indels 0; Gaps 0;

QY 25 YGWSGSHATFYGGDASGTMGACGYGNLYSGYGTNTVALSTALFNNGLSCGACFEHT 84
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 7 YGWSASHATFYGGSDASGTMGACGYGNLYSGYGTNTALSTALFNDGLSCGACYEHR 66
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 85 CTNDPKMCLPGTIRVTATNFCPPNFALPNNNGMCPNPLQHFDMAPFLQIAOYRAGIV 144
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 67 CNDDPQMKLPGLVTATNFCPPNFALPNDNGMCPNPLQHFDMAPFLKIAKRGIV 126
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 145 PVSFRPVPCKKGGVRFITNGHSYFNLVLTNNVGAGDVHVSIGKSRGTGMSRMNQ 204
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 127 PILYTRVPCLRKGRGIRFTNGHSYFNLVLTNNVGAGDVHVSIGKSRGTGMSRMNQ 186
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 205 NMOSNNYLNGLSLFQVTLSDGRTLTAVNLVPSNMQFGQTYEGSQ 249
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 187 NMOSNSYLNGLSLFQVTLSDGRTLVSNVAVPSNMQFGQTFEGSQ 231
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 3
T09818
expansin (clone pPexp2) - loblolly pine (fragment)
C:Species: Pinus taeda (loblolly pine)
C>Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 26-May-2000
C:Accession: T09818
R:Hutchinson, K.W.; Singer, P.B.; Diaz-Sala, C.; Greenwood, M.S.
submitted to the EMBL Data Library, July 1996
A:Description: Expansins are conserved in conifers and expressed in response to exogenous
A:Reference number: Z16866
A:Accession: T09818
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-232 <HUT>
A:Cross-references: EMBL:U64890; NID:g1778098; PID:g1778099
A:Experimental source: clone pPexp2; hypocotyl
C:Superfamily: expansin

Query Match
Best Local Similarity 82.2%; Score 1087; DB 2; Length 232;
Matches 185; Conservative 22; Mismatches 18; Indels 0; Gaps 0;

QY 25 YGWSGSHATFYGGDASGTMGACGYGNLYSGYGTNTVALSTALFNNGLSCGACFEHT 84
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 7 YGWSASHATFYGGSDASGTMGACGYGNLYSGYGTNTALSTALFNDGLSCGACYEHR 66
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 85 CTNDPKMCLPGTIRVTATNFCPPNFALPNNNGMCPNPLQHFDMAPFLQIAOYRAGIV 144
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 67 CNDDPQMKLPGLVTATNFCPPNFALPNDNGMCPNPLQHFDMAPFLKIAKRGIV 126
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 145 PVSFRPVPCKKGGVRFITNGHSYFNLVLTNNVGAGDVHVSIGKSRGTGMSRMNQ 204
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 127 PILYTRVPCLRKGRGIRFTNGHSYFNLVLTNNVGAGDVHVSIGKSRGTGMSRMNQ 186
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 205 NMOSNNYLNGLSLFQVTLSDGRTLTAVNLVPSNMQFGQTYEGSQ 249
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 187 NMOSNSYLNGLSLFQVTLSDGRTLVSNVAVPSNMQFGQTFEGSQ 231
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 4
T09826
expansin (clone pPexp5) - loblolly pine (fragment)
C:Species: Pinus taeda (loblolly pine)
C>Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 26-May-2000
C:Accession: T09826
R:Hutchinson, K.W.; Singer, P.B.; Diaz-Sala, C.; Greenwood, M.S.
submitted to the EMBL Data Library, July 1996
A:Description: Expansins are conserved in conifers and expressed in response to exogenous
A:Reference number: Z16866
A:Accession: T09826
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-232 <HUT>
A:Cross-references: EMBL:U64893; NID:g1778104; PID:g1778105
A:Experimental source: clone pPexp5
C:Superfamily: expansin

Query Match
Best Local Similarity 82.2%; Score 1085; DB 2; Length 232;
Matches 185; Conservative 23; Mismatches 17; Indels 0; Gaps 0;

QY 25 YGWSGSHATFYGGDASGTMGACGYGNLYSGYGTNTVALSTALFNNGLSCGACFEHT 84
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 7 YGWSASHATFYGGSDASGTMGACGYGNLYSGYGTNTALSTALFNDGLSCGACYEHR 66
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 85 CTNDPKMCLPGTIRVTATNFCPPNFALPNNNGMCPNPLQHFDMAPFLQIAOYRAGIV 144
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 67 CNDDPQMKLPGLVTATNFCPPNFALPNDNGMCPNPLQHFDMAPFLKIAKRGIV 126
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 145 PVSFRPVPCKKGGVRFITNGHSYFNLVLTNNVGAGDVHVSIGKSRGTGMSRMNQ 204
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 127 PILYTRVPCLRKGRGIRFTNGHSYFNLVLTNNVGAGDVHVSIGKSRGTGMSRMNQ 186
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 205 NMOSNNYLNGLSLFQVTLSDGRTLTAVNLVPSNMQFGQTYEGSQ 249
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 187 NMOSNSYLNGLSLFQVTLSDGRTLVSNVAVPSNMQFGQTFEGSQ 231
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 5
F84831
expansin (imported) - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C>Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 16-Feb-2001
C:Accession: F84831
R:Lin, X.; Kaul, S.; Roundley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; Vanden, S.E.; Umayam, L.; Tallon, L.;
euss, D.; Nieman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Frazer, C.M.; Venter, J.
Nature 402, 761-768, 1999
A:Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A:Reference number: A84420; MUID:20083487; PMID:10617197
A:Accession: F84831
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-253 <STO>
A:Cross-references: GB:A8002093; NID:g2651297; PIDN:AAB87577.1; GSPDB:GN00139
C:Genetics:
A:Gene: At2g40610
A:Map position: 2
C:Superfamily: expansin

Query Match
Best Local Similarity 77.9%; Score 1085; DB 2; Length 253;
Matches 194; Conservative 22; Mismatches 31; Indels 2; Gaps 2;

QY 4 SYSPSSFLPFPFV-FTPADYGGSHATFYGGDASGTMGACGYGNLYSGYGTN 62
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 5 SYLKYSIISIISVLPLOGTHGDGQGGHATFYGGSDASGTMGACGYGNLYSGYGTN 64
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 63 TVALSTALFNNGLSCGACFEHTCTNDPKMCLPGTIRVTATNFCPPNFALPNNNGMCPN 122
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
```

```
RESULT 6
T09826
expansin (clone pPexp5) - loblolly pine (fragment)
C:Species: Pinus taeda (loblolly pine)
C>Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 26-May-2000
C:Accession: T09826
R:Hutchinson, K.W.; Singer, P.B.; Diaz-Sala, C.; Greenwood, M.S.
submitted to the EMBL Data Library, July 1996
A:Description: Expansins are conserved in conifers and expressed in response to exogenous
A:Reference number: Z16866
A:Accession: T09826
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-232 <HUT>
A:Cross-references: EMBL:U64893; NID:g1778104; PID:g1778105
A:Experimental source: clone pPexp5
C:Superfamily: expansin

Query Match
Best Local Similarity 82.2%; Score 1085; DB 2; Length 232;
Matches 185; Conservative 23; Mismatches 17; Indels 0; Gaps 0;

QY 25 YGWSGSHATFYGGDASGTMGACGYGNLYSGYGTNTVALSTALFNNGLSCGACFEHT 84
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 7 YGWSASHATFYGGSDASGTMGACGYGNLYSGYGTNTALSTALFNDGLSCGACYEHR 66
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 85 CTNDPKMCLPGTIRVTATNFCPPNFALPNNNGMCPNPLQHFDMAPFLQIAOYRAGIV 144
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 67 CNDDPQMKLPGLVTATNFCPPNFALPNDNGMCPNPLQHFDMAPFLKIAKRGIV 126
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 145 PVSFRPVPCKKGGVRFITNGHSYFNLVLTNNVGAGDVHVSIGKSRGTGMSRMNQ 204
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 127 PILYTRVPCLRKGRGIRFTNGHSYFNLVLTNNVGAGDVHVSIGKSRGTGMSRMNQ 186
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 205 NMOSNNYLNGLSLFQVTLSDGRTLTAVNLVPSNMQFGQTYEGSQ 249
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 187 NMOSNSYLNGLSLFQVTLSDGRTLVSNVAVPSNMQFGQTFEGSQ 231
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 7
F84831
expansin (imported) - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C>Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 16-Feb-2001
C:Accession: F84831
R:Lin, X.; Kaul, S.; Roundley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; Vanden, S.E.; Umayam, L.; Tallon, L.;
euss, D.; Nieman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Frazer, C.M.; Venter, J.
Nature 402, 761-768, 1999
A:Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A:Reference number: A84420; MUID:20083487; PMID:10617197
A:Accession: F84831
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-253 <STO>
A:Cross-references: GB:A8002093; NID:g2651297; PIDN:AAB87577.1; GSPDB:GN00139
C:Genetics:
A:Gene: At2g40610
A:Map position: 2
C:Superfamily: expansin

Query Match
Best Local Similarity 77.9%; Score 1085; DB 2; Length 253;
Matches 194; Conservative 22; Mismatches 31; Indels 2; Gaps 2;

QY 4 SYSPSSFLPFPFV-FTPADYGGSHATFYGGDASGTMGACGYGNLYSGYGTN 62
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 5 SYLKYSIISIISVLPLOGTHGDGQGGHATFYGGSDASGTMGACGYGNLYSGYGTN 64
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 63 TVALSTALFNNGLSCGACFEHTCTNDPKMCLPGTIRVTATNFCPPNFALPNNNGMCPN 122
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
```

Db	65	TAALSTALFNNGLTCACYEEMKCNDDPRWCGLSTITVTATNVCSPNPGLSDNNGMNCNP	124
Qy	123	LQFDMADPEPFLQIAQYRAGIYVFSRRVPCKKGGVREFTINGHSYFNLVLTITVGGAGD	182
Db	125	LQFHDIAEPFLQIAQYRAGIYVFSRRVPCKKGGIPEFTINGHSYFNLVLTISVVGAGD	184
Qy	183	VHVSIVIKGSRT-QMOSMSRNRMGQNMNNYVLNGGLSPVYLTSDERTLTATNLVPSNQF	241
Db	185	VHVASIIGSKTQSGWMMSRNRMGQNMNSYNNDQSLSPVYTTSDERTLVSDVAVPSNQF	244
Qy	242	GQTYEGPQF 250	
Db	245	GQTYGGQF 253	

RESULT 6
T09825
expansin (clone ptxexp4) - loblolly pine (fragment)
C:Species: Pinus taeda (loblolly pine)
C:Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 26-May-2000
C:Accession: T09825
R:Hutchinson, K.W.; Singer, P.B.; Diaz-Sala, C.; Greenwood, M.S.
submitted to the EMBL Data Library, July 1996
A:Description: Expansins are conserved in conifers and expressed in response to exogenous
A:Reference number: Z16866
A:Accession: T09825
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-232 <HUT>
A:Cross-references: EMBL:U64892; NID:g1778102; PID:g1778103
A:Experimental source: EMBL:clone ptxexp4
C:Superfamily: expansin

	Query Match	Best Local Similarity	77.3%; Score 10777; DB 2; length 232;
	Matches	183; Conservative	81.3%; Pred. No. 6,9e-84;
		23; Mismatches	19; Indels
			0; Gaps
QY	25	YGMQSGHATITGGGDASGTWGAACGYNTLSQGYGINTVALSTALFNNGLSCGACPEMT	84
DB	7	YGMESALATPTGGSDASGTWGAACGYNTLSQGYGINTVALSTALFNDGLSCGACYEMQ	66
QY	85	CTNPQKMLPCTIRATATNFCPPNALNNNGMGNPFLQHPDMAEPALFIAOYRAQIV	144
DB	67	CNDPPQMLPCTIVITITATNFCPPNALPNDNGMGNPFLQHPDMAEPFLIAKRGQIV	126
QY	145	PVSEFRVPCMKKGVRFTINGHSYFNVLVTNNVGAGDVHSYSIKGSHTQMSRMNQ	204
DB	127	PILTRVPCILKGGIRFTVNGHSCFNILVLTNNVGAGDVHVAISIKGRSGQPMSRMNQ	186
QY	205	NMQSNNTYINGQLSPQVLTLSGRTLTAAVLVPSNNQPCQTEGPG	249
DB	187	NMQSNNTYINGQLSPQVLTLSGRTVYNNVAVSNMQPCQTEGSG	231

RESULT 7
T09786
expansin - upland cotton
C:Species: *Gossypium hirsutum* (upland cotton)
C:Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 26-May-2000
C:Accession: T09786
R:Orford, S.J.; Timmis, J.N.
Biochim. Biophys. Acta 1398, 342-6, 1998
A:Title: Specific expression of an expansin gene during elongation of cotton fibres
A:Reference number: Z14466; MUID:9655931; PMID:9655931
A:Accession: T09786
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-258 <ORF>
A:Cross-references: EMBL:AF043284; NID:g2811277; FID:g2811278
A:Experimental source: cultivar Siokra 1-2
C:Gene: Ghext1
C:Function:

A;Description: involved in cell wall modification
C;Superfamily: expansin

Query Match	75.4%	Score 1051;	DB 2;	Length 258;
Best Local Similarity	74.3%	Pred. No. 1.2e-81;		
Matches 182;	Conservative 25;	Mismatches 25;	Indels 10;	Gaps 1.

QY	16	FFEVFVFEFA-----	DYGMQSGHATFFGGDGASGTMGAGCGYGLYSQSYGYNTVA	65
		:	:	
Db	14	FFFLFVFCNSIFLGDANGDNGGMCQFAHATFFYGADATGTMGACGYGNYLSQGYGTSTAA		73
QY	66	LSTALLPNNLSGACAFEMTCITNDPKKCLPGITRTATNATPCPPNALPNNNGMGNPPLOH		12
		:	:	
Db	74	LSTALLPNNLSGACACEYELRCNNDPPMCISRTITVTATNFCPPNALSDNGMGCPREH		133
QY	126	FDMAEPALFQIAQYRAGIVPVSFRFVPPMKKGGVRFITNGHSYFNLVLTITVAGAGVHS		185
		:	:	
Db	134	FDLAERFLPRLIEYRAGIVPWFVFRVSCVKKGGIRITNGHSYNNMLITLGSAGDITS		193
QY	186	VSIKSGRTQWQSMSTRNMGQNMOSNNYLLNGGSLFQVTLSDGRLLTATNLVPSNMQPCQTY		245
		:	:	
Db	194	VSIKSGRTQWLTPLMSRNMGQNMOSNAYLLNGOSLSFQVTLSDGRITITAVNVVPAGQWQFQTF		253
QY	246	EGHQF 250		
Db	254	EGQGF 258		

RESULT 8
T03298
expansin 2 - rice
C:Species: *Oryza sativa* (rice)
C:Date: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 21-Jul-2000
C:Accession: T03298
R:Sticheban, T.Y.; Shi, J.; Durachko, D.M.; Gultinan, M.J.; McQueen-Mason, S.J.; Shieh
Proc. Natl. Acad. Sci. U.S.A. 92, 9245-9249, 1995
A:Title: Molecular cloning and sequence analysis of expansins--a highly conserved, multi-
A:Reference number: Z14894; MUID:96016146; PMID:7568110
A:Accession: T03298
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-251 <SHC>
A:Cross-references: EMBL:U30477; NID:G1041709; PIDN:AMB38074.1; PID:G1041710
C:Genetics:
A:Gene: EXP2
C:Function:
A:Description: induces extension (creep) in plant cell
C:Superfamily: expansin

[illegible]

RESULT 9

T04175
 expansin - rice
 C:Species: Oryza sativa (rice)
 C:Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 26-May-2000
 C:Accession: T04175
 R:Cho, H.T.; Kende, H.
 Plant Cell 9, 1661-1671, 1997
 A:Title: Expression of expansin genes is correlated with growth in deepwater ce.
 A:Reference number: Z15042; MUID:97480100; PMID:9338967
 A:Accession: T04175
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-246 <CHO>
 A:Cross-References: EMBL:U85246; NID:g1815680; PIDN:AAB81662.1; PID:g1815681
 A:Experimental source: cv. Pin Gaew 56
 C:Genetics:
 A:Gene: EXP4
 C:Superfamily: expansin

Query Match 74.5%; Score 1038; DB 2; Length 246;
 Best Local Similarity 77.1%; Pred. No. 1.5e-80;
 Matches 185; Conservative 21; Mismatches 34; Indels 0; Gaps 0;

QY 11 LFLPFFFTFADYCGMOSGHATFYGGDASGTWGCAGYGNLYSGYGTNTVALSTL 70
 |||
 DB 7 LFLPLARQASAGYGGWOSAHATFYGGDASGTWGCAGYGNLYSGYGTNTVALSTL 66
 QY 71 FNNGLSCGAFEMTCTNDPKMCLPGTIRYATNFCPPNFPALPNNNGMCPNLPLOHFDMAE 130
 |||
 DB 67 FNDGAACGSCYELRCMNASCLPGSITYTATNFCPPNGLSDGCMCPNRPHPDMAE 126
 QY 131 PAFLOIAQYRAGIVPVSPFRVPCMKKGYRFTINGHSYFNLYLITNVGAGDVHSYIKG 190
 |||
 DB 127 PAFELIAQYRAGIVPVSPFRVPCMKKGYRFTINGHSYFNLYLITNVGAGDVHSYIKG 186
 QY 191 SPTGMSMRNMGQNNNNYNGGLSFQVTLSDGRTLTANLYVPSNMQPQTYGPGP 250
 |||
 DB 187 SRTGQPMRSRMGQNNQSNAPLFDGSLSFQVTLSDGRTVTSNNVAHPMGQFQTEGGQF 246

RESULT 10

T50654
 expansin EXP1 [imported] - Arabidopsis thaliana (fragment)
 C:Species: Arabidopsis thaliana (mouse-ear cress)
 C:Date: 21-Jul-2000 #sequence_revision 21-Jul-2000 #text_change 02-Sep-2000
 C:Accession: T50654
 R:Shcherban, T.Y.; Shi, J.; Durachko, D.M.; Gultinan, M.J.; McQueen-Mason, S.J.; Shieh, Proc. Natl. Acad. Sci. U.S.A. 92, 9245-9249, 1995
 A:Title: Molecular cloning and sequence analysis of expansins--a highly conserved, multi
 A:Reference number: Z14894; MUID:96016146; PMID:7568110
 A:Accession: T50654
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-237 <SHC>
 A:Cross-References: EMBL:U30476; PIDN:AAB38070.1
 C:Genetics:
 A:Gene: EXP1
 C:Function:
 A:Description: induces extension (creep) in plant cell walls
 C:Superfamily: expansin
 C:Keywords: cell wall

Query Match 74.0%; Score 1032; DB 2; Length 237;
 Best Local Similarity 79.0%; Pred. No. 4.6e-80;
 Matches 177; Conservative 23; Mismatches 24; Indels 0; Gaps 0;

QY 26 GWMOSGHATFYGGDASGTWGCAGYGNLYSGYGTNTVALSTALPNNGLSCGAFEMTC 85
 |||
 DB 12 GWMVNAHATFYGGDASGTWGCAGYGNLYSGYGTNTVALSTALPNNGLSCGAFEMTC 71
 QY 86 TNDPKMCLPGTIRYATNFCPPNFPALPNNNGMCPNLPLOHFDMAEPAFLQIAQYRAGIVP 145

DB 72 QNDGKMCPLSGISVYATNFCPPNFPALPNNNGMCPNLPLOHFDLSQVFORIAQYRAGIVP 131
 |||

QY 146 VSFRRVPCMKKGVYRFTINGHSYFNLYLITNVGAGDVHSYIKSRTGQMSMRNMGON 205
 |||
 DB 132 VAYRRVPCVRRGIRFTINGHSYFNLYLITNVGAGDVHSYIKSRTGQMSMRNMGON 191

QY 206 WOSNNYNGGLSFQVTLSDGRTLTANLYVPSNMQPQTYGPGP 249
 |||
 DB 192 WQSNYLNQGLSFQVTLSDGRTVTSNNVAHPMGQFQTEGGQF 235

RESULT 11

T50656
 expansin EXP2 [imported] - Arabidopsis thaliana
 C:Species: Arabidopsis thaliana (mouse-ear cress)
 C:Date: 21-Jul-2000 #sequence_revision 21-Jul-2000 #text_change 28-Jul-2000
 C:Accession: T50656
 R:Shcherban, T.Y.; Shi, J.; Durachko, D.M.; Gultinan, M.J.; McQueen-Mason, S.J.; Shieh, Proc. Natl. Acad. Sci. U.S.A. 92, 9245-9249, 1995
 A:Title: Molecular cloning and sequence analysis of expansins--a highly conserved, multi
 A:Reference number: Z14894; MUID:96016146; PMID:7568110
 A:Accession: T50656
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-255 <SHC>
 A:Cross-References: EMBL:U30481; PIDN:AAB38073.1
 A:Experimental source: variety Columbia
 C:Genetics:
 A:Gene: EXP2
 C:Function:
 A:Description: induces extension (creep) in plant cell walls
 C:Superfamily: expansin
 C:Keywords: cell wall

Query Match 73.9%; Score 1030; DB 2; Length 255;
 Best Local Similarity 73.6%; Pred. No. 7.3e-80;
 Matches 184; Conservative 29; Mismatches 35; Indels 2; Gaps 2;

QY 3 FSYSPSSLFLIP-FVFTFADYCGMOSGHATFYGGDASGTWGCAGYGNLYSGYGT 61
 |||
 DB 6 YSHILFLISLCTLNFLCTYINSDDNGMGRGHATFYGADASGTWGCAGYGNLYSGYGL 65
 QY 62 NTVLSTALPNNGLSCGAFEMTCTNDPKMCLPGTIRYATNFCPPNFPALPNNNGMCPN 121
 |||
 DB 66 QPALSTALPNSGQKCGACFELTCEDEBWCIPGSIIVSATNFCPPNFPALANDNGMCPN 125
 QY 122 PLOHFDMAEPAFLQIAQYRAGIVPVSPFRVPCMKKGYRFTINGHSYFNLYLITNVGAG 181
 |||
 DB 126 PLKHDLEPAFLQIAQYRAGIVPVAFRRVPCMKKGYRFTINGHSYFNLYLITNVGAG 185
 QY 182 DVHSYIKSRTG-WQMSMRNMGQNNNNYNGGLSFQVTLSDGRTLTANLYVPSNMQ 240
 |||
 DB 186 DIRAVSLKSGSKTDQMSMRNMGQNNNTYLRGQSLSFQVTLSDGRTVSYDVVPHDQ 245
 QY 241 FQGTREGQF 250
 |||
 DB 246 FQGTREGQF 255

RESULT 12

C64444
 Probable expansin [imported] - Arabidopsis thaliana
 C:Species: Arabidopsis thaliana (mouse-ear cress)
 C:Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 16-Feb-2001
 C:Accession: C64444
 R:Lin, X.; Kaul, S.; Roundley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.; M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; Vanaken, S.E.; Umayam, L.; Tallon, L.; Eues, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Frazer, C.M.; Venter, J. Nature 402, 761-768, 1999
 A:Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
 A:Reference number: AB4420; MUID:20083487; PMID:10617197
 A:Accession: C64444

A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-248 <STO>
 A:Cross-references: GB:AE002093; NID:g3461833; PIDN:AAC32927.1; GSPDB:GN00139
 C:Genetics:
 A:Gene: AC2903090
 A:Map position: 2
 C:Superfamily: expansin

Query Match 73.5%; Score 1024; DB 2; Length 248;
 Best Local Similarity 78.1%; Pred. No. 2.3e-79;

Matches 175; Conservative 23; Mismatches 26; Indels 0; Gaps 0;

QY 27 GWSGHAFFYGGDASGTMGACGYNLYSGYGTNTVALSTALFNNGLSCGACFEMTCT 86
 DB 24 GWNNAHTFYGGSDASTMGACGYNLYSGYGTNTVALSTALFNNGLSCGACFELKQ 83
 QY 87 NDRKCLPGTIRVTATNFCPPNFPALPNNNGMCPNLPQHFDMAPFLQIAYRAGIVPV 146
 DB 84 SDAMCLPGAIIVTATNFCPPNFPALPNNNGMCPNLPQHFDMAPFLQIAYRAGIVPV 143
 QY 147 SPFRVPCMKKGVRTFNGHSYFNLVLTIVVGAGDVHSVSKSRGMSMRNMGQNW 206
 DB 144 SYRRVPCMRGGIRFTNGHSYFNLVLTIVVGAGDVHSVAVKSRTRMGQMSRNMGQNW 203
 QY 207 QSNVYNGQGLSFQVTLSDGRTLTAYNLVPSNQFGQTYEGPOF 250
 DB 204 QSNVYNGQGLSFQVTLSDGRTLTAYNLVPSNQFGQTYEGPOF 247

RESULT 13

probable expansin (imported) - Arabidopsis thaliana

C:Species: Arabidopsis thaliana (mouse-ear cress)
 C>Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 16-Feb-2001

C:Accession: D84820

R:Lin, X.; Kaul, S.; Roundley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.; M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; Vanaken, S.E.; Umayam, L.; Tallon, L.; Neuse, D.; Niemann, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J. Nature 402, 761-768, 1999

A:Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
 A:Reference number: A84420; MUID:20083487; PMID:10617197

A:Accession: D84820

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-257 <STO>

A:Cross-references: GB:AE002093; NID:g2795809; PIDN:AAB97125.1; GSPDB:GN00139

C:Genetics:

A:Gene: AC2939700

A:Map position: 2

C:Superfamily: expansin

Query Match 71.2%; Score 993; DB 2; Length 257;
 Best Local Similarity 71.4%; Pred. No. 9.9e-77;

Matches 177; Conservative 24; Mismatches 37; Indels 10; Gaps 2;

QY 13 LLEFFVFTFADY-----GWSGHAFFYGGDASGTMGACGYNLYSGYGTNTV 64
 DB 8 LLEFFVFTFADY-----GWSGHAFFYGGDASGTMGACGYNLYSGYGTNTV 67
 QY 65 ALSTALFNNGLSCGACFEMTCTNDPKWCLPG--TIRVTATNFCPPNFPALPNNNGMCPN 122
 DB 68 ALSTALFNNGLSCGACFELKQANDPKWCHSGSPILITANFCPPNLPALQSDNGMCPN 127
 QY 123 LQHFDMAPFLQIAYRAGIVPVSPFRVPCMKKGVRTFNGHSYFNLVLTIVVGAGD 182
 DB 128 REHFDMAPFLQIAYRAGIVPVSPFRVPCMKKGVRTFNGHSYFNLVLTIVVGAGD 187
 QY 183 VHSVSKSRGMSMRNMGQNSNLYNGQLSFQVTLSDGRTLTAYNLVPSNQFG 242
 DB 188 VHSVSKSRGMSMRNMGQNSNLYNGQLSFQVTLSDGRTLTAYNLVPSNQFG 247
 QY 243 QTYEGPOF 250

DB 248 QTFVGNKF 255

RESULT 14

expansin-like protein - Arabidopsis thaliana

N:Alternate names: protein T22E16.160

C:Species: Arabidopsis thaliana (mouse-ear cress)

C>Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 26-May-2000

C:Accession: T47689

A:Reference number: Z24472

A:Accession: T47689

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-260 <BEN>

A:Cross-references: EMBL:AL132975

A:Experimental source: cultivar Columbia; BAC clone T22E16

C:Genetics:

A:Map position: 3

A:Insertions: 52/1; 158/2

A:Note: T22E16.160

C:Superfamily: expansin

Query Match 70.2%; Score 979; DB 2; Length 260;
 Best Local Similarity 67.5%; Pred. No. 1.5e-75;

Matches 172; Conservative 28; Mismatches 45; Indels 10; Gaps 2;

QY 6 SPFSFLLEFFVFTFADY-----GWSGHAFFYGGDASGTMGACGYNLYSQ 57
 DB 4 NPILILITFLFLSLFTDAGIRPVSGSMQTAHTFYGNDASGTMGACGYNLYSQ 63
 QY 58 GYGTNTVALSTALFNNGLSCGACFEMTCTNDPKWCLPG--TIRVTATNFCPPNFPALPNN 115
 DB 64 GYGTNTVALSTALFNNGLSCGACFELKQANDPKWCHSGSPILITANFCPPNLPALQSDNG 123
 QY 116 GWSGHAFFYGGDASGTMGACGYNLYSGYGTNTVALSTALFNNGLSCGACFEMTCTNDPKWCLPG 175
 DB 124 GWSGHAFFYGGDASGTMGACGYNLYSGYGTNTVALSTALFNNGLSCGACFEMTCTNDPKWCLPG 183
 QY 176 NVGAGDVHSVSKSRGMSMRNMGQNSNLYNGQLSFQVTLSDGRTLTAYNLV 235
 DB 184 NVGAGDVHSVSKSRGMSMRNMGQNSNLYNGQLSFQVTLSDGRTLTAYNLV 243
 QY 236 PSNWQFGQTYEGPOF 250
 DB 244 PSNWQFGQTYEGPOF 258

RESULT 15

expansin 1 - tomato

C:Species: Lycopersicon esculentum (tomato)

C>Date: 14-May-1999 #sequence_revision 14-May-1999 #text_change 26-May-2000

C:Accession: T07630

R:Rose, U.K.C.; Lee, H.H.; Bennett, A.B.

Proc. Natl. Acad. Sci. U.S.A. 94, 5955-5960, 1997

A:Title: Expression of a divergent expansin gene is fruit-specific and ripening-regulat

A:Reference number: Z16063; MUID:97303239; PMID:9159182

A:Accession: T07630

A:Status: preliminary; translated from GB/EMBL/DBEST

A:Molecule type: mRNA

A:Residues: 1-261 <ROS>

A:Cross-references: EMBL:U82123; NID:g2062420; PIDN:AAC63088.1; PID:g2062421

A:Experimental source: cultivar Castlemart; fruit

C:Genetics:

A:Gene: EXP1

A:Note: specifically expressed in ripening fruit, regulated by ethylene

C:Superfamily: expansin

Query Match 68.1%; Score 949.5; DB 2; Length 261;

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 18, 2003, 17:45:48 ; Search time 18 Seconds
(without alignments)

653.149 Million cell updates/sec

Title: US-09-383-579c-10

Perfect score: 1394
Sequence: 1 MAFSYSPFSLFLPFEEVF.....AYNLVPSNMQFGQYEGPQP 250

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_41.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1085	77.8	253	1	EXP8_ARATH
2	1041	74.7	249	1	EX10_ARATH
3	1036.5	74.4	250	1	EXP1_ARATH
4	1030	73.9	255	1	EXP2_ARATH
5	1024	73.5	248	1	EX15_ARATH
6	993	71.2	257	1	EXP4_ARATH
7	979	70.2	260	1	EX16_ARATH
8	965	69.2	255	1	EX14_ARATH
9	944	67.7	262	1	EXP3_ARATH
10	939	67.0	259	1	EXP6_ARATH
11	934	67.0	258	1	EXP9_ARATH
12	889.5	63.8	255	1	EXP5_ARATH
13	865.5	62.1	252	1	EX11_ARATH
14	858.5	60.2	255	1	EX17_ARATH
15	748	53.7	273	1	EX22_ARATH
16	741	53.2	279	1	EX26_ARATH
17	735	52.7	269	1	EX23_ARATH
18	735	52.7	276	1	EX25_ARATH
19	718.5	51.5	262	1	EXP7_ARATH
20	711.5	49.6	312	1	EX24_ARATH
21	692	49.6	257	1	EX18_ARATH
22	679.5	48.7	266	1	EX13_ARATH
23	669	48.0	252	1	EX12_ARATH
24	613	44.0	256	1	EX21_ARATH
25	604	40.3	256	1	EX20_ARATH
26	283.5	20.0	264	1	EXB1_ARATH
27	279	19.8	271	1	EXB2_ARATH
28	276.5	19.6	259	1	EXB4_ARATH
29	243	17.6	269	1	EXB4_MAIZE
30	243	17.1	263	1	MPH1_PHLPR
31	239	16.7	265	1	MPH1_HOILA
32	232.5	16.4	263	1	MPH1_LOLPR
33	229	16.4	263	1	PL4946 lolium pere

34	228	16.4	246	1	MPCL_CYNDA	004701 cynodon dac
35	220.5	15.8	269	1	MPAL_PHAQA	041260 phalaris eq
36	217.5	15.6	265	1	EX11_ARATH	091274 arabidopsis
37	209	15.0	263	1	EX13_ARATH	091255 arabidopsis
38	206.5	14.8	250	1	EXR1_ARATH	023547 arabidopsis
39	206	14.8	265	1	EXL2_ARATH	095655 arabidopsis
40	203.5	14.6	264	1	EXB5_ARATH	092033 arabidopsis
41	192.5	13.8	263	1	MP01_ORYZA	040638 oryza sativ
42	185	13.3	191	1	EXB8_MAIZE	007154 zea mays (m
43	112.5	8.1	242	1	GUNS_TRIPE	P43317 trichoderma
44	111.5	8.0	123	1	EXR2_ARATH	090052 arabidopsis
45	99	7.1	1385	1	YMS5_CAEL	P34501 caenorhabdi

ALIGNMENTS

RESULT 1	EXP8_ARATH	STANDARD;	PRT;	253 AA.
ID	EXP8_ARATH			
AC	022874;			
DT	28-FEB-2003 (Rel. 41, Created)			
DT	28-FEB-2003 (Rel. 41, Last sequence update)			
DT	28-FEB-2003 (Rel. 41, Last annotation update)			
DE	Alpha-expansin 8 precursor (At-EXP8) (AtEx8) (Ath-ExpAlpha-1.11).			
GN	EXP8 OR AT2G40610 OR T2P4.4.			
OS	Arabidopsis thaliana (Mouse-ear cress).			
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;			
OC	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;			
OC	eurosid II; Brassicales; Brassicaceae; Arabidopsis.			
ON	NCBI_TaxID=3702;			
RX	1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=cv. Columbia;			
RX	MEDLINE=20083487; PubMed=10617197;			
RA	Liu X., Kaul S., Rounsley S.D., Shea T.P., Benito M.-I., Town C.D.,			
RA	Fuji C.Y., Mason T.M., Bowman C.L., Barnstead M.E., Feldblyum T.V.,			
RA	Buell C.R., Ketchum K.A., Lee J.J., Rouning C.M., Koo H.L.,			
RA	Moffet K.S., Cronin L.A., Shen M., Pat G., Van Aken S., Umayam L.,			
RA	Tallon L.J., Gill J.E., Adams M.D., Carrera A.J., Creasy T.H.,			
RA	Goodman H.M., Somerville C.R., Copenhaver G.P., Preuss D.,			
RA	Nierman W.C., White O., Bisen J.A., Salzberg S.L., Frazer C.M.,			
RA	Venter J.C.;			
RT	"sequence and analysis of chromosome 2 of the plant Arabidopsis			
RT	thaliana.";			
RL	Nature 402:761-768(1999).			
CC	-1- FUNCTION: Causes loosening and extension of plant cell walls by			
CC	disrupting noncovalent bonding between cellulose microfibrils and			
CC	matrix glucans. No enzymatic activity has been found (by			
CC	similarity).			
CC	-1- SUBCELLULAR LOCATION: Cell-wall bound.			
CC	-1- SIMILARITY: BELONGS TO THE EXPANSIN FAMILY.			
CC	-1- SIMILARITY: Contains 1 expansin-like EG45 domain.			
CC	-1- SIMILARITY: Contains 1 expansin-like CBD domain.			
CC	-1- DATABASE: NMB=EXPANSIN homepage;			
CC	WWW="http://www.bio.pau.edu/expansins/".			
CC	-----			
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration			
CC	between the Swiss Institute of Bioinformatics and the EMBL outstation -			
CC	the European Bioinformatics Institute. There are no restrictions on its			
CC	use by non-profit institutions as long as its content is in no way			
CC	modified and this statement is not removed. Usage by and for commercial			
CC	entities requires a license agreement (See http://www.isb-sib.ch/announce/			
CC	or send an email to license@isb-sib.ch).			
CC	-----			
DR	EMBL; AC002336; AAB87577.1; -			
DR	PIR; P84831; P84831.			
DR	InterPro; IPR007112; Expan_endogl.			
DR	InterPro; IPR007118; Expan_loi_pi.			
DR	InterPro; IPR007117; Expan_loi_pi_c.			
DR	Pfam; PF01357; Pollen_allergen; 1.			
DR	PRINTS; PR01225; EXPANSINPAMLY.			
DR	ProDom; PD002179; Expan_loi_pi_c; 1.			

```

DR PROSITE; PS50843; EXPANSIN_CBD; 1.
DR PROSITE; PS50842; EXPANSIN_EG45; 1.
KW Cell wall; Signal; Multigene family.
FT SIGNAL 1 25 POTENTIAL.
FT CHAIN 26 253 ALPHA-EXPANSIN 8.
FT DOMAIN 48 160 EXPANSIN-LIKE EG45.
FT DOMAIN 170 250 EXPANSIN-LIKE CBD.
SQ SEQUENCE 253 AA; 27260 MW; 08C42880D523DD8A CRC64;

Query Match
Best Local Similarity 77.8%; Score 1085; DB 1; Length 253;
Matches 194; Conservative 22; Mismatches 31; Indels 2; Gaps 2;

QY 4 SYSPSSFLPLPPFY-FFPADYGMQSGHATFYGGSDASGTMGACGCGNLVSGYGTN 62
DB 5 SYLKSTSIISIVLFQGTGHGDGQGGCHATFYGGEDASGTMGACGCGNLVSGYGTN 64
QY 63 TVALSTALFNNGLSGACFEMTCTNDPKMCLPGTRVFTATNFCPPALPNNNGMCNPP 122
DB 65 TVALSTALFNNGLSGACFEMTCTNDPKMCLPGTRVFTATNFCPPALPNNNGMCNPP 124
QY 123 LQHPMAEPFLQIAQYRAGIVPVSPFRVPCMKKGGVFTINGHSYFNLVLTNNGACD 182
DB 125 LQHPMAEPFLQIAQYRAGIVPVSPFRVPCMKKGGVFTINGHSYFNLVLTNNGACD 184
QY 183 VHSVSIKSGRT-GMQSMSPNNQGNQSNLYLNGGLSFVYTTSDGRTLTAVNLVPSNQPF 241
DB 185 VHAVSIKSGRTQSWQMSRNNQGNQSNLYLNGGLSFVYTTSDGRTLTAVNLVPSNQPF 244
QY 242 GQTYGSGQPF 250
DB 245 GQTYGSGQPF 253

RESULT 2
EX10 ARAWH STANDARD; PRT; 249 AA.
ID EX10 ARAWH
AC Q9LDR3;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE ALPHA-expansin 10 precursor (Ac-EXP10) (AtEXP10) (Ach-Exp1alpha-1.1).
GN EXP10 OR AT1G26770 OR T24P13_14 OR T24P13.15.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eucoside II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_Taxid=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Columbia;
RX MEDLINE=20402612; PubMed=10931949;
RA Buehler E., Chan A., Chao Q., Chen H., Cheuk R.F., Chin C.W.,
RA Chung M.K., Conn L., Conway A.B., Conway A.R., Creasy T.H., Dewar K.,
RA Dunn P., Eguu P., Feildlyum T.V., Feng J.-D., Fong B., Fujii C.Y.,
RA Gill J.E., Goldsmith A.D., Haas B., Hansen N.F., Hughes B., Huizer L.,
RA Hunter J.L., Jenkins J., Johnson-Hopson C., Khan S., Khaykin E.,
RA Kim C.-U., Koo H.L., Kremenetskaia I., Kurtz D.B., Kwan A., Lam B.,
RA Langin-Hooper S., Lee A., Lee J.M., Lenz C.A., Li J.H., Li Y.-P.,
RA Lin X., Liu S.X., Liu Z.A., Lueros J.S., Malt R., Marziani A.,
RA Miltischer J., Miranda M., Nguyen M., Niemman W.C., Osborne B.I.,
RA Pal G., Peterson J., Pham P.K., Rizzo M., Rooney T., Rowley D.,
RA Sakano H., Salzberg S.L., Schwartz J.R., Shinn P., Southwick A.M.,

```

```

RA Sun H., Tallon L.J., Tambunga G., Toriumi M.J., Town C.D.,
RA Uteerbock T., Van Aken S., Vayenberg M., Vysotskaia V.S., Walker M.,
RA Wu D., Yu G., Fraser C.M., Venter J.C., Davis R.W.;
RA "Sequence and analysis of chromosome 1 of the plant Arabidopsis
RA thaliana.";
RL Nature 408:816-820 (2000).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Columbia;
RA Shinozaki K., Davis R.W., Ecker J.R., Theologis A.;
RT "Riken Arabidopsis full length cDNA clones (RAFLs) sequenced by the
RT SSP consortium (Salk/Stanford/PGE)" ;
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: Causes loosening and extension of plant cell walls by
CC disrupting noncovalent bonding between cellulose microfibrils and
CC matrix glycans. No enzymatic activity has been found. Plays a
CC major role in control of leaf growth and influences the mechanical
CC breakage behavior of the pedicel.
CC -1- SUBCELLULAR LOCATION: Cell-wall bound.
CC -1- TISSUE SPECIFICITY: Most highly expressed in the young leaf
CC petiole and midrib, in trichomes and at the base of the pedicel.
CC -1- DEVELOPMENTAL STAGE: Expression is first seen at the base of the
CC emerging first two true leaves but not of the cotyledons. As leaf
CC development progresses expression begins in the base of the
CC petiole and gradually extends toward the whole midrib and later it
CC is restricted to the vasculature of the petiole and leaf blade and
CC disappears as the leaf matures.
CC -1- SIMILARITY: BELONGS TO THE EXPANSIN FAMILY.
CC -1- SIMILARITY: Contains 1 expansin-like EG45 domain.
CC -1- SIMILARITY: Contains 1 expansin-like CBD domain.
CC -1- DATABASE: NAME=EXPANSIN homepage;
CC WWW="http://www.bio.psu.edu/expansins/".
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation
CC at the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; AF229437; AAF61712.1; -
DR EMBL; AF229431; AAF61713.1; -
DR EMBL; AC006535; AAF87031.1; -
DR EMBL; AY052247; AAK97717.1; -
DR InterPro; IPR007112; Expan_endogl.
DR InterPro; IPR007118; Expan_lo1_pi.
DR InterPro; IPR007117; Expan_lo1_pi_C.
DR Pfam; PF01357; Pollen_allergen_1.
DR PRINTS; PR01225; EXPANSINPMLX.
DR PRODOM; PD002179; Expan_lo1_pi_C; 1.
DR PROSITE; PS50843; EXPANSIN_CBD; 1.
DR PROSITE; PS50842; EXPANSIN_EG45; 1.
KW Cell wall; Signal; Multigene family.
FT SIGNAL 1 21 POTENTIAL.
FT CHAIN 22 249 ALPHA-EXPANSIN 10.
FT DOMAIN 44 156 EXPANSIN-LIKE EG45.
FT DOMAIN 166 245 EXPANSIN-LIKE CBD.
SQ SEQUENCE 249 AA; 26428 MW; 63D014410D4ABBA1 CRC64;

Query Match
Best Local Similarity 74.7%; Score 1041; DB 1; Length 249;
Matches 179; Conservative 23; Mismatches 23; Indels 0; Gaps 0;

QY 26 GSGMGHATFYGGSDASGTMGACGCGNLVSGYGTNTVALSTALFNNGLSGACFEMTC 85
DB 24 GSHINAHATFYGGSDASGTMGACGCGNLVSGYGTSTALSTALFNNGLSGSCGCEINC 83
QY 86 TNDPWCPLPGTRVATNFCPPNFPALPNNNGMCNPPLOHPMAEPFLQIAQYRAGIYP 145
DB 84 ENDGKWCPLPGSIVATNFCPPNFPALPNNNGMCNPPLEHPFLAOPVFORIAQYRAGIYP 143
QY 146 VSPFRVPCMKKGGVFTINGHSYFNLVLTNNGACGADVHVSISKSGRTQSWQMSRNNQGN 205

```



```

DB 144 VSTRVRCRRRGGRFTINGHSYNLVLITVNGAGVHSAIGSPRTVQMSRNGON 203
QY 206 MOSNNYINCOGLSFQVTLSDGRTLTAVNLVPSNMQFQVGPQF 250
DB 204 MOSNYINCOGLSFQVTLSDGRTLTAVNLVPSNMQFQVGPQF 248

RESULT 3
EXPL_ARATH STANDARD; PRT; 250 AA.
AC 09C554: 038863;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DE Alpha-expansin 1 precursor (At-EXP1) (AtEx1) (Ath-ExpAlpha-1.2).
GN EXP1 OR AT1G69530 OR P10D13.18.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OC NCBI_TaxID=3702;
RN 1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Columbia;
RX MEDLINE=21016719; PubMed=11130712;
RA Theologis A., Ecker J.R., Palm C.J., Federspiel N.A., Kaul S.,
RA White O., Alonso J., Altieri H., Araujo R., Bowman C.L., Brooks S.Y.,
RA Buehler E., Chan A., Chao Q., Chen H., Cheuk R.F., Chin C.W.,
RA Chung M.K., Conn L., Conway A.B., Conway A.R., Creasy T.H., Dewar K.,
RA Dunn P., Egu P., Feldblum T.V., Fang J.-D., Fong B., Fujii C.Y.,
RA Gali J.E., Goldsmith A.D., Haas B., Hansen N.F., Hughes B., Hutzar L.,
RA Hunter J.L., Jenkins J., Johnson-Hopson C., Khan S., Khaykin E.,
RA Kim C.J., Koo H.L., Kremenetskaia I., Kurtz D.B., Kwan A., Lam B.,
RA Langin-Hooper S., Lee A., Lee J.M., Lenz C.A., Li J.H., Li Y.-P.,
RA Lin X., Liu S.X., Liu Z.A., Lueros U.S., Maltl R., Marzilli A.,
RA Milschker J., Miranda M., Nguyen M., Nierman W.C., Osborne B.I.,
RA Pal G., Peterson J., Pham P.K., Rizzo M., Rooney T., Rowley D.,
RA Sakano H., Salzberg S.L., Schwartz J.R., Shinn P., Southwick A.M.,
RA Sun H., Tallon L.J., Tambunga G., Tortum M.J., Town C.D.,
RA Uterback T., Van Aken S., Vaysberg M., Vysotskaia V.S., Walker M.,
RA Wu D., Yu G., Fraser C.M., Venter J.C., Davis R.W.;
RT "Sequence and analysis of chromosome 1 of the plant Arabidopsis
RT thaliana."
RL Nature 408:816-820(2000).
RN 2]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Columbia;
RA Shinzaki K., Davis R.W., Ecker J.R., Theologis A.;
RT "RIKEN Arabidopsis full length cDNA clones (RAFLs) sequenced by the
RT SGP consortium (Salk/Stanford/PGEC).";
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
RN 3]
RP SEQUENCE OF 14-250 FROM N.A.
RX MEDLINE=96016146; PubMed=7568110;
RA Sheehar T.Y., Shi J., Duracko D.M., Gullitman M.J.,
RA McQueen-Nason S.J., Shieh M., Cosgrove D.J.;
RT "Molecular cloning and sequence analysis of expansin - a highly
RT conserved, multigene family of proteins that mediate cell wall
RT extension in plants."
RL Proc. Natl. Acad. Sci. U.S.A. 92:9245-9249(1995).
RN 4]
RP TISSUE SPECIFICITY.
RA Duracko D.M., Cosgrove D.J.;
RT "Expression patterns for selective expansin genes in Arabidopsis.";
RL (in) Abstracts of Plant Biology '99: The annual meeting of the
RL American Society of Plant Physiologists, abstract#56, Baltimore
RL (1999).
CC -1- FUNCTION: Causes loosening and extension of plant cell walls by
CC disrupting noncovalent bonding between cellulose microfibrils and
CC matrix glucans. No enzymatic activity has been found (by
CC similarity).
CC -1- SUBCELLULAR LOCATION: Cell-wall bound.

```

```

CC -1- TISSUE SPECIFICITY: Expressed in stomatal guard cells and very
CC young vascular bundles throughout the plant.
CC -1- SIMILARITY: BELONGS TO THE EXPANSIN FAMILY.
CC -1- SIMILARITY: Contains 1 expansin-like EG45 domain.
CC -1- SIMILARITY: Contains 1 expansin-like CBD domain.
CC -1- DATABASE: NAME=EXPANSIN homepage;
CC WWW=http://www.bio.psu.edu/expansins/.
CC -----
CC THIS SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.iesb.ch/announce/
CC or send an email to license@iesb-sib.ch).
CC -----
DR EMBL; AC073178; AAG60095.1; -
DR EMBL; AF360291; AAK26001.1; -
DR EMBL; AY051047; AAK93724.1; -
DR EMBL; AY058193; AAL25606.1; -
DR EMBL; U30476; AAB38070.1; -
DR PIR; T50654; T50654.
DR InterPro; IPR007112; Expan_endogl.
DR InterPro; IPR007118; Expan_lo1_pi.
DR InterPro; IPR007117; Expan_lo1_pi_C.
DR Pfam; PF01357; Pollen allergen; 1.
DR PRINTS; PR01225; EXPANSINFAMLY.
DR ProDom; PD002179; Expan_lo1_pi_C; 1.
DR PROSITE; PS50843; EXPANSIN_CBD; 1.
DR PROSITE; PS50842; EXPANSIN_EG45; 1.
KW Cell wall; Signal; Multigene family.
FT SIGNAL 1 17 POTENTIAL.
FT CHAIN 18 250 ALPHA-EXPANSIN 1.
FT DOMAIN 45 157 EXPANSIN-LIKE EG45.
FT DOMAIN 167 246 EXPANSIN-LIKE CBD.
FT CONFLICT 14 18 AMTSH -> NSARD (IN REF. 1).
SQ SEQUENCE 250 AA; 26518 MW; 1D95EBA24FCFB7E5 CRC64;

Query Match 74.4%; Score 1036.5; DB 1; Length 250;
Best Local Similarity 73.6%; Pred. No. 2.2e-81;
Matches 181; Conservative 25; Mismatches 31; Indels 9; Gaps 1;

QY 13 LRPFFVFPFADY-----GGMOSGATFFYGGDASGTMGACGYNLYSGYGTNT 63
DB 3 LVTFLEFATIGANTSHVNGAGGWNNAHATFFGCGDASGTMGACGYNLYSGYGTNT 62
QY 64 VALSTALPNNGLSCGACFENCTNDPRKCLPGTIRVATNFCPPNFPALPNNNGCMCNPL 123
DB 63 AALSTALPNNGLSCGACFETRCQNDGKMLPGSIVVTATNFCPPNFPALPNNNGCMCNPL 122
QY 124 QHEDMAEPALQIAQVRAGIVPSPRRVPCMKKGVRFTINGHSYNFLVLTIVGAGADV 183
DB 123 QHFDLSQPVFORIAQVRAGIVPAPVRRVPCVRGGIRFTINGHSYNFLVLTIVGAGADV 182
QY 184 HSYISIGSRGTMOSMSRNMGMQNSNNYINCOGLSFQVTLSDGRTLTAVNLVPSNMQFQ 243
DB 183 HSMVWGSRTGMQMSRNMGMQNSNNYINCOGLSFQVTLSDGRTLTAVNLVPSNMQFQ 242
QY 244 TYEGPQ 249
DB 243 TFGAQ 248

RESULT 4
EXPL_ARATH STANDARD; PRT; 255 AA.
AC 038866: 09FLC5;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DE Alpha-expansin 2 precursor (At-EXP2) (AtEx2) (Ath-ExpAlpha-1.12).
GN EXP2 OR AT5G05290 OR K18123.9.
OS Arabidopsis thaliana (Mouse-ear cress).

```

```

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eustoid II; Brassicales; Brassicaceae; Arabidopsis.
OK NCBI_TaxID=3702;
(1)
RN SEQUENCE FROM N.A.
RP MEDLINE=96016146; PubMed=7568110;
RX Shcherban T.Y., Shi J., Durachko D.M., Gultinan M.J.,
RA McQueen-Mason S.J., Shien M., Cosgrove D.J.;
RT "Molecular cloning and sequence analysis of expansins - a highly
RT conserved, multigene family of proteins that mediate cell wall
RT extension in plants.";
RL Proc. Natl. Acad. Sci. U.S.A. 92:9245-9249(1995).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Columbia;
RX MEDLINE=98344145; PubMed=9679202;
RA Kaneko T., Koriaki H., Nakamura Y., Sato S., Asamizu E., Miyajima N.,
RA Tabata S.;
RT "Structural analysis of Arabidopsis thaliana chromosome 5. V. Sequence
RT features of the regions of 1,381,565 bp covered by twenty one
RT physically assigned P1 and TAC clones.";
RL DNA Res. 5:131-145(1998).
CC -1- FUNCTION: Causes loosening and extension of plant cell walls by
CC disrupting noncovalent bonding between cellulose microfibrils and
CC matrix glucans. No enzymatic activity has been found (By
CC similarity).
CC -1- SUBCELLULAR LOCATION: Cell-wall bound.
CC -1- SIMILARITY: BELONGS TO THE EXPANSIN FAMILY.
CC -1- SIMILARITY: Contains 1 expansin-like EG45 domain.
CC -1- SIMILARITY: Contains 1 expansin-like CBD domain.
CC -1- DATABASE: NAME=EXPANSIN homepage;
CC WWW="http://www.bio.psu.edu/expansins/".
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL, U30481; AAB38073.1; -.
DR EMBL, AB010692; BAB09972.1; -.
DR PIR, T50656; T50656.
DR InterPro: IPR007112; Expan_endogl.
DR InterPro: IPR007118; Expan_Lol_PI.
DR InterPro: IPR007117; Expan_Lol_PI_C.
DR Pfam: PF01357; Pollen_allergen.1.
DR PRINTS: PR01225; EXPANSIN_FAMLY.
DR ProDom: PD002179; Expan_Lol_PI_C; 1.
DR PROSITE, PS50843; EXPANSIN_CBD; 1.
DR PROSITE, PS50842; EXPANSIN_EG45; 1.
DR Cell wall, Signal; Multigene family.
FT SIGNAL 1 26 POTENTIAL.
FT CHAIN 27 255 ALPHA-EXPANSIN 2.
FT DOMAIN 50 162 EXPANSIN-LIKE EG45.
FT DOMAIN 172 252 EXPANSIN-LIKE CBD.
FT CONFLICT 88 88 T -> Q (IN REF. 2).
FT CONFLICT 255 255 AA; 27722 MW; 2785F0827A285500 CRC64;
SQ SEQUENCE 255 AA; 27722 MW; 2785F0827A285500 CRC64;
Query Match 73.9%; Score 1030; DB 1; Length 255;
Best Local Similarity 73.6%; Pred. No. 8.1e-81;
Matches 184; Conservative 29; Mismatch 35; Indels 2; Gaps 2;
3 FSYSPSPSFLLPF-FVFETPADYGGMGSHATFYGGSGASGTMGACGYNYSGGYG 61
6 YSHILFLSLCTLANFCIYSTNSDNGMGWEGHATFYGGADSGMGACGYNLHSGGYGL 65
62 NTVALSTALFNNGLSCGACFEMTCTNDPKMCLPGITRVATINFCPNFALPNNNGCMCP 121
66 QTPAALSTALFNSQKGCACGACELTCDPEMCIPIGSLIVSATINCPNPFALANDNGCMCP 125

```

```

QY 122 PLOHFMABEAPLQIAOYRAGIVPVSFRRVPCMKKGAVFTLNGSYFNLVLITNVGAG 181
DB 126 PUKHFDLBPAPLQIAOYRAGIVPVSFRRVPCMKKGAVFTLNGSYFNLVLITNVGAG 185
QY 182 DVHSVSIKSGSRGTG-WQSMRNMGMQMSNNYLNQGLSFQVTLSDGRTLTAYNLPSNMQ 240
DB 186 DIRAVSLKSGSKTDQMSRNMGMQMSNNYLNQGLSFQVTLSDGRTLTAYNLPSNMQ 245
QY 241 FQGTTEGGPOF 250
DB 246 FQGTTEGGPOF 255
RESULT 5
EX15_ARATH STANDARD; PRT; 248 AA.
ID EX15_ARATH
AC 080622;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Alpha-expansin 15 precursor (Ac-EXP15) (Atch-Expalpha-1.3).
GN EXP15 OR AT2G03090 OR T17M13.26.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eustoid II; Brassicales; Brassicaceae; Arabidopsis.
OK NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Columbia;
RX MEDLINE=20083487; PubMed=10617197;
RA Lin X., Kaul S., Rounsley S.D., Shea T.P., Benito M.-I., Town C.D.,
RA Fujii C.Y., Mason T.M., Bowman C.L., Barnstead M.E., Feldblum T.V.,
RA Buehl C.R., Ketchum K.A., Lee J.J., Rongting C.M., Koo H.L.,
RA Moffat K.S., Cronin L.A., Shen M., Pal G., Van Aken S., Umayam L.,
RA Tallon L.J., Gill J.E., Adams M.D., Carrera A.J., Creasy T.H.,
RA Goodman H.M., Somerville C.R., Copenhaver G.P., Preuss D.,
RA Nierman W.C., White O., Eisen J.A., Salzberg S.L., Fraser C.M.,
RA Venter J.C.;
RT "Sequence and analysis of chromosome 2 of the plant Arabidopsis
RT thaliana.";
RL Nature 402:761-768(1999).
CC -1- FUNCTION: Causes loosening and extension of plant cell walls by
CC disrupting noncovalent bonding between cellulose microfibrils and
CC matrix glucans. No enzymatic activity has been found (By
CC similarity).
CC -1- SUBCELLULAR LOCATION: Cell-wall bound.
CC -1- SIMILARITY: BELONGS TO THE EXPANSIN FAMILY.
CC -1- SIMILARITY: Contains 1 expansin-like EG45 domain.
CC -1- SIMILARITY: Contains 1 expansin-like CBD domain.
CC -1- DATABASE: NAME=EXPANSIN homepage;
CC WWW="http://www.bio.psu.edu/expansins/".
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL, AC004138; AAC32927.1; -.
DR PIR, C84444; C84444.
DR InterPro: IPR007112; Expan_endogl.
DR InterPro: IPR007118; Expan_Lol_PI.
DR InterPro: IPR007117; Expan_Lol_PI_C.
DR Pfam: PF01357; Pollen_allergen.1.
DR PRINTS: PR01225; EXPANSIN_FAMLY.
DR ProDom: PD002179; Expan_Lol_PI_C; 1.
DR PROSITE, PS50843; EXPANSIN_CBD; 1.
DR PROSITE, PS50842; EXPANSIN_EG45; 1.
DR Cell wall, Signal; Multigene family.
FT SIGNAL 1 20 POTENTIAL.

```

```

FT CHAIN 21 248 ALPHA-EXPANSIN 15.
FT DOMAIN 43 155 EXPANSIN-LIKE EG45.
FT DOMAIN 165 244 EXPANSIN-LIKE CBD.
SQ SEQUENCE 248 AA; 26482 MW; 29E3199269B71271 CRC64;

Query March 73.5%; Score 1024; DB 1; Length 248;
Best Local Similarity 78.1%; Pred. No. 2.5e-80;
Matches 175; Conservative 23; Mismatches 26; Indels 0; Gaps 0;

QY 27 GWSGHATFYGGDASGTMGACGYNLYSGYGTNTVALSTALFNNGLSGACPEMCT 86
DB 24 GVVNAHATFYGGSDASGTMGACGYNLYSGYGTNTVALSTALFNNGLSGACPEMCT 83
QY 87 NDPKMLPRTTRVATATNFCPPNFALPNNNGWCNPPLOHFMABPAFLQIAQYRAGIVPV 146
DB 84 SDGAMCIEGALIVATATNFCPPNFALPNNAGWCNPPLOHFMABPAFLQIAQYRAGIVPV 143
QY 147 SFRVPCMKKGGVFTTNGHSYFNLVLTNAGAGDVHVSIGKSGRTGWSNRNMGQNW 206
DB 144 SYRRVPCMRGGRGIRTTNGHSYFNLVLTNAGAGDVHVSIVKSGRTGWSNRNMGQNW 203
QY 207 QSNVYNGQGLSFQVTLSDGRTLTPAVNLVPSNMOPGQYEGPOF 250
DB 204 QSNVYNGQGLSFQVTLSDGRTLTPAVNLVPSNMOPGQYEGPOF 247

RESULT 6
EXP4 ARATH STANDARD; PRT; 257 AA.
ID EXP4 ARATH STANDARD; PRT; 257 AA.
AC 04818;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DE 28-FEB-2003 (Rel. 41, Last annotation update)
DE Alpha-expansin 4 precursor (At-EXP4) (AtEx4) (Ath-ExpAlpha-1.6).
GN EXP4 OR AT2G39700 OR F17A14.7.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC euroids II; Brassicales; Brassicaceae; Arabidopsids.
OX NCBI_TaxID=3702;
RN 1;
RP SEQUENCE FROM N.A.
RC MEDLINE=20083487; PubMed=10617197;
RX Lin X., Kaul S., Rounsley S.D., Shea T.P., Benito M.-I., Town C.D.,
RA Fujii C.Y., Mason T.M., Bowman C.L., Barnstead M.E., Feldhym T.V.,
RA Buell C.R., Ketchum K.A., Lee J.J., Roming C.M., Koo H.L.,
RA Moffat K.S., Cronin L.A., Shen M., Pai G., Van Aken S., Umeyam L.,
RA Tallon L.J., Gill J.E., Adams M.D., Carrera A.J., Creasy T.H.,
RA Goodman H.M., Somerville C.R., Coppenhaver G.P., Preuss D.,
RA Nierman W.C., White O., Eisen J.A., Salzberg S.L., Fraser C.M.,
RA Venter J.C.;
RT "Sequence and analysis of chromosome 2 of the plant Arabidopsis
thaliana.";
RU Nature 402:761-768(1999).
RN 2;
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Columbia;
RA Shinozaki K., Davis R.W., Ecker J.R., Theologis A.;
RT "RIKEN Arabidopsis full length cDNA clones (RAFLs) sequenced by the
SSP consortium (Salk/Stanford/PSEC).";
RU Submitted (Aug-2001) to the EMBL/GenBank/DBJ databases.
RN 3;
RP TISSUE SPECIFICITY.
RA Durachko D.M., Cosgrove D.J.;
RT "Expression patterns for selective expansin genes in Arabidopsis.";
RU (In) Abstracts of Plant Biology '99: The annual meeting of the
American Society of Plant Physiologists, abstract#56, Baltimore
(1999).
RL -1- FUNCTION: Causes loosening and extension of plant cell walls by
disrupting noncovalent bonding between cellulose microfibrils and
matrix glucans. No enzymatic activity has been found (By
similarity).

```

```

CC -1- SUBCELLULAR LOCATION: Cell-wall bound.
CC -1- TISSUE SPECIFICITY: Expressed in the vascular bundles throughout
CC the plant.
CC -1- SIMILARITY: BELONGS TO THE EXPANSIN FAMILY.
CC -1- SIMILARITY: Contains 1 expansin-like EG45 domain.
CC -1- SIMILARITY: Contains 1 expansin-like CBD domain.
CC -1- DATABASE: NAME=EXPANSIN homepage;
CC WWW="http://www.bio.psu.edu/expansin/".
CC -----
CC This SWISS-PROT entry is copyrighted. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation-
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb.ch/announce/
CC or send an email to license@isb.ch).
CC -----
DR EMBL; AC003674; AAB97125.1; -
DR EMBL; AF410277; AAK95263.1; -
DR PIR; D84820; D84820.
DR InterPro; IPR007112; Expan_endogl.
DR InterPro; IPR007118; Expan_lo1_pi.
DR InterPro; IPR007117; Expan_lo1_pi_c.
DR Pfam; PF01357; Pollen_allergen; 1.
DR PRINTS; PR01225; EXPANSIN_FAMLY.
DR ProDom; PD002179; Expan_lo1_pi_c_1.
DR PROSITE; PS50843; EXPANSIN_CBD_1.
DR PROSITE; PS50842; EXPANSIN_EG45; 1.
DR KEGG; K01179; Signal; Multigene family.
FT SIGNAL 1 20
FT CHAIN 21 257 ALPHA-EXPANSIN 4.
FT DOMAIN 49 163 EXPANSIN-LIKE EG45.
FT DOMAIN 173 252 EXPANSIN-LIKE CBD.
SQ SEQUENCE 257 AA; 27847 MW; 5C510E930A35B736 CRC64;

Query March 71.4%; Score 993; DB 1; Length 257;
Best Local Similarity 71.4%; Pred. No. 1.2e-77;
Matches 177; Conservative 24; Mismatches 37; Indels 10; Gaps 2;

QY 13 LLPFFFTFTADY-----GWSGHATFYGGDASGTMGACGYNLYSGYGTNTV 64
DB 8 LFTTFVLFSLDARIPGIVSGAMQNAHATFYGGSDASGTMGACGYNLYSGYGTNTA 67
QY 65 ALSTALFNNGLSGACPEMCTNDPKKCLG--TIRVATNFCPPNFALPNNNGWCNPP 122
DB 68 ALSTALFNNGLSGACPEMCTNDPKKCLG--TIRVATNFCPPNFALPNNNGWCNPP 127
QY 123 LOHFDNAEPALQIAQYRAGIVPVSFRVPCMKKGGVFTTNGHSYFNLVLTNAGAGD 182
DB 128 REHFDLAMPVFLKIAQYRAGIVPVSFRVPCMRGGRGIRTTNGHSYFNLVLTNAGAGD 187
QY 183 VHSVSTGSGRTGWSNRNMGQNWQSNVYNGQGLSFQVTLSDGRTLTPAVNLVPSNMOPG 242
DB 188 IVRASVSGSGRTGWSNRNMGQNWQSNVYNGQGLSFQVTLSDGRTLTPAVNLVPSNMOPG 247
QY 243 QTEYEGPOF 250
DB 248 QTEYGNKF 255

RESULT 7
EX16 ARATH STANDARD; PRT; 260 AA.
ID EX16 ARATH STANDARD; PRT; 260 AA.
AC 02M25;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Alpha-expansin 16 precursor (At-Exp16) (AtEx16) (Ath-ExpAlpha-1.7).
GN EXP16 OR AT2G55500 OR T22E16.160.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC euroids II; Brassicales; Brassicaceae; Arabidopsids.

```

```

OK NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Columbia;
RX MEDLINE=21016720; PubMed=11130713;
RA Salomondat M., Lemcke K., Rieger M., Anseorge W., Unseld M.,
RA Fairman B., Valle G., Bloeker H., Perez-Alonso M., Oermeier B.,
RA Delany M., Boutry M., Grivell L.A., Maché R., Pulgomech P.,
RA De Simone V., Choiane N., Artiguenave F., Robert C., Brothier P.,
RA Winkler P., Cattoico L., Weissenbach J., Saurin W., Queller F.,
RA Schefer M., Mueller-Auer S., Gabel C., Fuchs M., Benes V.,
RA Wurmbach E., Drzonek H., Erle H., Jordan N., Bangert S.,
RA Wiedemann R., Kranz H., Holland R., Brandt P., Nyakatura G.,
RA Vezzi A., D'Angelo M., Pallavicini A., Toppi S., Simionati B.,
RA Conrad A., Hornischer K., Kauer G., Loehner T.-H., Nordstiek G.,
RA Reichelt J., Schaefer M., Schoen O., Barques M., Terol J., Clement J.,
RA Navarro P., Collado C., Perez-Perez A., Oetleweider B., Duchemin D.,
RA Cooke R., Lande M., Berger-Llauro C., Purnelle B., Maury D.,
RA de Haan M., Maarse A.C., Alcaraz J.-P., Cortet A., Casacuberta E.,
RA Montfort A., Argitrou A., Flores M., Liguori R., Vitale D.,
RA Manhaupt G., Haase D., Schoof H., Rudd S., Zaccaria P., Mewes H.-W.,
RA Mayer K.F.X., Kaul S., Town C.D., Koo H.L., Tallon L.J., Jenkins J.,
RA Rooney T., Rizzo M., Walts A., Utterback T., Fujii C.Y., Shea T.P.,
RA Cressy T.H., Haas B., Maiti R., Wu D., Peterson J., Van Aken S.,
RA Pai G., Wiltseher J., Sellers P., Gill J.E., Feldblyum T.V.,
RA Preuss D., Lin X., Nierman W.C., Salzberg S.L., White O., Venter J.C.,
RA Frazer C.M., Kaneo T., Nakamura Y., Sato S., Kato T., Asamizu E.,
RA Sasamoto S., Kimura T., Ideawa K., Kawashima K., Kishida Y.,
RA Kiyokawa C., Kohara M., Matsumoto M., Matsumoto A., Muraki A.,
RA Nakayama S., Nakazaki N., Shimo S., Takeuchi C., Mada T.,
RA Watanabe A., Yamada M., Yasuda M., Tabata S.;
RT "Sequence and analysis of chromosome 3 of the plant Arabidopsis
RT thaliana.";
RL Nature 408:822(2000).
CC -!- FUNCTION: Causes loosening and extension of plant cell walls by
CC disrupting noncovalent bonding between cellulose microfibrils and
CC matrix glucans. No enzymatic activity has been found (By
CC similarity).
CC -!- SUBCELLULAR LOCATION: Cell-wall bound.
CC -!- SIMILARITY: BELONGS TO THE EXPANSIN FAMILY.
CC -!- SIMILARITY: Contains 1 expansin-like EG45 domain.
CC -!- SIMILARITY: Contains 1 expansin-like CBD domain.
CC -!- DATABASE: NAME=EXPANSIN homepage;
CC WWW="http://www.bio.psu.edu/expansins/".
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: AL132975; CAB75908.1; -.
CC FIR; T47689; 147689.
CC InterPro: IPR007112; Expan_endogl.
CC InterPro: IPR007118; Expan_lo1_pi.
CC InterPro: IPR007117; Expan_lo1_pi_C.
CC Pfam: PF01357; Pollen_allergen.1.
CC PRINTS: PR01225; EXPANSIN_FAM1.
CC PRODOM: PD002179; Expan_lo1_pi_C.1.
CC DR PROSITE: PS00843; EXPANSIN_CBD.1.
CC DR PROSITE: PS00842; EXPANSIN_EG45.1.
CC KW Cell wall; Signal; Multigene family.
CC FT SIGNAL 1 23
CC FT CHAIN 1 260
CC FT DOMAIN 52 166
CC FT DOMAIN 176 255
CC FT SEQUENCE 1260 AA; 28162 MW; 1428C01FCD4E994 CRC64;
Query Match 70.2%; Score 979; DB 1; Length 260;
Best Local Similarity 67.5%; Pred. No. 1.8e-76;
Matches 172; Conservative 28; Mismatches 45; Indels 10; Gaps 2;

```

```

QY 6 SPFSLLPLPPFFVETADY-----GMSQGHATFYGGDASCTMGACGYGNLYSQ 57
DB 4 NEPLILITIFPLFLLSFTDAGIPRVFSGSGSQTAATFYGGDASCTMGACGYGNLYSQ 63
QY 58 GYNTVTLSTALPNNGLSCACFEPTCTNDPKMCLPG:-TIRVATNFCPPNLPNN 115
DB 64 GYNTVTLSTLSTLSPFSGSCGACFEIKCVNDPKMCHPNPVSFTATNFCPPNLPN 123
QY 116 GGMCPNPLQHPMAEPALQIAYRAGIVPVSPRRVPCMKKGVFTINGHSYFNLVLT 175
DB 124 GGMCPNPRSHPLAMPVFLKIAEYRAGIVPISYRVACRKSQGFRTINGHRYFNLVLT 183
QY 176 NYGAGDVHVSIVSKSRFGWQSMNRNMQMNSNYLNGGCLSPVYTLSDGRTTLAVLV 235
DB 184 NYAGAGDIALRISVKSSTGVMWSLTNNMQMNSNVLVQSLSPFRVTSDDRTSTSWNIA 243
QY 236 PSNMQFGOTYEGPOF 250
DB 244 PSNMQFGOTYEGKNF 258
RESULT 8
EX14_ARATH STANDARD; PRT; 255 AA.
ID EX14_ARATH
AC Q9FMA0;
DT 28-FEB-2003 (rel. 41, Created)
DT 28-FEB-2003 (rel. 41, Last sequence update)
DT 28-FEB-2003 (rel. 41, Last annotation update)
DE Putative alpha-expansin 14 precursor (At-EX14) (AtEX14) (Ath-
DE Exp14p1-15)
GN EXP14 OR AT5G56320 OR MCD7.4.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosid II; Brassicales; Brassicaceae; Arabidopsie.
OK NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Columbia;
RX MEDLINE=98290546; PubMed=9628582;
RA Sato S., Kaneo T., Kotani H., Nakamura Y., Asamizu E., Miyajima N.,
RA Tabata S.;
RT "Structural analysis of Arabidopsis thaliana chromosome 5. IV.
RT Sequence features of the regions of 1,456,315 bp covered by nineteen
RT physically assigned P1 and TAC clones.";
RL DNA Res. 5:41-54(1998).
CC -!- FUNCTION: Causes loosening and extension of plant cell walls by
CC disrupting noncovalent bonding between cellulose microfibrils and
CC matrix glucans. No enzymatic activity has been found (By
CC similarity).
CC -!- SUBCELLULAR LOCATION: Cell-wall bound.
CC -!- SIMILARITY: BELONGS TO THE EXPANSIN FAMILY.
CC -!- SIMILARITY: Contains 1 expansin-like EG45 domain.
CC -!- SIMILARITY: Contains 1 expansin-like CBD domain.
CC -!- DATABASE: NAME=EXPANSIN homepage;
CC WWW="http://www.bio.psu.edu/expansins/".
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: AB009049; BAB11259.1; -.
CC InterPro: IPR007112; Expan_endogl.
CC InterPro: IPR007118; Expan_lo1_pi.
CC InterPro: IPR007117; Expan_lo1_pi_C.
CC Pfam: PF01357; Pollen_allergen.1.
CC PRINTS: PR01225; EXPANSIN_FAM1.
CC PRODOM: PD002179; Expan_lo1_pi_C.1.

```

DR PROSITE; PSS0843; EXPANSIN_CBD; 1.
 DR PROSITE; PSS0842; EXPANSIN_EG45; 1.
 KM Hypothetical protein; Cell wall; Signal; Multigene family.
 FT SIGNAL 1 24 POTENTIAL.
 FT CHAIN 25 255 PUTATIVE ALPHA-EXPANSIN 14.
 FT DOMAIN 47 155 EXPANSIN-LIKE EG45.
 FT DOMAIN 169 248 EXPANSIN-LIKE CBD.
 SQ SEQUENCE 255 AA; 27733 MW; 22A7DD423381CB4E CRC64;
 Query Match 69.2%; Score 965; DB 1; Length 255;
 Best Local Similarity 75.4%; Pred. No. 2.8e-75;
 Matches 163; Conservative 18; Mismatches 37; Indels 0; Gaps 0;
 QY 27 GWSGHATFYGGSGDASGTMGACGYNLYSQGYGNTVATLSTALFNNGLSCGACFEWCT 86
 DB 28 GWNVATATFYGGADASGTMGACGYNLYSQGYGNTVATLSTALFNNGLSCGACFEWCT 87
 QY 87 NDRPWCLPTITRTATNFCPPNFALPNNNGWCNPLQHPDMAEPALQIAYRAGI 146
 DB 88 DDPKMCIGTITVTGTNFCPPNFALPNNNGWCNPLQHPDMAEPALQIAYRAGI 147
 QY 147 SFRVPCKKKGVFTNGHSYFNLVLTIVGAGDVHSVSIKSRGQSMSSRNWGM 206
 DB 148 QYRVARCKRGGIFETNGHSYFNLVLTIVGAGDVHSVSIKSRGQSMSSRNWGM 207
 QY 207 QSNVNYLNGQGLSFQVTLSDGRTLTAVNLVPSNMQFGQTYGCP 250
 DB 208 QSNVNYLNGQGLSFQVTLSDGRTLTAVNLVPSNMQFGQTYGCP 251
 RESULT 9
 EXP6_ARATH STANDARD; PRT; 262 AA.
 ID EXP6_ARATH
 AC Q80933;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Alpha-expansin 3 precursor (At-EXP3) (AtEX3) (Ath-ExpAlpha-1.9).
 GN EXP3 OR AT2G37640 OR F13M22.14.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsids.
 OC NCBI_TaxID=3702;
 RP SEQUENCE FROM N.A.
 RC STRAIN=cv. Columbia;
 RX MEDLINE=20083487; PubMed=10617197;
 RA Lin X., Kaul S., Rounsley S.D., Shea T.P., Benito M.-I., Town C.D.,
 RA Fujii C.Y., Mason T.M., Bowman C.L., Barnstead M.E., Feldblum T.V.,
 RA Buell C.R., Ketchum K.A., Lee J.C., Rinning C.M., Koh H.L.,
 RA Moffett K.S., Cronin L.A., Shen M., Pai G., Van Aken S., Umayam L.,
 RA Tallon L.J., Gill J.E., Adams M.D., Carrera A.J., Creasy T.H.,
 RA Goodman H.M., Somerville C.R., Copenhaver G.P., Preuss D.,
 RA Niernan W.C., White O., Eisen J.A., Salzberg S.L., Frazer C.M.,
 RA Venter J.C.;
 RA "Sequence and analysis of chromosome 2 of the plant Arabidopsis
 thaliana";
 RT Nature 402:761-768(1999).
 RL Nature 402:761-768(1999).
 CC - FUNCTION: Causes loosening and extension of plant cell walls by
 disrupting noncovalent bonding between cellulose microfibrils and
 matrix glucans. No enzymatic activity has been found (by
 similarity).
 CC - SUBCELLULAR LOCATION: Cell-wall bound.
 CC - SIMILARITY: BELONGS TO THE EXPANSIN FAMILY.
 CC - SIMILARITY: Contains 1 expansin-like EG45 domain.
 CC - SIMILARITY: Contains 1 expansin-like CBD domain.
 CC - DATABASE: NAME=EXPANSIN homepage;
 CC WWW="http://www.bio.psu.edu/expansins/".
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its

CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.1sb-sib.ch/announcement/>
 CC or send an email to license@1sb-sib.ch).
 CC -----
 DR EMBL; AC004684; AAC3634.1; -.
 DR PIR; T02530; T02530.
 DR InterPro; IPR007112; Expan_endogl.
 DR InterPro; IPR007118; Expan_Lol_P1.
 DR InterPro; IPR007117; Expan_Lol_P1_C.
 DR Pfam; PF01357; Pollen_allergen; 1.
 DR PRINTS; PR01225; EXPANSINFAMLY.
 DR ProDom; PD002179; Expan_Lol_P1_C; 1.
 DR PROSITE; PSS0843; EXPANSIN_CBD; 1.
 DR PROSITE; PSS0842; EXPANSIN_EG45; 1.
 KM Cell wall; Signal; Multigene family.
 FT SIGNAL 1 25 POTENTIAL.
 FT CHAIN 26 262 ALPHA-EXPANSIN 3.
 FT DOMAIN 54 168 EXPANSIN-LIKE EG45.
 FT DOMAIN 178 257 EXPANSIN-LIKE CBD.
 SQ SEQUENCE 262 AA; 28266 MW; AFC4D0EC599B4882 CRC64;
 Query Match 67.7%; Score 944; DB 1; Length 262;
 Best Local Similarity 71.8%; Pred. No. 1.8e-73;
 Matches 163; Conservative 27; Mismatches 35; Indels 2; Gaps 1;
 QY 26 GWSGHATFYGGSGDASGTMGACGYNLYSQGYGNTVATLSTALFNNGLSCGACFEWCT 85
 DB 34 GWNVATATFYGGADASGTMGACGYNLYSQGYGNTVATLSTALFNNGLSCGACFEWCT 93
 QY 86 TNDPKMCLPG--TIRVTATNFCPPNFALPNNNGWCNPLQHPDMAEPALQIAYRAGI 143
 DB 94 TDDPRKCVBPNSILVTATNFCPPNFALPNNNGWCNPLQHPDMAEPALQIAYRAGI 153
 QY 144 VPSFRVPCKKKGVFTNGHSYFNLVLTIVGAGDVHSVSIKSRGQSMSSRNWGM 203
 DB 154 VPSFRVPCKKKGVFTNGHSYFNLVLTIVGAGDVHSVSIKSRGQSMSSRNWGM 213
 QY 204 QSNVNYLNGQGLSFQVTLSDGRTLTAVNLVPSNMQFGQTYGCP 250
 DB 214 QSNVNYLNGQGLSFQVTLSDGRTLTAVNLVPSNMQFGQTYGCP 260
 RESULT 10
 EXP6_ARATH STANDARD; PRT; 259 AA.
 ID EXP6_ARATH
 AC Q3865; O81065;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Alpha-expansin 6 precursor (At-EXP6) (AtEX6) (Ath-ExpAlpha-1.8).
 GN EXP6 OR AT2G28950 OR T914.3.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsids.
 OC NCBI_TaxID=3702;
 RP SEQUENCE FROM N.A.
 RC STRAIN=cv. Columbia;
 RX MEDLINE=20083487; PubMed=7568110;
 RA Shecharben T.Y., Shi J., Durachko D.M., Gullitnan M.J.,
 RA McQueen-Mason S.J., Shieh M., Cosgrove D.J.;
 RA "Molecular cloning and sequence analysis of expansins - a highly
 RT conserved, multigene family of proteins that mediate cell wall
 RT extension in plants";
 RL Proc. Natl. Acad. Sci. U.S.A. 92:9245-9249(1995).
 CC -
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its

RA Buell C.R., Ketchum K.A., Lee J.J., Roming C.M., Koo H.L.,
RA Moffat K.S., Cronin L.A., Shen M., Raj G., Van Aken S., Unayam L.,
RA Tallon L.J., Gill J.E., Adams M.D., Carreira A.J., Creasy T.H.,
RA Goodman H.M., Somerville C.R., Copenhaver G.P., Preuss D.,
RA Nieman W.C., White O., Eisen J.A., Salzberg S.L., Fraser C.M.,
RA Venter J.C.,
RT "Sequence and analysis of chromosome 2 of the plant *Arabidopsis*
RT *thaliana*".
RL Nature 402:761-766(1999).
CC -1- FUNCTION: Causes loosening and extension of plant cell walls by
CC disrupting noncovalent bonding between cellulose microfibrils and
CC matrix glucans. No enzymatic activity has been found (By
CC similarity).
CC -1- SUBCELLULAR LOCATION: Cell-wall bound.
CC -1- SIMILARITY: BELONGS TO THE EXPANSIN FAMILY.
CC -1- SIMILARITY: Contains 1 expansin-like EG45 domain.
CC -1- SIMILARITY: Contains 1 expansin-like CBD domain.
CC -1- DATABASE: NAME=EXPANSIN homepage;
CC WWW="http://www.bio.psu.edu/expansins/".
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: U30480; AAC8072.1; -
CC EMBL: AC005315; AAC33223.1; -
CC PIR: T02727; T02727.
CC PIR: T50653; T50653.
CC InterPro: IPR007112; Expan_endogl.
CC InterPro: IPR007117; Expan_lool_pi.
CC DR Pfam: PF01357; Pollen_allergen; 1.
CC DR PRINTS: PRO1225; EXPANSIN_FAMLY.
CC DR ProDom: PD002179; Expan_lool_pi_C; 1.
CC DR PROSITE: PS50843; EXPANSIN_CBD; 1.
CC DR PROSITE: PS50842; EXPANSIN_EG45; 1.
CC Cell wall; Signal; Multigene family.
CC FT SIGNAL: 1 22 POTENTIAL.
CC FT CHAIN: 23 259 ALPHA-EXPANSIN 6.
CC FT DOMAIN: 51 165 EXPANSIN-LIKE EG45.
CC FT DOMAIN: 175 254 EXPANSIN-LIKE CBD.
CC FT CONFLICT: 11 12 MISSING (IN REF. 2).
CC SEQ SEQUENCE 259 AA; 28004 MW; B0C8089F0222C908 CRC64;

Query Match 67.4%; Score 939; DB 1; Length 259;
Best Local Similarity 70.9%; Pred. No. 4.7e-73;
Matches 161; Conservative 29; Mismatches 35; Indels 2; Gaps 1;

DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Alpha-expansin 9 precursor (At-EXP9) (AtEX9) (Ath-Exp1alpha-1.10).
GN EXP9 OR A15G02260 OR T1822.20.
OS *Arabidopsis thaliana* (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliopsida; eudicotyledons; core eudicots; Rosidae;
OC eucosids II; Brassicales; Brassicaceae; Arabidopsids.
OC NCBI_TaxId=3702;
OK NCBI_TaxId=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Columbia;
RX MEDLINE=21016721; PubMed=11130714;
RA Tabata S., Kaneko T., Nakamura Y., Kotani H., Kato T., Asamizu E.,
RA Miyajima N., Sasamoto S., Kimura T., Hosouchi T., Kawashima K.,
RA Kohara M., Matsuno M., Matsuno A., Muraki A., Nakayama S.,
RA Nakazaki N., Nanno K., Okumura S., Shino S., Takeuchi C., Wada T.,
RA Watanabe A., Yamada M., Sato S., de la Bastide M.,
RA Huang E., Spiegel L., Gnoj L., O'Shaughnessy A., Preston R.,
RA Habermann K., Murray J., Johnson D., Kohliffing T., Nelson J.,
RA Stoeckling T., Pepin K., Spieth J., Sekhon M., Armstrong J., Becker M.,
RA Belter E., Cordum H., Cordes M., Courtney L., Courtney W., Dante M.,
RA Du H., Edwards J., Fryman J., Haakensen B., Lamar E., Latreille P.,
RA Leonard S., Meyer R., Mulvaney E., Ozersky P., Riley A., Stromatt C.,
RA Wagner-McPherson C., Wollam A., Yeakum M., Bell M., Dedhia N.,
RA Parnell L., Shah R., Rodriguez M., Hoon See L., Vil D., Baker J.,
RA Kirchoff K., Toth K., King L., Bahret A., Miller B., Marra M.,
RA Marienssen R., McCombie W.R., Wilson R.K., Murphy G., Bancroft I.,
RA Volckaert G., Wambut R., Dueseterehoelt A., Stiekema W., Pohl T.,
RA Entlan K.-D., Terryn N., Hartley N., Bent E., Johnson S.,
RA Langham S.-A., McCullagh B., Robben J., Gyrompierrez B., Zimmermann W.,
RA Ramberger U., Wedler H., Balke K., Wedler E., Peters S.,
RA van Staveren T., Dikse W., Wooljman P., Klein Lamhocht R.,
RA Welzenegger T., Bothe G., Rose M., Hauf J., Bernessee S., Hempel S.,
RA Felpanusch M., Lamberth S., Villarroel R., Gietlen J., Ardlies W.,
RA Bents O., Lemcke K., Kolesov G., Mayer K.F.X., Rüd S., Schoof H.,
RA Scheller C., Zaccaria P., Mewes H.-W., Bevan M., Franz P.;
RT "Sequence and analysis of chromosome 5 of the plant *Arabidopsis*
RT *thaliana*".
RL Nature 408:823-826(2000).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Columbia;
RA Shinozaki K., Davis R.W., Ecker J.R., Theologis A.;
RT "RIKEN *Arabidopsis* full length cDNA clones (RAFLs) sequenced by the
RT SSP consortium (Salk/Stanford/PGEC)".
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: Causes loosening and extension of plant cell walls by
CC disrupting noncovalent bonding between cellulose microfibrils and
CC matrix glucans. No enzymatic activity has been found (By
CC similarity).
CC -1- SUBCELLULAR LOCATION: Cell-wall bound.
CC -1- SIMILARITY: BELONGS TO THE EXPANSIN FAMILY.
CC -1- SIMILARITY: Contains 1 expansin-like EG45 domain.
CC -1- SIMILARITY: Contains 1 expansin-like CBD domain.
CC -1- DATABASE: NAME=EXPANSIN homepage;
CC WWW="http://www.bio.psu.edu/expansins/".
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: AL162874; CAB85531.1; -
CC EMBL: AY054586; AK96777.1; -
CC PIR: T48247; T48247.
CC InterPro: IPR007112; Expan_endogl.
CC InterPro: IPR007117; Expan_lool_pi.
CC InterPro: IPR007117; Expan_lool_pi_C.

DR Pfam; PF01357; Pollen allergen; 1.
 DR PRINTS; PR01225; EXPANSIN_FAMLY.
 DR PRODOM; PD002179; Expan_Lol PI C; 1.
 DR PROSITE; PS50843; EXPANSIN_CBD; 1.
 DR PROSITE; PS50842; EXPANSIN_EG45; 1.
 DR Cell wall; Signal; Multigene family.
 FT SIGNAL 1 21 POTENTIAL.
 FT CHAIN 22 258 ALPHA-EXPANSIN 9.
 FT DOMAIN 50 164 EXPANSIN-LIKE EG45.
 FT DOMAIN 174 253 EXPANSIN-LIKE CBD.
 SQ SEQUENCE 258 AA; 27749 MW; 61AE7AD0C32A1FF9 CRC64;

Query Match 67.0%; Score 934; DB 1; Length 258;
 Best Local Similarity 72.2%; Pred. No. 1.2e-72;
 Matches 164; Conservative 21; Mismatches 40; Indels 2; Gaps 1;

DB 26 GCMQSGHATFYGGDASGTGAGAGYGNLYSGYGTNTVALSTLFPNNGISCGCFEMTC 85
 30 GPMINAHATFYGGDASGTGAGAGYGNLYSGYGTNTVALSTLFPNNGISCGCFELKC 89

QY 86 TNDPKMCLPG--TIRVATNFCPPNFALPNNNGCMCPLOHFMABEPAFLQIAQYRAGI 143
 90 INDEGKCLPKNPSLITRATNFCPPNFQASDNGCMCPREHFDLAMPFLSLAKYRAGI 149

DB 144 VPVSFRFPVPCMKKGVFTTNGHSYFNLVLTITVNGAGDVHVSISKSGRTGQMSRHWG 203
 150 VPVSYRIRPCRRKKGIRFTTNGHSYFNLVLTITVNGAGDVHVSISKSGRTGQMSRHWG 209

QY 204 QNMOSNNYLNQGLSFQVTLSDGRTLTAVNLVPSNMQFGQTYEGPOF 250
 210 QNMOSNNYLNQGLSFQVTLSDGRTLTAVNLVPSNMQFGQTYEGPOF 256

RESULT 12

EXP5_ARATH STANDARD; PRT; 255 AA.
 AC Q38864;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Alpha-expansin 5 precursor (At-EXP5) (ACEX5) (Ath-ExpAlpha-1.4).
 GN EXP5 OR AT3G29030 OR K5K13_14 OR K5K13.16.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eurosid II; Brassicales; Brassicaceae; Arabidopsids.
 OC NCBI_TaxID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA MEDLINE=6016146; PubMed=7568110;
 RA Sheehar T.Y., Shi J., Duracko D.M., Gultitan M.J.,
 RA McQueen-Mason S.J., Shieh M., Coe D.J.,
 RT "Molecular cloning and sequence analysis of expansins - a highly
 RT conserved, multigene family of proteins that mediate cell wall
 RT extension in plants";
 RL Proc. Natl. Acad. Sci. U.S.A. 92:9245-9249(1995).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=cv. Columbia;
 RA MEDLINE=20277480; PubMed=10819329;
 RA Sato S., Nakamura Y., Kaneko T., Katoh T., Asamizu E., Tabata S.;
 RT "Structural analysis of Arabidopsis thaliana chromosome 3. I. Sequence
 RT features of the regions of 4,504,864 bp covered by sixty P1 and TAC
 RT clones";
 RL DNA Res. 7:131-135(2000).
 CC -1- FUNCTION: loosening and extension of plant cell walls by
 CC disrupting noncovalent bonding between cellulose microfibrils and
 CC matrix glucans. No enzymatic activity has been found (by
 CC similarity).
 CC -1- SUBCELLULAR LOCATION: Cell-wall bound.
 CC -1- SIMILARITY: BELONGS TO THE EXPANSIN FAMILY.
 CC -1- SIMILARITY: Contains 1 expansin-like EG45 domain.
 CC -1- SIMILARITY: Contains 1 expansin-like CBD domain.

CC -1- DATABASE: NAME=EXPANSIN homepage;
 CC WWW="http://www.bio.psu.edu/expansins/".

CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.ebi.ac.uk/announcements> or send an email to license@ebi.ac.uk).

CC EMBL; U30478; AAB38071.1; -.
 CC EMBL; AB025615; BAA95756.1; -.
 CC PIR; T50655; T50655.
 DR InterPro; IPR007112; Expan_endogl.
 DR InterPro; IPR007118; Expan_Lol PI.
 DR InterPro; IPR007117; Expan_Lol PI C.
 DR Pfam; PF01357; Pollen allergen; 1.
 DR PRINTS; PR01225; EXPANSIN_FAMLY.
 DR PRODOM; PD002179; Expan_Lol PI C; 1.
 DR PROSITE; PS50843; EXPANSIN_CBD; 1.
 DR PROSITE; PS50842; EXPANSIN_EG45; 1.
 DR Cell wall; Signal; Multigene family.
 FT SIGNAL 1 22 POTENTIAL.
 FT CHAIN 23 255 ALPHA-EXPANSIN 5.
 FT DOMAIN 56 161 EXPANSIN-LIKE EG45.
 FT DOMAIN 171 250 EXPANSIN-LIKE CBD.
 SQ SEQUENCE 255 AA; 27611 MW; 7580595A30DC414B CRC64;

Query Match 63.8%; Score 889.5; DB 1; Length 255;
 Best Local Similarity 69.5%; Pred. No. 7.5e-69;
 Matches 157; Conservative 26; Mismatches 34; Indels 9; Gaps 2;

QY 26 GCMQSGHATFYGGDASGTGAGAGYGNLYSGYGTNTVALSTLFPNNGISCGCFEMTC 85
 36 GPMINAHATFYGGDASGTGAGAGYGNLYSGYGTNTVALSTLFPNNGISCGCFELKC 95

DB 86 TNDPKMCLPG--TIRVATNFCPPNFALPNNNGCMCPLOHFMABEPAFLQIAQYRAGI 144
 96 VNDPQMCIRKRSIVTIRATNFCPP-----GACDPPNHFDSQTYEKIALYKSGII 147

QY 145 VPVSFRFPVPCMKKGVFTTNGHSYFNLVLTITVNGAGDVHVSISKSGRTGQMSRHWG 204
 148 VPVSYRIRPCRRKKGIRFTTNGHSYFNLVLTITVNGAGDVHVSISKSGRTGQMSRHWG 207

QY 205 QNMOSNNYLNQGLSFQVTLSDGRTLTAVNLVPSNMQFGQTYEGPOF 250
 208 QNMOSNNYLNQGLSFQVTLSDGRTLTAVNLVPSNMQFGQTYEGPOF 253

RESULT 13

EX11_ARATH STANDARD; PRT; 252 AA.
 AC Q01UN3;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Alpha-expansin 11 precursor (At-Exp11) (AtEX11) (Ath-ExpAlpha-1.14).
 GN EXP11 OR AT1G01900 OR T2OH2.4 OR T2OH2.5.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eurosid II; Brassicales; Brassicaceae; Arabidopsids.
 OC NCBI_TaxID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=cv. Columbia;
 RA MEDLINE=21016719; PubMed=11130712;
 RA Theologis A., Ecker J.R., Palm C.U., Federspiel N.A., Kaul S.,
 RA White O., Alonso J., Altieri H., Araujo R., Bowman C.L., Brookes S.Y.,
 RA Buehler E., Chan A., Chen Q., Chen H., Cheuk R.F., Chin C.W.,
 RA Chung M.K., Conn L., Conway A.B., Conway A.R., Creasy T.H., Dewar K.,
 RA Dunn P., Egu P., Feldblyum T.V., Feng J.-D., Fong B., Fujii C.Y.,

Qy 145 PVSFRVPCMKKGVRFTINGHSYENLVLITNYGAGDVHSVISIKSRTGMSRNGO 204
| | : | | | | | : | | : | | | | | : | | : | | : | |
Db 167 PVRYRRI PCSKTGCVK FETKGNPYFLMVLIVNVGAGDIKYVKGKNTGWTMKKNWGO 226
Qy 205 NMQSNMYLNGQGLSFQVTLSDGRRLTAYNIVPSNMOFGOTYEG 247
| | : | | | | | : | | : | | | | | : | | : | | : | |
Db 227 NMTTITVLTGQGLSFRVTTSDGTTKDFMNVMPKKNMGFGOTFDG 269

Search completed: December 18, 2003, 17:48:59
Job time : 19 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using SW model

Run on: December 18, 2003, 17:46:23 ; Search time 35 Seconds
(without alignments)
1843.233 Million cell updates/sec

Title: US-09-383-579C-10

Perfect score: 1394
Sequence: 1 MAFSYSPFSSLLPLPFEPVF.....AYNLVPSNMQFGQYEGPQF 250

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

SPTREMBL_23:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_virus:*
16: sp_bacteriap:*
17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1394	100.0	250	10	Q39625
2	1160.5	83.2	254	10	Q82093
3	1152.5	82.7	260	10	Q9FNT0
4	1151.5	82.6	254	10	Q9FUM3
5	1143.5	82.0	245	10	Q9FLM3
6	1130.5	81.1	253	10	Q9LLB2
7	1125	80.7	247	10	Q82625
8	1118	80.2	249	10	Q92P35
9	1117.5	80.2	253	10	Q9SMT1
10	1116.5	80.1	253	10	Q9SMD4
11	1116	80.1	254	10	Q8RYK6
12	1113.5	79.9	253	10	Q93XP2
13	1111	79.9	252	10	Q9FS30
14	1108	79.5	252	10	Q8L5S6
15	1105	79.3	252	10	Q8L133
16	1102.5	79.1	255	10	Q8RYK4

17	1101.5	79.0	253	10	Q9SWM1	Q9SWY1
18	1092	78.3	232	10	P93493	P93493
19	1087	78.0	232	10	P93492	P93492
20	1085	77.8	232	10	P93495	P93495
21	1077	77.3	232	10	P93494	P93494
22	1063	76.3	248	10	Q8L5G5	Q8L5G5
23	1059	76.0	258	10	Q8LKK3	Q8LKK3
24	1058	75.9	251	10	Q946J1	Q946J1
25	1053	75.5	252	10	Q8WVW8	Q8WVW8
26	1051	75.4	258	10	Q49194	Q49194
27	1050	75.3	249	10	Q93XP1	Q93XP1
28	1048	75.2	248	10	Q8L5G4	Q8L5G4
29	1043	74.8	251	10	Q40636	Q40636
30	1041.5	74.7	247	10	Q9M5T7	Q9M5T7
31	1041	74.7	249	10	Q8L5T9	Q8L5T9
32	1039	74.5	246	10	Q946J0	Q946J0
33	1038	74.5	246	10	P93442	P93442
34	1037	74.4	252	10	Q9FUM2	Q9FUM2
35	1032	74.0	258	10	Q8LKK2	Q8LKK2
36	1030	73.9	250	10	Q8L5S0	Q8L5S0
37	1030	73.9	250	10	Q8L5S1	Q8L5S1
38	1029	73.8	250	10	Q8L5R7	Q8L5R7
39	1027	73.7	248	10	Q8LKK8	Q8LKK8
40	1027	73.7	249	10	Q9M5I5	Q9M5I5
41	1027	73.7	253	10	Q94KT7	Q94KT7
42	1024	73.5	253	10	Q8VYD1	Q8VYD1
43	1022	73.3	249	10	Q92P36	Q92P36
44	1008.5	72.3	242	10	Q9L1B1	Q9L1B1
45	1002	71.9	250	10	Q9FVQ9	Q9FVQ9

ALIGNMENTS

RESULT 1

ID Q39625 PRELIMINARY; PRT; 250 AA.
AC Q39625;
DT 01-NOV-1996 (T-REMBLrel. 01, Created)
DT 01-NOV-1996 (T-REMBLrel. 01, Last sequence update)
DE 01-MAR-2003 (T-REMBLrel. 23, Last annotation update)
DE EXPANSIN SL.
GN CS-EXPI.
OS Cucumis sativus (Cucumber).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids I; Cucurbitales; Cucurbitaceae; Cucumis.
OX NCBI_TaxID=1659;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Burpee Pickler;
RX MEDLINE=96016146; PubMed=7568110;
RA Shcherban T.Y., Shi J., Durachko D.M., Gullitnan M.J.,
RA McQueen-Mason S.J., Shieh M., Cosgrove D.J.;
RT "Molecular cloning and sequence analysis of expansins--a highly
RT conserved, multigene family of proteins that mediate cell wall
RT extension in plants.";
RT Proc. Natl. Acad. Sci. U.S.A. 92:9245-9249(1995).
RL -1- SIMILARITY: BELONGS TO THE EXPANSIN FAMILY.
RC EMBL; U03082; AAB37746.1; .
DR InterPro: IPR007112; Expan_endogl.
DR InterPro: IPR007118; Expan_lo1_P1_C.
DR InterPro: IPR007117; Expan_lo1_P1_C.
DR Pfam: PF01357; Pollen_allergen; 1.
DR PRINTS; PR01225; EXPANSINPAMLY.
DR PRODOM; PD002179; Expan_lo1_P1_C; 1.
DR PROSITE; PS00843; EXPANSIN_CBD; 1.
DR PROSITE; PS00842; EXPANSIN_BG45; 1.
FT CHAIN 24 250
SQ SEQUENCE 250 AA; 27215 MW; 60651BC47E4186DA CRC64;
Query Match 100.0%; Score 1394; DB 10; Length 250;
Best local Similarity 100.0%; Pred. No. 7,1e-116;

```

Matches 250; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAFSYPSSSLFLPFVFTPADYGMQSGHATFYGGDASGTMGACGYGNLYSQGYG 60
    |||
DB 1 MAFSYPSSSLFLPFVFTPADYGMQSGHATFYGGDASGTMGACGYGNLYSQGYG 60
    |||

QY 61 TMTVALSTALFNNNGSCGACFEMTCTNDPKCLPGTIRATATNFCPPNFALPNNNGMGN 120
    |||
DB 61 TMTVALSTALFNNNGSCGACFEMTCTNDPKCLPGTIRATATNFCPPNFALPNNNGMGN 120
    |||

QY 121 PLOHEDMAEPALQIAQYRAGIVPVSFRVPCMKKGVRFTINGHSYFNVLITVNGA 180
    |||
DB 121 PLOHEDMAEPALQIAQYRAGIVPVSFRVPCMKKGVRFTINGHSYFNVLITVNGA 180
    |||

QY 181 GGVHSVSIKSGRTGMQSMRNQNNYLNQGLSFQVTLSDGRTLTAYNLVPSNMQ 240
    |||
DB 181 GGVHSVSIKSGRTGMQSMRNQNNYLNQGLSFQVTLSDGRTLTAYNLVPSNMQ 240
    |||

QY 241 FQOTYEGPOF 250
    |||
DB 241 FQOTYEGPOF 250
    |||

RESULT 2
082093 PRELIMINARY; PRT; 254 AA.
AC 082093;
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Expansion.
GN PA-Expt1.
OS Prunus armeniaca (Apricot).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC euroside 1; Rosales; Rosaceae; Amygdaloideae; Prunus.
OX NCBI_TaxID=36596;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Bergeon; TISSUE=Mesocarp, and Exocarp;
RA Mbequie-A-Mbequie D., Gomez R.-M., File-Lycan B.;
RT "Molecular cloning and nucleotide sequence of expansin 1 (PA-Expt1)
RT from apricot fruit.";
RL Submitted (DEC-1997) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: BELONGS TO THE EXPANSIN FAMILY.
DR EMBL; U93167; AAC33529.1; -.
DR InterPro; IPR007112; Expan_endogl.
DR InterPro; IPR007118; Expan_Lol_P1.
DR InterPro; IPR007117; Expan_Lol_P1_C.
DR Pfam; PF01357; Pollen_allergen; 1.
DR PRINTS; PR01225; EXPANSINFAMILY.
DR ProDom; PD002179; Expan_Lol_P1_C; 1.
DR PROSITE; PS50843; EXPANSIN CBD; 1.
DR PROSITE; PS50842; EXPANSIN EG45; 1.
SQ SEQUENCE 254 AA; 27264 MW; 88068D75933FDBE1 CRC64;

Query Match 83.2%; Score 1160.5; DB 10; Length 254;
Best Local Similarity 82.4%; Pred. No. 8.6e-97;
Matches 206; Conservative 15; Mismatches 28; Indels 1; Gaps 1;

QY 2 AFSYSPFS-SLFLPFVFTPADYGMQSGHATFYGGDASGTMGACGYGNLYSQGYG 60
    |||
DB 5 AUSTALALSLVLFNHLHGAIFADYGMGEGAHATFYGGDASGTMGACGYGNLYSQGYG 64
    |||

QY 61 TMTVALSTALFNNNGSCGACFEMTCTNDPKCLPGTIRATATNFCPPNFALPNNNGMGN 120
    |||
DB 61 TMTVALSTALFNNNGSCGACFEMTCTNDPKCLPGTIRATATNFCPPNFALPNNNGMGN 124
    |||

QY 121 PLOHEDMAEPALQIAQYRAGIVPVSFRVPCMKKGVRFTINGHSYFNVLITVNGA 180
    |||
DB 121 PLOHEDMAEPALQIAQYRAGIVPVSFRVPCMKKGVRFTINGHSYFNVLITVNGA 184
    |||

QY 181 GGVHSVSIKSGRTGMQSMRNQNNYLNQGLSFQVTLSDGRTLTAYNLVPSNMQ 240
    |||
DB 181 GGVHSVSIKSGRTGMQSMRNQNNYLNQGLSFQVTLSDGRTLTAYNLVPSNMQ 240
    |||

```

```

DB 185 GGVHSVSIKSGRTGMQSMRNQNNYLNQGLSFQVTLSDGRTLTAYNLVPSNMQ 244
    |||
QY 241 FQOTYEGPOF 250
    |||
DB 245 FQOTYEGPOF 254
    |||

RESULT 3
09FNT0 PRELIMINARY; PRT; 260 AA.
AC 09FNT0;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Expansion.
OS Cicer arietinum (Chickpea) (Garbanzo).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC euroside 1; Fabales; Fabaceae; Papilionoideae; Ciceraceae; Cicer.
OX NCBI_TaxID=3827;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Castellana; TISSUE=Etioolated epicotyl;
RA Dopico B., Sanchez M.A., Labrador E.;
RT "An second expansin is expressed in chickpea epicotyls.";
RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: BELONGS TO THE EXPANSIN FAMILY.
DR EMBL; AJ291817; CAC19184.1; -.
DR InterPro; IPR007112; Expan_endogl.
DR InterPro; IPR007118; Expan_Lol_P1.
DR InterPro; IPR007117; Expan_Lol_P1_C.
DR InterPro; IPR00504; RNA_rec_mot.
DR Pfam; PF01357; Pollen_allergen; 1.
DR PRINTS; PR01225; EXPANSINFAMILY.
DR ProDom; PD002179; Expan_Lol_P1_C; 1.
DR PROSITE; PS50843; EXPANSIN CBD; 1.
DR PROSITE; PS50842; EXPANSIN EG45; 1.
DR PROSITE; PS00030; RRM_RNP_1; 1.
SQ SEQUENCE 260 AA; 28266 MW; 32A70368BD2883E9 CRC64;

Query Match 82.7%; Score 1152.5; DB 10; Length 260;
Best Local Similarity 81.9%; Pred. No. 4.7e-96;
Matches 203; Conservative 18; Mismatches 20; Indels 7; Gaps 1;

QY 10 SLFLPFVFTPADYGMQSGHATFYGGDASGTMGACGYGNLYSQGYGN 62
    |||
DB 13 SLVKGGLFLFNNMMQSAIADYGMGEGAHATFYGGDASGTMGACGYGNLYSQGYGN 72
    |||

QY 63 TMTVALSTALFNNNGSCGACFEMTCTNDPKCLPGTIRATATNFCPPNFALPNNNGMGN 122
    |||
DB 73 TMTVALSTALFNNNGSCGACFEMTCTNDPKCLPGTIRATATNFCPPNFALPNNNGMGN 132
    |||

QY 123 LOHFDMAEPALQIAQYRAGIVPVSFRVPCMKKGVRFTINGHSYFNVLITVNGAGD 182
    |||
DB 133 LOHFDMAEPALQIAQYRAGIVPVSFRVPCMKKGVRFTINGHSYFNVLITVNGAGD 192
    |||

QY 183 VHSVSIKSGRTGMQSMRNQNNYLNQGLSFQVTLSDGRTLTAYNLVPSNMQFG 242
    |||
DB 193 VHSVSIKSGRTGMQSMRNQNNYLNQGLSFQVTLSDGRTMTSYNVAPSNMQFG 252
    |||

QY 243 QOTYEGPOF 250
    |||
DB 253 QOTYEGPOF 260
    |||

RESULT 4
09FUM3 PRELIMINARY; PRT; 254 AA.
AC 09FUM3;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)

```

DE Expansin 1.
 GN EXP1 OR EXP2.
 OS Prunus avium (Cherry), and
 OS Prunus cerasus.
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC Eucosids I; Rosales; Rosaceae; Amygdaloideae; Prunus.
 NCBI_TaxID=42229, 140311;
 [1]
 RP SEQUENCE FROM N.A.
 RC SPECIES=P.avium;
 RA Wu Z., Wiersma P.A.;
 RT "Differential Expression of Expansin Genes Isolated from Sweet Cherry
 (Prunus avium L.) During Fruit Ripening."
 RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC SPECIES=P.cerasus; TISSUE=Fruit;
 RA Yoo S.-D., Gao Z., Cantini C., Loeschner W., van Nocker S.;
 RT "Coordinated expression of genes encoding expansins and other cell
 wall-modifying enzymes is associated with pectin-related changes in
 the cell wall during ripening of cherry (P. cerasus) fruit."
 RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: BELONGS TO THE EXPANSIN FAMILY.
 DR EMBL: AF297521; AAG13982.1; -
 DR EMBL: AF350937; AAK4846.1; -
 DR InterPro: IPR007112; Expan_endogl.
 DR InterPro: IPR007118; Expan_lo1_pi.
 DR InterPro: IPR007117; Expan_lo1_pi_C.
 DR Pfam: PF01357; Pollen_allergen; 1.
 DR PRINTS: PR01225; EXPANSINFAMILY.
 DR ProDom: PD002179; Expan_lo1_pi_C; 1.
 DR PROSITE: PSS0843; EXPANSIN_CBD; 1.
 DR PROSITE: PSS0842; EXPANSIN_EG45; 1.
 SQ SEQUENCE 254 AA; 27278 MW; 953A7BB2491D081 CRC64;

Query Match 82.6%; Score 1151.5; DB 10; Length 254;
 Best Local Similarity 82.0%; Pred. No. 5.6e-96;
 Matches 205; Conservative 14; Mismatches 30; Indels 1; Gaps 1;

QY 2 AFSVSPSS-SLFLPFFVFTFADYGGWQSGHATFYGGDASGTMGACGYNLYSGCYG 60
 DB 5 ALSIAPLALSIVLFLNLHGAFAFYGGWQSGHATFYGGDASGTMGACGYNLYSGCYG 64
 QY 61 TTTVALSTALFNNGLSCGACFEMTCTNDPKMCLPGTIRVATNFCPPNFALPNNNGWCN 120
 DB 65 TTTVALSTALFNNGLSCGSCYEMRCNDPDKMCLPGTIRVATNFCPPNFALPNNNGWCN 124
 QY 121 PPIOHFMAEPAPLQIAQYAGIVPVSFRVPCMKKGGVFTTNGHSYFNLVLTNVGA 180
 DB 125 PPIOHFMAEPAPLQIAQYAGIVPVSFRVPCMKKGGVFTTNGHSYFNLVLTNVGA 184
 QY 181 GDVHSVSIKSGRTGWSMSRNMGQNNNYLNGQGLSFQVLTSDGRTLTAYNLVPSNMQ 240
 DB 185 GDVHSVSIKSGRTGWSMSRNMGQNNNYLNGQGLSFQVLTSDGRTLTAYNLVPSNMQ 244
 QY 241 FGQTYEGPOF 250
 DB 245 FGQTFGGQF 254

RESULT 5

Q9LUB2

Q9LUB2 PRELIMINARY; PRT; 245 AA.

AC Q9LUB2; 01-OCT-2000 (Tremblrel. 15, Created)
 DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
 DT 01-MAR-2003 (Tremblrel. 23, Last annotation update)
 DE Expansin 2.
 OS Zinnia elegans.
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 OC Asteridae; Campanulids; Asterales; Asteraceae; Asteroideae;

OC Heliantheae; Zinnia.
 NCBI_TaxID=34245;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC MEDLINE=20317189; PubMed=10859177;
 RA Im K.H., Coggrove D.J., Jones A.M.;
 RT "Subcellular localization of expansin mRNA in xylem cells."
 RL Plant Physiol. 123:463-470(2000).
 CC -1- SIMILARITY: BELONGS TO THE EXPANSIN FAMILY.
 DR EMBL: AF230332; AAF35901.1; -
 DR InterPro: IPR007112; Expan_endogl.
 DR InterPro: IPR007118; Expan_lo1_pi.
 DR InterPro: IPR007117; Expan_lo1_pi_C.
 DR Pfam: PF01357; Pollen_allergen; 1.
 DR PRINTS: PR01225; EXPANSINFAMILY.
 DR ProDom: PD002179; Expan_lo1_pi_C; 1.
 DR PROSITE: PSS0843; EXPANSIN_CBD; 1.
 DR PROSITE: PSS0842; EXPANSIN_EG45; 1.
 SQ SEQUENCE 245 AA; 26201 MW; F66E26114C27E360 CRC64;

Query Match 82.0%; Score 1143.5; DB 10; Length 245;
 Best Local Similarity 81.2%; Pred. No. 2.8e-95;
 Matches 203; Conservative 20; Mismatches 22; Indels 5; Gaps 1;

QY 1 MAFSVSPSS-SLFLPFFVFTFADYGGWQSGHATFYGGDASGTMGACGYNLYSGCYG 60
 DB 1 MAISTFTIVSLVSSFRV-----YGGWQSGHATFYGGDASGTMGACGYNLYSGCYG 55
 QY 61 TTTVALSTALFNNGLSCGACFEMTCTNDPKMCLPGTIRVATNFCPPNFALPNNNGWCN 120
 DB 56 TTTVALSTALFNNGLSCGSCYEMRCNDPDKMCLPGTIRVATNFCPPNFALPNNNGWCN 115
 QY 121 PPIOHFMAEPAPLQIAQYAGIVPVSFRVPCMKKGGVFTTNGHSYFNLVLTNVGA 180
 DB 116 PPIOHFMAEPAPLQIAQYAGIVPVSFRVPCMKKGGVFTTNGHSYFNLVLTNVGA 175
 QY 181 GDVHSVSIKSGRTGWSMSRNMGQNNNYLNGQGLSFQVLTSDGRTLTAYNLVPSNMQ 240
 DB 176 GDVHSVSIKSGRTGWSMSRNMGQNNNYLNGQGLSFQVLTSDGRTLTAYNLVPSNMQ 235
 QY 241 FGQTYEGPOF 250
 DB 236 FGQTFGGQF 245

RESULT 6

Q8LS57

Q8LS57 PRELIMINARY; PRT; 253 AA.

AC Q8LS57; 01-OCT-2002 (Tremblrel. 22, Created)
 DT 01-OCT-2002 (Tremblrel. 22, Last sequence update)
 DT 01-MAR-2003 (Tremblrel. 23, Last annotation update)
 DE Expansin 7 precursor.
 GN EXP7.
 OS Rumex palustris.
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 OC Caryophyllidae; Caryophyllales; Polygonaceae; Rumex.
 NCBI_TaxID=50298;
 [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Root/shoot junction;
 RA Colmer T., Wagemaker C.A.M., Vriezen W., Vooeeneek L.A.C.J.,
 RA Peeters A.J.M.;
 RT "The expression of expansin genes in roots during waterlogging of
 Rumex palustris."
 RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: BELONGS TO THE EXPANSIN FAMILY.
 DR EMBL: AF428174; AAM22521.1; -
 DR InterPro: IPR007112; Expan_endogl.
 DR InterPro: IPR007118; Expan_lo1_pi.
 DR InterPro: IPR007117; Expan_lo1_pi_C.
 DR Pfam: PF01357; Pollen_allergen; 1.

DR PRINTS; PRO1225; EXPANSIN_FAMLY.
 DR PRODOM; PD002179; Expan_Lol_PI_C; 1.
 DR PROSITE; PSS0843; EXPANSIN_CBD; 1.
 DR PROSITE; PSS0842; EXPANSIN_EG45; 1.
 KW Signal.
 FT SIGNAL.
 SQ SEQUENCE 253 AA; 26765 MW; 5AD64CA8563306C7 CRC64; POTENTIAL.

Query Match 81.1%; Score 1130.5; DB 10; Length 253;
 Best Local Similarity 81.0%; Pred. No. 4.4e-94;
 Matches 205; Conservative 14; Mismatches 31; Indels 3; Gaps 2;

QY 1 MAFSSPESLFLPP--FFVTFADYGG-WDSGHATFYGGDASGTMGACGYGNLYSQ 57
 DB 1 MAFQAFASLLLIARQHVSSAFGDYGDWNGHATFYGGDASGTMGACGYGNLYSQ 60
 QY 58 GYGTNTVALSTALFNNGSCGACFEWTCNDPKMCLPGTIRVATNFCPPNFALPNNGG 117
 DB 61 GYGTSTALSTALFNNGSCGACFEWTCNDPKMCLPGTIRVATNFCPPNFALPNNGG 120
 QY 118 WCNPLQHPDMAEPALQIAQYRAGIVPVSFRRVPCMKKGVRFTINGHSYFNLYITNV 177
 DB 121 WCNPLQHPDMAEPALQIAQYRAGIVPVSFRRVPCMKKGVRFTINGHSYFNLYITNV 180
 QY 178 GAGADVHSYISIGSRGTGMSRNMGNMNSNYLNGQSLSFQVTLSDRITLAVNLVVS 237
 DB 181 GAGADVHSYISIGSRGTGMSRNMGNMNSNYLNGQSLSFQVTLSDRITLAVNLVVS 240
 QY 238 NMQFGQYEGPOF 250
 DB 241 NMQFGQYEGPOF 253

RESULT 7
 ID 082625 PRELIMINARY; PRT; 247 AA.
 AC 082625;
 DT 01-NOV-1998 (TREMBLrel. 08, Created)
 DT 01-NOV-1998 (TREMBLrel. 08, Last sequence update)
 DE 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
 DE EXPANSIN.
 GN LEXXP2.
 OS Lycopersicon esculentum (Tomato).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 OC Asteridae; lamids; Solanales; Solanaceae; Solanum.
 OC NCBI_Taxid=4081;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Hypocotyl;
 RA Catala C., Rose J.K.C., Bennett A.B.;
 RA "Hormonal regulation and expression patterns of LEXXP2, a new tomato
 RT expansin.";
 RL Submitted (OCT-1998) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=cv. VFN8;
 RA Caderas D., Muster M., Vogler H., Mandel T., Rose J.,
 RA McQueen-Mason S., Kuhnlemaier C.;
 RA "Limited correlation between expansin gene expression and elongation
 RT growth rate.";
 RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: BELONGS TO THE EXPANSIN FAMILY.
 DR EMBL; AF096776; AAC64201.1; -;
 DR EMBL; AJ239068; CAB43197.1; -;
 DR InterPro; IPR007112; Expan_endogl.
 DR InterPro; IPR007118; Expan_Lol_PI_C.
 DR InterPro; IPR007117; Expan_Lol_PI_C.
 DR Pfam; PF01357; Pollen_allergen; 1.
 DR PRINTS; PRO1225; EXPANSIN_FAMLY.
 DR PRODOM; PD002179; Expan_Lol_PI_C; 1.
 DR PROSITE; PSS0843; EXPANSIN_CBD; 1.
 DR PROSITE; PSS0842; EXPANSIN_EG45; 1.

SQ SEQUENCE 247 AA; 26470 MW; 99E6F53F84F7A3E1 CRC64;
 Query Match 80.7%; Score 1125; DB 10; Length 247;
 Best Local Similarity 81.6%; Pred. No. 1.3e-93;
 Matches 195; Conservative 21; Mismatches 23; Indels 0; Gaps 0;

QY 12 FLPPFFVTFADYGGWDSGHATFYGGDASGTMGACGYGNLYSQGYNTVALSTALF 71
 DB 9 FLPSFCFTSTFDYGGWDSGHATFYGGDASGTMGACGYGNLYSQGYNTVALSTALF 68
 QY 72 NNGSCGACFEWTCNDPKMCLPGTIRVATNFCPPNFALPNNGMWCNPLQHPDMAEP 131
 DB 69 NNGGLTCGACYELTCNNAQWCLQGTITVATNFCPPNPSLPNNMGWCNPLQHPDMAEP 128
 QY 132 AFLQIAQYRAGIVPVSFRRVPCMKKGVRFTINGHSYFNLYITNVGAGDVHSYISIGS 191
 DB 129 AFLQIAQYRAGIVPVSFRRVPCMKKGVRFTINGHSYFNLYITNVGAGDVHSYISIGS 188
 QY 192 RTGMSRNMGNMNSNYLNGQSLSFQVTLSDRITLAVNLVPSNMQFGQYEGPOF 250
 DB 189 NTGQWMSRNMGNMNSNYLNGQSLSFQVTLSDRITLAVNLVPSNMQFGQYEGPOF 247

RESULT 8
 ID 092P35 PRELIMINARY; PRT; 249 AA.
 AC 092P35;
 DT 01-MAY-1999 (TREMBLrel. 10, Created)
 DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)
 DE 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
 DE NT-EXPS.
 GN Nicotiana tabacum (Common tobacco).
 OS Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 OC Asteridae; lamids; Solanales; Solanaceae; Nicotiana.
 OC NCBI_Taxid=4097;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=cv. BY2;
 RA MEDLINE=99026292; PubMed=9808735;
 RA Link B.M., Cosgrove D.J.;
 RA "Acid-growth response and alpha-expansins in suspension cultures of
 RT bright yellow 2 tobacco.";
 RL Plant Physiol. 118:907-916(1998).
 CC -1- SIMILARITY: BELONGS TO THE EXPANSIN FAMILY.
 DR EMBL; AF049354; AAC96081.1; -;
 DR InterPro; IPR007112; Expan_endogl.
 DR InterPro; IPR007118; Expan_Lol_PI_C.
 DR InterPro; IPR007117; Expan_Lol_PI_C.
 DR Pfam; PF01357; Pollen_allergen; 1.
 DR PRINTS; PRO1225; EXPANSIN_FAMLY.
 DR PRODOM; PD002179; Expan_Lol_PI_C; 1.
 DR PROSITE; PSS0843; EXPANSIN_CBD; 1.
 DR PROSITE; PSS0842; EXPANSIN_EG45; 1.
 KW Signal.
 FT NON_TER
 FT SIGNAL
 FT CHAIN
 SQ SEQUENCE 249 AA; 26663 MW; 98323A43CA952879 CRC64; POTENTIAL.
 ALPHA-EXPANSIN.

Query Match 80.2%; Score 1118; DB 10; Length 249;
 Best Local Similarity 81.4%; Pred. No. 5.8e-93;
 Matches 201; Conservative 19; Mismatches 23; Indels 4; Gaps 1;

QY 8 PSLFLPPFFVTFADYGGWDSGHATFYGGDASGTMGACGYGNLYSQGYNT 63
 DB 3 PSILSLFFFSFCCHATFADYGGWDSGHATFYGGDASGTMGACGYGNLYSQGYNT 62
 QY 64 VALSTALFNNGSCGACFEWTCNDPKMCLPGTIRVATNFCPPNFALPNNGMWCNPL 123
 DB 63 ALSTALFNNGSCGACFEWTCNDPKMCLPGTIRVATNFCPPNFALPNNGMWCNPL 122

QY 124 QHFMADPAFLQIAQYRAGIVPSFRVPCMKKGAVFTINGHSYFNLVLTNNVGAGDV 183
 DB 123 QHFDLPAPFLQIAQYRAGIVPSFRVPCMKKGAVFTINGHSYFNLVLTNNVGAGDV 182
 QY 184 HSYSIKSRRTGWSMSRNNQNNNNYLNQGLSFQVTLSDGRTLTAVNLVPSNNQPGQ 243
 DB 183 QSVISIKSSNTGWTMSRNNQNNNNYLNQGLSFQVTLSDGRTLTAVNLVPSNNQPGQ 242
 QY 244 TYEGPQF 250
 DB 243 TFEBAQF 249

RESULT 9

Q9SBT1 PRELIMINARY; PRT; 253 AA.
 ID Q9SBT1
 AC Q9SBT1
 DT 01-MAY-2000 (Tremblrel. 13, Created)
 DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
 DT 01-MAR-2003 (Tremblrel. 23, Last annotation update)
 DE Expansin.
 GN EXP2.
 OS Fragaria ananassa (Strawberry).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC euroside 1; Rosales; Rosaceae; Rosoideae; Fragaria.
 OC NCBI_TaxID=3747;
 RN
 RP SEQUENCE FROM N.A.
 RC STRAIN=cv. Chandler;
 RA Clivello P.M., Sebenat A., Powell A.L.T., Bennett A.B.;
 RT "An expansin gene expressed in ripening strawberry fruit is auxin-independent."
 RL Plant Physiol. 12:1273-1279 (1999).
 CC -1- SIMILARITY: BELONGS TO THE EXPANSIN FAMILY.
 DR EMBL: AF159563; AF21101.1; -;
 DR InterPro: IPR007112; Expan_endogl.
 DR InterPro: IPR007118; Expan_Lol.pl.
 DR InterPro: IPR007117; Expan_Lol.pl.C.
 DR InterPro: IPR00408; Reg.chr.condens.
 DR Pfam: PF01357; Pollen.allergen; 1.
 DR PRINTS: PR01225; EXPANSINFAMILY.
 DR ProDom: PD002179; Expan_Lol.pl.C.1.
 DR PROSITE: PSS0843; EXPANSIN_CBD; 1.
 DR PROSITE: PSS0842; EXPANSIN_BG45; 1.
 DR PROSITE: PSS0626; RCC1_2; 1.
 SO SEQUENCE 253 AA; 26887 MW; CE39CF00ADEAICEF CRC64;
 Query Match 80.4%; Score 1117.5; DB 10; Length 253;
 Best Local Similarity 85.3%; Pred. No. 6.5e-93;
 Matches 197; Conservative 15; Mismatches 18; Indels 1; Gaps 1;
 QY 21 TFPADYG-GWOSGHAFTFGGSDAGTNGGACGYGNYSGYGTNTVALSTALFNNGLSCGA 79
 DB 23 TYADYGGWVGCHATFYGGDAGTNGGACGYGNYSGYGTNTVALSTALFNDGLSCGS 82
 QY 80 CFEMTCTNDPKWCLPGTIRVTATNFCPPNFPALPNNNGKCNPPLOHDMAPFLQIAQY 139
 DB 83 CYMRCDNDPKWCLPGSITVTATNFCPPNFPANQANDNGKCNPPLOHDMAPFLQIAQY 142
 QY 140 RAGIVPSFRVPCMKKGAVFTINGHSYFNLVLTNNVGAGDVHSYSIKSRRTGWSMS 199
 DB 143 RAGIVPSFRVPCMKKGAVFTINGHSYFNLVLTNNVGAGDVHSYSIKSRRTGWSMS 202
 QY 200 RNNQNNQNNNNYLNQGLSFQVTLSDGRTLTAVNLVPSNNQPGQTYEGPQF 250
 DB 203 RNNQNNQNNNNYLNQGLSFQVTLSDGRTLTAVNLVPSNNQPGQTYEGPQF 253
 RESULT 10
 Q9SMD4 PRELIMINARY; PRT; 253 AA.
 ID Q9SMD4
 AC Q9SMD4;

DT 01-MAY-2000 (Tremblrel. 13, Created)
 DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
 DT 01-MAR-2003 (Tremblrel. 23, Last annotation update)
 DE Expansin.
 GN EXP1.
 OS Rumex palustris.
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 OC Caryophyllidae; Caryophyllales; Polygonaceae; Rumex.
 OC NCBI_TaxID=50298;
 RN
 RP SEQUENCE FROM N.A.
 RC TISSUE=Leaf;
 RX MEDLINE=20330988; Pubmed=10872228;
 RA Vriezen W.H., De Graaf B., Mariani C., Voeseenck L.A.C.J.;
 RT "Submergence induces expansin gene expression in flooding-tolerant Rumex palustris and not in flooding-intolerant R. acetosa."
 RL Planta 210:956-963 (2000).
 CC -1- SIMILARITY: BELONGS TO THE EXPANSIN FAMILY.
 DR EMBL: AF167360; AAD4956.1; -;
 DR InterPro: IPR007112; Expan_endogl.
 DR InterPro: IPR007118; Expan_Lol.pl.
 DR InterPro: IPR007117; Expan_Lol.pl.C.
 DR Pfam: PF01357; Pollen.allergen; 1.
 DR PRINTS: PR01225; EXPANSINFAMILY.
 DR ProDom: PD002179; Expan_Lol.pl.C.1.
 DR PROSITE: PSS0843; EXPANSIN_CBD; 1.
 DR PROSITE: PSS0842; EXPANSIN_BG45; 1.
 DR PROSITE: PSS0626; RCC1_2; 1.
 SO SEQUENCE 253 AA; 27063 MW; 7DC75610C80B23A8 CRC64;
 Query Match 80.4%; Score 1116.5; DB 10; Length 253;
 Best Local Similarity 79.4%; Pred. No. 8e-93;
 Matches 201; Conservative 16; Mismatches 33; Indels 3; Gaps 2;
 QY 1 MAFYSPPSSFLLPF-FVFTPADYGG-GWOSGHAFTFGGSDAGTNGGACGYGNYSG 57
 DB 1 MAFQAFASLLILIVFOHFTISSAFQYGGDMNGHATFYGGDAGTNGGACGYGKLYSQ 60
 QY 58 GYGTNTVALSTALFNNGLSCGAFEMTCTNDPKWCLPGTIRVTATNFCPPNFPALPNNNG 117
 DB 61 GYGTSTALSTALFNNGLSCGAFEMTCTNDPKWCLPGTIRVTATNFCPPNFPALPNNNG 120
 QY 118 WCNPPLOHDMAPFLQIAQYRAGIVPSFRVPCMKKGAVFTINGHSYFNLVLTNN 177
 DB 121 WCNPPLOHDMAPFLQIAQYRAGIVPSFRVPCMKKGAVFTINGHSYFNLVLTNN 180
 QY 178 GGAGDVHSYSIKSRRTGWSMSRNNQNNNNYLNQGLSFQVTLSDGRTLTAVNLVPS 237
 DB 181 GGAGDVHSYSIKSRRTGWSMSRNNQNNNNYLNQGLSFQVTLSDGRTLTAVNLVPS 240
 QY 238 NNQPGQTYEGPQF 250
 DB 241 NNQPGQTYEGPQF 253

RESULT 11

Q8RVK6 PRELIMINARY; PRT; 254 AA.
 ID Q8RVK6
 AC Q8RVK6
 DT 01-JUN-2002 (Tremblrel. 21, Created)
 DT 01-JUN-2002 (Tremblrel. 21, Last sequence update)
 DT 01-MAR-2003 (Tremblrel. 23, Last annotation update)
 DE Expansin 1.
 GN EXP1.
 OS Malus domestica (apple) (Malus sylvestris).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC euroside 1; Rosales; Rosaceae; Maloideae; Malus.
 OC NCBI_TaxID=3750;
 RN
 RP SEQUENCE FROM N.A.
 RC STRAIN=cv. Granny Smith; TISSUE=Ripening fruit pulp;
 RT Clivello P.K., Solomos T.;

RT "Characterization of expansin cDNA from apple."
 RU Submitted (MAR-2002) to the EMBL/Genbank/DBJ databases.
 CC -1- SIMILARITY: BELONGS TO THE EXPANSIN FAMILY.
 DR EMBL: AY083166; AAM08928.1; -
 DR InterPro: IPR007112; Expan_endogl.
 DR InterPro: IPR007117; Expan_Lol PI C.
 DR InterPro: IPR000408; Reg chr condens.
 DR Pfam: PF01357; Pollen_allergen.1.
 DR ProDom: PD002179; Expan_Lol PI C; 1.
 DR PROSITE: PS50843; EXPANSIN_CBD; 1.
 DR PROSITE: PS50842; EXPANSIN_EG45; 1.
 DR PROSITE: PS00626; RCC1.2; 1.
 SQ SEQUENCE 254 AA; 27246 MW; 23FED3E8B0B3D6D CRC64;

Query Match 80.1%; Score 1116; DB 10; Length 254;
 Best Local Similarity 82.2%; Pred. No. 9e-93;
 Matches 198; Conservative 13; Mismatches 30; Indels 0; Gaps 0;

QY 10 SLFLPFFVFTFADY-GGWSGHATFYGGDASGTWGAAGYGNLYSGGYGNTVALSTA 69
 DB 14 SLVLENLHLHGLVATYGSWEVHAIFYGGDASATWGAAGYGNLYSGGYGNTVALSTA 73
 QY 70 LFNNGISCGACFEMTCTNDPKMLPGTIRVTATNFCPPNFALPNNNGMCNPLQHFDMA 129
 DB 74 LFNNGISCGSCYEMMCNNDPRMCRPGSIIVTATNFCPPNFABSDNDGMCNPLQHFDLA 133
 QY 130 EBAFLQIAQYRAGIVPSFRVPCMKKGVRFTNGHSYFNLYLTNVGAGDVHSVSIK 189
 DB 134 EBAFLQIAQYRAGIVPSFRVPCMKKGIRFTNGHSYFNLYLTNVGAGDVHSVSIK 193
 QY 190 GSRTGQMSRNMGMQMSNNYLNQGLSFQVTLSDGRITLVNLYPSMWRQGTGEGNO 249
 DB 194 GSRTGQMSRNMGMQMSNNYLNQGLSFQVTLSDGRITLVNLYPSMWRQGTGEGNO 253

QY 250 F 250
 DB 254 F 254

RESULT 12
 Q93XP2 PRELIMINARY; PRT; 253 AA.
 AC Q93XP2;
 DT 01-DEC-2001 (Tremblrel. 19, Created)
 DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)
 DT 01-MAR-2003 (Tremblrel. 23, Last annotation update)
 DE Expansin.
 GN EXP1.
 OS Prunus cerasus.
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC euroside I; Rosales; Rosaceae; Amygdaloideae; Prunus.
 OX NCB1_TaxID=140311;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=fruit;
 RA Yoo S.-D., Gao Z., Cantini C., Loescher W., van Nocker S.;
 RT "Coordinated expression of genes encoding expansins and other cell
 wall-modifying enzymes is associated with pectin-related changes in
 the cell wall during ripening of cherry (P. cerasus) fruit."
 RT Submitted (FEB-2001) to the EMBL/Genbank/DBJ databases.
 CC -1- SIMILARITY: BELONGS TO THE EXPANSIN FAMILY.
 DR EMBL: AF350936; AAK48845.1; -
 DR InterPro: IPR007112; Expan_endogl.
 DR InterPro: IPR007118; Expan_Lol PI C.
 DR InterPro: IPR007117; Expan_Lol PI C.
 DR Pfam: PF01357; Pollen_allergen.1.
 DR PRINTS: PR01225; EXPANSINFAMILY.
 DR ProDom: PD002179; Expan_Lol PI C; 1.
 DR PROSITE: PS50843; EXPANSIN_CBD; 1.
 DR PROSITE: PS50842; EXPANSIN_EG45; 1.
 SQ SEQUENCE 253 AA; 26861 MW; 9C24484F14AA52CD CRC64;

Query Match 79.9%; Score 1113.5; DB 10; Length 253;
 Best Local Similarity 79.4%; Pred. No. 1.5e-92;
 Matches 201; Conservative 23; Mismatches 26; Indels 3; Gaps 3;

QY 1 MAF-SYSPSSLP-LLPFFVFTFADY-GGWSGHATFYGGDASGTWGAAGYGNLYSQ 57
 DB 1 MAFSHLTLALFVSVNLCLQGTGYDGGWEGHATFYGGDASGTWGAAGYGNLYSQ 60
 QY 58 GYGTNTVALSTALFNNGISCGACFEMTCTNDPKMLPGTIRVTATNFCPPNFALPNNNG 117
 DB 61 GYGTNTVALSTALFNDGLSCGSCYEMRCDSPKMLPGSIIVTATNFCPPNFALQSDNDG 120
 QY 118 WCNPLQHFDMAPFAFLQIAQYRAGIVPSFRVPCMKKGVRFTNGHSYFNLYLTNV 177
 DB 121 WCNPLQHFDMAPFAFLQIAQYRAGIVPSFRVPCVKKGIRFTNGHSYFNLYLTNV 180
 QY 178 GGAGDVHSVSIKSGRTGQMSRNMGMQMSNNYLNQGLSFQVTLSDGRITLVNLYPS 237
 DB 181 GGAGDVHSVSIKSGRTGQMSRNMGMQMSNNYLNQGLSFQVTLSDGRITLVNLYPS 240
 QY 238 NMFGQGTGEGNOF 250
 DB 241 NMFGQGTGEGNOF 253

RESULT 13
 Q9FS30 PRELIMINARY; PRT; 252 AA.
 AC Q9FS30;
 DT 01-MAR-2001 (Tremblrel. 16, Created)
 DT 01-MAR-2001 (Tremblrel. 16, Last sequence update)
 DT 01-MAR-2003 (Tremblrel. 23, Last annotation update)
 DE Expansin.
 GN PPEXP1.
 OS Prunus persica (Peach).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC euroside I; Rosales; Rosaceae; Amygdaloideae; Prunus.
 OX NCB1_TaxID=3760;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Hayama H.;
 RT "Homolog to expansin in peach fruit."
 RT Submitted (JUN-1999) to the EMBL/Genbank/DBJ databases.
 CC -1- SIMILARITY: BELONGS TO THE EXPANSIN FAMILY.
 DR EMBL: AB029083; BAB19676.1; -
 DR InterPro: IPR007112; Expan_endogl.
 DR InterPro: IPR007118; Expan_Lol PI C.
 DR InterPro: IPR007117; Expan_Lol PI C.
 DR Pfam: PF01357; Pollen_allergen.1.
 DR PRINTS: PR01225; EXPANSINFAMILY.
 DR ProDom: PD002179; Expan_Lol PI C; 1.
 DR PROSITE: PS50843; EXPANSIN_CBD; 1.
 DR PROSITE: PS50842; EXPANSIN_EG45; 1.
 SQ SEQUENCE 252 AA; 26743 MW; BF0B86FE0C060482 CRC64;

Query Match 79.7%; Score 1111; DB 10; Length 252;
 Best Local Similarity 80.2%; Pred. No. 2.5e-92;
 Matches 203; Conservative 21; Mismatches 25; Indels 4; Gaps 4;

QY 1 MAF-SYSPSSLP-LLPFFVFTFADY-GGWSGHATFYGGDASGTWGAAGYGNLYSQ 57
 DB 1 MAFSHLTLALFVSVNLCLQGTGYDGGWEGHATFYGGDASGTWGAAGYGNLYSQ 60
 QY 58 GYGTNTVALSTALFNNGISCGACFEMTCTNDPKMLPGTIRVTATNFCPPNFALPNNNG 117
 DB 61 GYGTNTVALSTALFNDGLSCGSCYEMRCDSPKMLPGSIIVTATNFCPPNFALQSDNDG 120
 QY 118 WCNPLQHFDMAPFAFLQIAQYRAGIVPSFRVPCMKKGVRFTNGHSYFNLYLTNV 177
 DB 121 WCNPLQHFDMAPFAFLQIAQYRAGIVPSFRVPCVKKGIRFTNGHSYFNLYLTNV 180
 QY 178 GGAGDVHSVSIKSGRTGQMSRNMGMQMSNNYLNQGLSFQVTLSDGRITLVNLYPS 237

Db 181 GGAGDVHSYISKSSKTKGMQMSRNMQNMNSYINGALSFQVTTSDGRITVS-NAVPA 235

QY 238 NMQFGQTYEGPQF 250

Db 240 NMQFGQTFSSGQF 252

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: December 18, 2003, 23:23:52 ; Search time 2047 Seconds
(without alignments)
2968.304 Million cell updates/sec

Title: US-09-383-579C-10
Perfect score: 1194
Sequence: 1 MAFSYPSSSLFLPFFVF.....AYNLVPSNMVFGQYEGPQF 250

Scoring table:
BLOSUM62
Xgapop 10.0, Xgapext 0.5
Ygapop 10.0, Ygapext 0.5
Fgapop 6.0, Fgapext 7.0
Delop 6.0, Delext 7.0

Searched: 22781392 segs, 1215238056 residues

Total number of hits satisfying chosen parameters: 45562784

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
-MODEL=frame+ p2n model -DEV=xld
-Q/cgnt_1/USFTO.spool/p/US933579/runat.18122003.171927.28784/app.query.fasta.1.391
-DB=EST -QPM=fastcap -SUFFIX=ret -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bite -START=1 -END=1 -MATRIX=blsum62 -TRANS=human40.cdi -LIST=45
-DOCALLIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pct -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USRR=US09383579 @CGN 1.1 3549 @runat.18122003.171927.28784 -NCPU=6 -ICPU=3
-NMR MAP -LARGEOUTRY -NBS SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :
EST:
1: em_estba:*
2: em_estbnum:*
3: em_estin:*
4: em_estnu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_hnc:*
9: gb_est1:*
10: gb_est2:*
11: gb_hnc:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: em_gss_hum:*
18: em_gss_inv:*
19: em_gss_pln:*
20: em_gss_vtc:*
21: em_gss_fun:*
22: em_gss_mam:*
23: em_gss_mus:*
24: em_gss_pro:*
25: em_gss_rnd:*
26: em_gss_phg:*
27: em_gss_vrl:*
28: gb_gss1:*

29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1173.5	84.2	880	14	CD574577
2	1153.5	82.7	816	14	CD575807
3	1144.5	82.1	809	14	CB291406
4	1138	81.6	838	14	CB980842
5	1134.5	81.4	799	14	CB293003
6	1123.5	80.6	798	10	BG581975
7	1100.5	78.9	736	14	CD486517
8	1099	78.8	772	14	CB980777
9	1097.5	78.7	788	14	CB290960
10	1081	77.5	767	12	BI932999
11	1078	77.3	864	14	CB822230
12	1070.5	76.8	881	14	CD484188
13	1061	76.1	845	10	BE131139
14	1060	76.0	747	13	BQ990398
15	1059	76.0	685	13	BUR15493
16	1056	75.8	816	10	BG645633
17	1045.5	75.0	770	12	BW780176
18	1044	74.9	656	13	BQ986992
19	1044	74.8	878	14	CD574625
20	1043	74.8	786	13	BQ165503
21	1042	74.7	868	10	BG446553
22	1041	74.7	843	14	CB979649
23	1039.5	74.6	719	14	CA785153
24	1027	73.7	730	14	CA917809
25	1027	73.7	1106	14	AY104146
26	1026	73.6	859	14	CD574696
27	1022	73.3	688	14	CB8007302
28	1021.5	73.3	723	14	CB292105
29	1019	73.1	699	14	CA840495
30	1015	72.8	646	9	AW574064
31	1014	72.7	656	13	BUR92415
32	1013.5	72.7	727	14	CA917661
33	1008	72.3	966	10	BE055631
34	999	71.7	656	13	BUR93884
35	998.5	71.6	620	13	BU044752
36	997.5	71.4	611	13	BU044997
37	996	71.4	792	12	BI179439
38	995	71.4	745	9	AW299054
39	994.5	71.3	733	14	CB978414
40	991	71.1	775	10	BE034856
41	989	70.9	710	12	BI931078
42	987.5	70.8	754	12	BI978130
43	986.5	70.8	741	12	BI909709
44	981	70.4	617	13	BO852261
45	980	70.3	727	14	CA800212

ALIGNMENTS

RESULT 1
CD574577
LOCUS
DEFINITION
CD574577
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

880 bp mRNA linear EST 12-JUN-2003
UCRPT01_06.G11.T3 Poncirus trifoliata CTV-challenged cDNA library -
UCR Poncirus trifoliata cDNA clone UCRPT01_06.G11, mRNA sequence.
CD574577.1 GI:31670479
EST.
Poncirus trifoliata
Poncirus trifoliata
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids
; eurosids II; Sapindales; Rutaceae; Poncirus.

FEATURES
Source

Location/Qualifiers
1. 816
/organism="Poncirus trifoliata"
/mol_type="mRNA"
/cultiyar="Pomeyoy Op"
/db_xref="taxon:37690"
/clone="UCRPT01.01a606"
/issue_type="Phloem"
/dev_stage="10 - 30 cm shoots"
/lab_host="E. coli TUC121"
/clone_lib="Poncirus trifoliata CTV-challenged cDNA library - AGI"
/note="Vector: Lambda Uni-ZAP XR, excised phagemid; Site 1: EcoRI, Site 2: XhoI; Plants were grown in the greenhouse at University of California, Riverside. The section was an open-pollinated (very probably selfed) seedling of Poncirus trifoliata cv Pomeyoy that was selected as homozygous for the CTV resistance gene. The rootstock was sweet orange infected with citrus tristeza virus (CTV) isolate T514 over 1 year before sampling (CTV infects sweet orange, but not genotypes carrying the CTV resistance gene. Shoots 10-30 cm long were harvested in October 2000, and the green phloem (bark) was removed and frozen quickly in dry ice. Total RNA was extracted using Trizol reagent (Gibco). Poly(A) RNA was purified, a cDNA library was made, and 0.5 million primary lambda cDNA clones were in vivo excised to give a population of phagescript SK(-) phagemids. All steps to this point were performed in the MU-Rose lab at the University of California, Riverside by X. Ye. Phagemids were plated, plasmid DNA purified, cDNA clones archived, and DNA sequences determined bi-directionally using an ABI3730 at the Arizona Genomics Institute, University of Arizona (Collura, Feuerbacher, Kim, Kudrna, Ming, Yu). Chromatogram files were transmitted to UC Riverside (by Yu), then processed at UC Riverside (by Manamaker) using the HarVest pipeline (http://harvest.ucr.edu) to remove vector and cloning oligo sequences and various contaminants, and to trim to a high quality region. Sequences that retained a phred 17 region of at least 100 bases were deposited to GenBank."

BASE COUNT 210 a 196 c 195 g 215 t
ORIGIN

Alignment Scores:

Pred. No.: 7.82e-98 Length: 816
Score: 1153.50 Matches: 206
Percent Similarity: 90.65% Conservative: 17
Best Local Similarity: 83.74% Mismatches: 22
Query Match: 82.75% Indels: 1
DB: 14 Gaps: 1

US-09-383-579C-10 (1-250) x CD575807 (1-816)

QY 1 MetAlaPheSerTyrSerProPheSerSerLeuPheLeuPheValPhe 20
Db 77 ATTGACGACATCATCTAGTGTGCTCTCTTTGTTGTGCTCAATTTGCTTCGCGC 136
QY 21 ThrPheAlaAspTyr--GlyGlyTTPGlnSerGlyHisAlaThrPheTyrGlyGly 39
Db 137 ACAATTGGACATCATGTGTGTGGTGGCAAGTGGCATCACTTCTATGAGGGGGT 196
QY 40 AspAlaSerGlyThrMetGlyValAlaCysGlyTyrTyrGlyLeuTyrSerGlnGlyTyr 59
Db 197 GAGGCTTCGGGCAACATGGGTGGTGTGGGATGACCAATTTGATACCAAGGCTAT 256
QY 60 GlyThrAsnThrValAlaLeuSerThrAlaLeuPheAsnAsnGlyLeuSerCysGlyAla 79
Db 257 GGGACTAACACTGAGACCTTAGTACCGCTCTATCAACAATGGCCTTAAGCTGGGTCA 316
QY 80 CysPheGluMetCysThrAsnAspProlCysTyrCysLeuProlGlyThrIleArgVal 99
Db 317 TGGTATGAATGAATGTGAATGACCCCAAGTGGTCTCCCGGCTCCATCATTTGTC 376

QY 100 ThrAlaThrAsnPheCysProPheAsnPheAlaLeuProAsnAsnGlyGlyTyrCys 119
Db 377 ACCGACCAACCACTTTCGCCACCTTAACCTTGCTGTACTAACGACCAAGCGGTGGTGC 436
QY 120 AsnProProlGlnGlnHisPheAspMetAlaGlnProlAlaPheLeuGlnIleAlaGlnTyr 139
Db 437 AATCTTCCTCCGACGACTTGAACATGCTGACCGCCCTTTCTTCAAAATGGCCCAATAC 496
QY 140 ArgAlaGlyIleValProValSerPheAsnArgValProCysMetGlyGlyVal 159
Db 497 CGTCCCGTATCGTCCCAATTTCTTCAGAGAGATCCGTGTGGAAGAAAGAGGAAATA 556
QY 160 ArgPheThrIleAsnGlyHisSerTyrPheAsnLeuValLeuIleThrAsnValGlyGly 179
Db 557 AGGTTTACCTCATGACACTCATCTACTTCACTGTTTGTATCAAAATGTCGAGGA 616
QY 180 AlaGlyAspValHisSerValSerIleGlySerArgThrGlyTyrGlnSerMetSer 199
Db 617 GCAGGAGATGTGATTCAGTATCAATCAACAGGTTCAAGACTGATGCAAGCAATGTCA 676
QY 200 ArgAsnTyrGlyGlnGlnSerTyrGlnSerAsnAsnTyrIleAsnGlyGlnGlyLeuSerPhe 219
Db 677 AGGAACTGGGGCCCAAAATGGCAGAGCAATCTTATCTTAAACGCAAGCTTTCTTTC 736
QY 220 GlnValThrLeuSerAspGlyArgThrLeuThrAlaThrAsnLeuValProSerAsnTyr 239
Db 737 CAAGTACAGCCAGCTGACGACGACGACTGTACTACGACAAATGTGTGCTGCAAAATGG 796
QY 240 GlnPheGlyGlnThrTyr 245
Db 797 CAATTGGGCAACCTT 814

RESULT 3

CB291406

LOCUS

DEFINITION

CB291406 809 bp mRNA linear EST 28-FEB-2003
UCRCS01_02dd11.g1 Washington Navel orange cold acclimated flavedo & albedo cDNA library Citrus sinensis cDNA clone UCRCS01_02dd11, mRNA sequence.

ACCESSION

CB291406
CB291406.1 GI:28616863

VERSION

KEYWORDS

EST.

SOURCE

Citrus sinensis

ORGANISM

Bakaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosids ; eurosids II; Sapindales; Rutaceae; Citrus.

REFERENCE

1 (bases 1 to 809)
Close,T.J., Collura,K., Fenton,R.D., Feuerbacher,O., Kim,H.R., Kudrna,D., Manamaker,S., Ming,R. and Yu,Y.

TITLE

Development of EST Resources and New Genetic Markers for California Citrus

JOURNAL

Unpublished
Contact: Timothy Close

COMMENT

Department of Botany & Plant Sciences, University of California
Riverside, CA, 92521-0124

AUTHORS

Tel: 9097873318
Fax: 9097874437
Email: timothy.close@ucr.edu
Seq primer: T3.

FEATURES

Source

1. 809
/organism="Citrus sinensis"
/mol_type="mRNA"
/cultiyar="Washington Navel"
/db_xref="taxon:2711"
/clone="UCRCS01_02dd11"
/issue_type="Rind containing flavedo and albedo"
/dev_stage="Mature fruit"
/lab_host="E. coli TUC121"
/clone_lib="Washington Navel orange cold acclimated flavedo & albedo cDNA library"
/note="Vector: Lambda Uni-ZAP XR, excised phagemid;

Site 1: Ecobri; Site 2: Xhol; Plants were grown in the field at University of California, Riverside Agricultural Operations since 1983. The scion was Washington Navel Orange and the rootstock Carizzo Citrange. Tissue from mature fruit was harvested at mid-day in January 2002 during a cold spell, when pre-dawn temperatures were approximately -2 to 2 degree C. Approximately 2 cm median sections of the rind were excised in the field from several fruits, then wrapped in aluminum foil and frozen quickly in dry ice. Total RNA was extracted using a phenol extraction procedure described in J. Japanese Soc. Hort. Sci. (1996) 64:809-814. Poly(A) RNA was purified. A cDNA library was made, and 1 million primary lambda cDNA clones were in vivo excised to give a population of plasmid clones SK(-) phagemids. All steps to this point were performed in the JV Close lab at the University of California, Riverside (Penton). Phagemids were plated, plasmid DNA purified, cDNA clones archived, and DNA sequences determined bi-directionally using an ABI3130 at the Arizona Genomics Institute, University of Arizona (Collura, Feuerbacher, Kim, Kudrna, Wing, Yu). Chromatogram files were transmitted to UC Riverside (by Yu), then processed at UC Riverside (by Manamaker) using the Harvest pipeline (<http://harvest.ucr.edu>) to remove vector and cloning oligo sequences and various contaminants, and to trim to a high quality region. Sequences that retained a paired 17 region of at least 100 bases were deposited to GenBank."

BASE COUNT 210 a 196 c 191 g 212 t
ORIGIN

Alignment Scores:

Pred. No.: 5,38e-97 Length: 809
Score: 1144.50 Matches: 204
Percent Similarity: 90.61% Conservative: 18
Best Local Similarity: 83.27% Mismatches: 22
Query Match: 82.10% Indels: 1
DB: 14 Gaps: 1

US-09-383-579c-10 (1-250) x CB291406 (1-809)

Qy 1 MetAlaPheSerTySerProPheSerSerLeuPheLeuLeuProPhePheValPhe 20
Db 73 ATTGACAGCATCTAGTGTGTGCTCTCTTTGTTGCTCAATTTTGTCTTCTGCGC 132
Qy 21 ThrPheAlaAspTy--GlyGlyTTPGInSerGlyVHAlaThrPheTyGlyGly 39
Db 133 ACATTGGAGACTATGTGTGGTGGCAAGGCGCATGCACTTCTATGGCGGGGT 192
Qy 40 AspAlaSerGlyThrMetGlyGlyAlaCysGlyTYTGGlyAsnLeuTYTSerGInGly 59
Db 193 GATGCTTCGGGCAATGGGTGTGTGTGGTATGGCAATTTGTACAGCCAAAGCTAT 252
Qy 60 GlyThrAsnThrValAlaLeuSerThrAlaLeuPheAsnAsnGlyLeuSerCysGlyAla 79
Db 253 GGGACTAACACTGCATCACTCACTACCGCTCTATTACAACTAGCCTTAGCTGTGTA 312
Qy 80 CysPheGluMetThrCysThrAsnAspProGlyTTPCysLeuProGlyThrIleArgVal 99
Db 313 TCTATGAATGAAATGTAAATGACCCCAAGTGTGCTCCCGGCTTCATCATTTGTC 372
Qy 100 ThrAlaThrAsnPheCysProProAsnPheAlaLeuProAsnAsnAsnGlyTTPCys 119
Db 373 ACCGCGACCAACTCTGCGCACCTTACCTTGCCCTCTCTAACGACAAACGGCGTGTGC 432
Qy 120 AsnProProLeuGlnHisPheAspMetAlaGluProAlaPheLeuGlnIleAlaGlnTY 139
Db 433 AATCTCCCTCCAGACCTTTGACATGCTGAGCCGCTTTCTTGCAATTTGCCCAATTC 492
Qy 140 ArgAlaGlyIleValProValSerPheArgValProCysMetIysGlyGlyVal 159
Db 493 CGGCGCGATGTGCTCCCAATTTCTTCAAGAGATCCCGGTGCGAAGAAAGAGAAATA 552
Qy 160 ArgPheThrIleAsnGlyHisSerTyPheAsnLeuValLeuIleThrAsnValGlyGly 179

Db 553 AGCTTACCGGTAAATGACACCTCATCTTCAACCTGCTTTTCATACAAATTCGAGGA 612
Qy 180 AlagIAspValHisSerValSerIleLeuSerArgThGlyTTPGInSerMetSer 199
Db 613 CGAGAGATGTACATTCACTGATATCAATCAAGAGGTTCAAGAGCTGATGCGAACATGTCA 672
Qy 200 ArgAsnTTPGlyGlnAsnTTPGInSerAsnAsnTYTLeuAsnGlyGlnGlyLeuSerPhe 219
Db 673 AGGAACGTGGGCGCAAAATTTGCGAGCAATTTTATCTTAAAGGGCAAGTTTCTTTC 732
Qy 220 GlnValThrLeuSerAspGlyArgThrLeuThrAlaTYAAsnLeuValProSerSerTTP 239
Db 733 CAATTGACAGCCAGATGACGCGACGACTGTGACTACACAAATGTTGTGCTGAAATTGG 792
Qy 240 GlnPheGlyGlnThr 244
Db 793 CAATTGGCGAACC 807

RESULT 4

CB980842

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

FEATURES

source

Expressed sequence tags from cabernet sauvignon berries at various developmental stages
Unpublished
Contact: Douglas Cook, PhD
CAES Genome Facility
UC Davis, Plant Pathology
One Shields Ave, Davis, CA 95616, USA
Tel: 530 754 6561
Fax: 530 754 6617
Email: drcoc@ucdavis.edu
Seq primer: GCCAAGCATGTCTAG.
Location/Qualifiers
1..838
/organism="Vitis vinifera"
/mol_type="mRNA"
/cultivar="Cabernet Sauvignon"
/db_xref="taxon:29760"
/clone="CAB70003_Iiar_A03"
/sex="Hermaphrodite"
/dev_stage="Post-Veraison, 18-19 brix"
/lab_host="DHSalpa"
/clone_lib="Cabernet Sauvignon Berry Post-Veraison - CAB7"
/note="Organ: Berry; Vector: pDNR; Site 1: S11; Site 2: S11; CAB7 is a cDNA library of Cabernet Sauvignon Clone 8 berries. Samples were collected post-veraison from field-grown vines during stage III of berry growth at 89 days after full bloom. Berries soluble solid concentration ranged between 18-19 brix. Sampled vines were located at the University of California, Davis, Experimental Vineyard. cDNAs were made by oligo-dT priming and directly cloned. 5' and 3' adaptors were used in cloning as follows: 5'-AAGCAGTGTATCAAGCAGAGCGCATACGCGCG-3' and 5'-ATTCTAGAGCCGAGCGCGCACATG-dT(30)-NN-3'. Library was constructed using the Clontech Creator SMART kit and size-selected to contain the 0.5-3 kb size fraction."

BASE COUNT 192 a 233 c 219 g 194 t
ORIGIN

Db 540 GGAATCAGATTCAATTAATGACACTCATCTTCAACTGTTTGGTTCACAATGTT 599

Qy 178 G1yG1yAlaG1yAspValHisSerValSerIleLeuGlySerArgThrGlyTrpGlnSer 197

Db 600 GGTGGAGCTGGAGATGATCATCTGTGTCTCCATCAAGGATCAAGAGATCGATGCAAGCT 659

Qy 198 MetSerArgAsnTrpGlyGlnAsnTrpGlnSerAsnAsnTrpLeuAsnGlyGlnGlyLeu 217

Db 660 ATGCTGAGAACTGGGGGCAAGACTGGCAAGCAATCACTATCTCAATGTGCAAGCTC 719

Qy 218 SerPheGlnValThrLeuSerAspGlyArgThrLeuThrAlaTrpAsnLeuValProSer 237

Db 720 TCATTCAGAGCTACAGAGATGATGAGATCACTACTAGCAACAAAGCTTGCTCCG 779

Qy 238 AsnTrpGlnPheGlyGln 243

Db 780 AATTGGCAATTGGACAG 797

RESULT 7

CD486517 736 bp mRNA linear EST 04-JUN-2003

LOCUS CRH3.3F02 Cotton Root and Hypocotyl Lambda ZIPLOX Library (CRH)

DEFINITION Gossypium hirsutum cDNA clone CRH3.3F02 5' similar to expansin,

ACCESSION CD486517

VERSION CD486517.1 GI:31407482

KEYWORDS EST.

SOURCE Gossypium hirsutum (upland cotton)

ORGANISM Gossypium hirsutum

REFERENCE Baskaraya; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids ; eucosids II; Malvales; Malvaceae; Malvoideae; Gossypium.

AUTHORS 1. (bases 1 to 736)

TITLE Dowd, C., Wilson, I. and McFadden, H.

JOURNAL Different Gene Expression Responses in Cotton Root and Hypocotyl tissues during infection with Fusarium wilt disease

COMMENT Unpublished (2003)

CONTACT: Cairtriona Dowd, Helen McFadden

COMMONWEALTH Scientific and Industrial Research Organisation

DIVISION of Plant Industry

BLACK MOUNTAIN Laboratories, Cnr Clunies Ross Street & Barry Drive,

Black Mountain, Canberra, ACT, 2601, Australia

TEL: 61 2 6246 4914, 6246 5377

FAX: 61 2 6246 5000

EMAIL: Cairtriona.Dowd@csiro.au, Helen.McFadden@csiro.au

VECTOR clipped sequences Bases 1-17 (GTGACCCACGCGTCCG): SalI adapter

Seq primer: M13 reverse primer

High quality sequence stop: 736.

FEATURES

source

1..736

/organism="Gossypium hirsutum"

/mol_type="mRNA"

/cultiivar="DeltaEMERALD"

/db_xref="taxon:3635"

/clone="CRH3.3F02"

/tissue_type="Root and hypocotyl tissues"

/dev_stage="5 day old seedlings"

/lab_host="Y1090(ZL)"

/library="lib=Cotton Root and Hypocotyl Lambda ZIPLOX Library (CRH)"

/notes="Vector: Lambda ZIPLOX; Site 1: SalI; Site 2: NotI; mRNA was prepared from root and hypocotyl tissues of the cotton cultivar DeltaEMERALD. cDNA was synthesised from a NotI-oligo(dT) primer/adaptor using the manufacturers protocols (Life Technologies) and then ligated to a SalI adaptor to facilitate directional cloning. The cDNA was cloned into the SalI and NotI sites of the Lambda ZIPLOX phage vector (Life Technologies). Constructed by Cairtriona Dowd and Helen McFadden."

BASE COUNT 182 a 188 c 176 g 190 t

ORIGIN

Alignment Scores:

Pred. No.: 6,36e-93 Length: 736

Score: 1100.50 Matches: 198

Percent Similarity: 90.60% Conservative: 14

Best Local Similarity: 84.62% Mismatches: 17

Query Match: 78.95% Indels: 5

DB: 14 Gaps: 2

US-09-383-579c-10 (1-250) x CD486517 (1-736)

Qy 6 SerProPheSerSer-----LeuPheLeuLeuProPhePheValPheThr 21

Db 33 TCACCATTTTCTACTCTTCTTAATCTTCACTTTCACCTTGAGAACACC 92

Qy 22 PheAlaAspTyr---GlyGlyTrpGlnSerGlyHisAlaThrPheTyrGlyGlyAsp 40

Db 93 ATTGTGACTATGAGTGGAGATGGAGGATGGATGATGATGATGATGATGATGATGAT 152

Qy 41 AlaSerGlyThrMetGlyGlyAlaCyGlyGlyTrpGlyAsnLeuTyrSerGlnGlyTyrGly 60

Db 153 GCATCCGGACCAATGGAGAGTCTTGATGATGATGATGATGATGATGATGATGATGAT 212

Qy 61 ThrAsnThrValAlaLeuSerThrAlaLeuPheAsnAsnGlyLeuSerCyGlyAlaCys 80

Db 213 ACCAACACACACACACACTTACACTGCTTTCACATGAGGTTGAGCTGTTCTTGT 272

Qy 81 PheGluMetThrCysThrAsnAspProLeuTyrProGlyThrIleArgValThr 100

Db 273 TATGAAATGAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 332

Qy 101 AlaThrAsnPheCysProProAsnPheAlaLeuProAsnAsnGlyGlyTyrCyAsn 120

Db 333 GCCACCAATTTTGTGCTCCCTTAATTTTGTCTTGCATATATATGATGATGATGATGAT 392

Qy 121 ProProLeuGlnHisPheAspMetAlaGlnProAlaPheLeuGlnIleAlaGlnTyrArg 140

Db 393 CTTCCATTTGCCAACACTTGTATTTGGCCGACCTGCTTTTGCACAAATAGCTCAATACGT 452

Qy 141 AlaGlyIleValProValSerPheArgValProCysMetLeuGlyGlyValArg 160

Db 453 GCTGGATTTGTACCGTTTATTCAGAGAGTCCAGTATTAAGAAAGAGAGATCGCA 512

Qy 161 PheThrIleAsnGlyHisSerTyrPheAsnLeuValLeuIleThrAsnValGlyAla 180

Db 513 TTCAACATCAAGCGCCACTATCTTCACTTGTCTTAATCACTTAACGTTGGCGCGCC 572

Qy 181 GlyAspValHisSerValSerIleLeuGlySerArgThrGlyTrpGlnSerMetSerArg 200

Db 573 GGAAGATGCCACTCGGTGTGATCAAGGCTGCAAACTGGTGGCAAGCAATGTCAAG 632

Qy 201 AsnTrpGlyGlnAsnTrpGlnSerAsnAsnTrpLeuAsnGlyGlnGlyLeuSerPheGln 220

Db 633 AACTGGGGCCAGAACTGGCAGACCAACACTTACTCAACGCGCAACCCCTGCTTTCCAA 692

Qy 221 ValThrLeuSerAspGlyArgThrLeuThrAlaTrpAsnLeu 234

Db 693 GTCAACCAAGAGATGGCAAGACTTCAACCACTCAACCTC 734

RESULT 8

CB980777 772 bp mRNA linear EST 01-MAY-2003

LOCUS CAB70003.11AF_A03 Cabernet Sauvignon Berry Post-Version - CAB7

DEFINITION Vitis vinifera cDNA clone CAB70003.11AF_A03 5', mRNA sequence.

ACCESSION CB980777

VERSION CB980777.1 GI:30303983

KEYWORDS EST.

SOURCE Vitis vinifera

ORGANISM Vitis vinifera

REFERENCE Baskaraya; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids ; Vitaceae; Vitis.

AUTHORS 1. (bases 1 to 772)

Goes da Silva, F., Iandolo, A., Lim, H., Baek, J., Jones, K. and Cook

TITLE 'D. Expressed sequence tags from cabernet sauvignon berries at various developmental stages
JOURNAL unpublished
COMMENT Contact: Douglas Cook, PhD

BASE COUNT ORIGIN	175 a	222 c	202 g	172 t	1 others
----------------------	-------	-------	-------	-------	----------

Alignment Scores:	
Pred. No.:	9, 24e-93
Score:	1099.00
Percent Similarity:	87.04%
Best Local Similarity:	78.54%
Query Match:	78.84%
OB:	14
Length:	772
Matches:	194
Conservative:	21
Mismatches:	28
Indels:	1
Gaps:	1

US-09-383-579C-10 (1-250) x CB980777 (1-772)

```

Oy 1 MetalAlaPheSerTyrSerProPheSerSerLeuPheLeuLeuProPhePheValPhe 20
Db 31 CTCTCAATGGCTACTGACGACGACATTTCTTTCTATCTCTCTTGGCCCTCTTCTCTCTGTGCTA 90
Oy 21 -----ThrPheAlaAspTyrGlyGlyTyrGlnSerGlyHisAlaThrPheTyr 36
Db 91 TGCTTCCAAAGGACCAAAATGGTACTATATGGGGGTGGGAAGGTGGACATGCCAATTCTAT 150
Oy 37 GlyGlyGlyAspAlaSerGlyThrMetGlyGlyAlaCysGlyTyrGlyAsnLeuTyrSer 56
Db 151 GCGCGGTGGTGAAGCCCTCAGGACCAATGGGTGGGGCTTGTGGTATATGGCACTTGTAAGC 210
Oy 57 GlnGlyTyrGlyThrAsnThrValAlaLeuSerThrAlaLeuPheAsnAsnGlyLeuSer 76
Db 211 CAAGGGTATAGGGAGCCAAACACTGACGCTCTCAGACACGCTCTCTTCCAACAGTGGGCTAGC 270
Oy 77 CysGlyAlaCysPheGlnMetThrCysThrAsnAspProLysTyrTyrCysLeuProGlyThr 96
Db 271 TGTGGGGCAATGTTATCAGATGAAATCCAAAGCAAGAACCCCAAAATGGTGCTCCACGGAGAC 330
Oy 97 IleArgValThrAlaThrAsnPheCysProProAsnPheAlaLeuProAsnAsnAsnGly 116
Db 331 CTAACTGTACTGCGCCCAAACTTCTGTGGCTCTCTTAATCTGGCTTGTGTCCAACCAACGAGC 390

```

Oy	117	GI ¹ TrpCysAsnProProlLeuGlnHisPheAspMetAlaGluProAlaPheLeuGlnIle	136
		:::	
Db	391	GGAGGTGGCAATCCCCCTTCAGCACTTGATGCTACTAGCTGGCTTCCTTCACATT	450
Oy	137	AlaGlnTyrArgAlaGlyIleValProValSerPheArgArgValProCysMetLeuLys	156
		:::	
Db	451	GCCAGTATCCGAGCTGGATCGATACCTGTCTCTTCGAAAGAGTCCCTGTGTGAAGAAA	510
Oy	157	GI ¹ GlyValAlaArgPheThrIleAsnGlyHisSerTyrPheAsnLeuValIleThrAsn	176
		:::	
Db	511	GGAGGAGTATCCGCTTTACCATCAACAGGCGCACTCCACTTCAACTGGTGCTATCAACAC	570
Oy	177	ValGI ¹ GlyIleValIleAspValHisSerValSerIleLeuGlySerArgThrGlyTrpGln	196
		:::	
Db	571	GTGGCCGGAGCGGGAGACGTCAAGGCGAGTCAATAAGGGGGCTTAAGACCGGGTGGCAG	630
Oy	197	SerMetSerAlaArgAsnTrpGlyGlnAsnTrpGlnSerAsnAsnTyrLeuAsnGlyGlnGly	216
		:::	
Db	631	CCCATGTTCAGAGAACTGGGGCCAGAACTGGCCAGAGCAATCAATCACTCAACCGGMAACC	690
Oy	217	LeuSerPheGlnValThrLeuSerAspGlyArgThrLeuThrAlaTyrAsnLeuValPro	236
		:::	
Db	691	CTTCATTTCCAAAGTCAAGACGAGGAGTGGCCGGACCATATCAAGCCTCAATGTGGCGCT	750
Oy	237	SerAsnTrpGlnPheGlyGln	243
		:::	
Db	751	GCTGGCTGGCAGTTGGGCAA	771

LOCUS	DEFINITION
CB290960	788 bp mRNA linear EST 28-FEB-2003
CB290960	UCCSC01_02af04 g1 Washington Naval orange cold acclimated flavedo & albedo cDNA library Citrus sinensis cDNA clone UCCSC01_02af04, mRNA sequence.

ACCESSION	CB290960
VERSION	CB290960.1
	GI:28616417

KEYWORDS
SOURCE

ORGANISM

1 (bacc 1 to 700)
1 eurosids II; Sapindales; Rutaceae; Citrus.

REFERENCE
1. Leases L. C. 1981.
Close, T. J., Coltura, K., Fenton, R. D., Feuerbacher, O., Kim, H. R.,
Kudrna, D., Wamamater S., Wing P. and Yu Y.

TITLE
Development of EST Resources and New Genetic Markers for California Citrus

JOURNAL Unpublished
COMMENT Contact: Timothy Close

Department of Botany & Plant Sciences, University of California
Riverside, CA, 92521-0124

Tel: 9097873318
Fax: 9097874437

Email: timothy.close@ucr.edu
Seq primer: T3.

FEATURES	Location/Qualifiers
source	1. .788

```
/organism="Citrus sinensis"  
/mol_type="mRNA"
```

```
/cultivar="Washington Navel"
/db_xref="taxon:2711"
/1="200001 00 000"
```

```

/clone="UCRCS01_02a104"
/tissue_type="Rind containi
/feature="Mature fruit"

```

```
/dev_stage=matrice_l1ulc
/lab_host="E. coli TJC121"
/clone_lib="Washington Navya
```

```

/clone_id="hahhngcon.nave
flavado & albedo cdna libra
/nota="Vector: lambda phi+2

```

```

/Note: vector: Lambda unit 2
Site_1: EcORI; Site_2: XhoI
field at University of Cali

```

Operations since 1983. The orange and the rootstock Ca

mature fruit was harvested at mid-day in January 2002

during a cold spell, when pre-dawn temperatures were approximately -2 to 2 degree C. Approximately 2 cm median sections of the rind were excised in the field from several fruits, then wrapped in aluminum foil and frozen quickly in dry ice. Total RNA was extracted using a phenol extraction procedure described in J. Japanese Soc. Hort. Sci. (1996) 64:809-814. Poly(A) RNA was purified, a cDNA library was made, and 1 million primary lambda cDNA clones were in vivo excised to give a population of plasmid SK(-) phagemids. All steps to this point were performed in the TJ Close lab at the University of California, Riverside (Renton). Phagemids were placed, plasmid DNA purified, cDNA clones archived, and DNA sequences determined bi-directionally using an ABI3130 at the Arizona Genomics Institute, University of Arizona (Collura, Feuerbacher, Kim, Kudrna, Ming, Yu). Chromatogram files were transmitted to UC Riverside (by Yu), then processed at UC Riverside (by Wamamaker) using the HarVest pipeline (<http://harvest.ucr.edu>) to remove vector and cloning oligo sequences and various contaminants, and to trim to a high quality region. Sequences that retained a phred 17 region of at least 100 bases were deposited to Genbank."

BASE COUNT 202 a 199 c 186 g 201 t
ORIGIN
Alignment Scores:
Pred. No.: 1.3e-92 Length: 788
Score: 1097.50 Matches: 197
Percent Similarity: 90.30% Conservative: 17
Best Local Similarity: 83.12% Mismatches: 22
Query Match: 78.73% Indels: 1
DB: 14 Gaps: 1

US-09-383-579C-10 (1-250) x CB290960 (1-788)

Qy 1 MetAlaPheSerTyRserProPheSerSerleuPheleuPheProPhePheValPhe 20
Db 76 ATTGCACATCATCTACGCTGCTCTCTTTGTTTGCTCAATTTCCTTCGTGAC 135
Qy 21 ThrPheAlaAspTyR---GlyGlyTTPGlnSerGlyHisAlaThrPheTyRGlYglYglY 39
Db 136 ACATTTCGAGACTATGGTGGTGGGCGCAAGTGGCATGCACTTTCATGGCGGGGT 195
Qy 40 AspAlaSerGlyThrMetGlyGlyAlaCyeglyTyRGlYAsnLeuTyRserGlnGlyTYR 59
Db 196 GATGCTTCGGGCAATGGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 255
Qy 60 GlyThrAsnThrValAlaLeuSerThrAlaLeuPheAsnAnglyLeuSerCyeglyAla 79
Db 256 GGGACTAACACTGACGACTTACCGCTTATTCATCAATGGCTTACCTGATGATCA 315
Qy 80 CysPheGlnMetThrCysThrAsnAspProlyserTyRProGlyThrIleAsnVal 99
Db 316 TGCATGAAATGAAATGAAATGAAATGAAATGAAATGAAATGAAATGAAATGAAATG 375
Qy 100 ThrAlaThrAsnPheCysProProAsnPheAlaLeuProAsnAsnAnglyGlyTYR 119
Db 376 ACCGCCACCACTTCTGCCACCTTACCTTCTCTCTCTCTCTCTCTCTCTCTCTCT 435
Qy 120 AsnProProLeuGlnHisPheAspMetAlaGlnProAlaPheLeuGlnIleAlaGlnTYR 139
Db 436 AATCTCTCCCTCCGACGACTTGAATGAGTGGAGCCGCTTCTTCAAAATGGCCATAC 495
Qy 140 ArgAlaGlyIleValProValSerPheArgValProCysMetIleValGlyVal 159
Db 496 CGGCGCGGCAATCGCCCAATTCCTTCAGAGAGATCCCGTGTCCCAAGAAAGAGAGATA 555
Qy 160 ArgPheThrIleAsnGlyHisSerTyRPhaAsnLeuValLeuIleThrAsnValGlyGly 179
Db 556 AGGTTTACCTCATATGACACTCATCTGTTTGGTCAAAATGTCGAGAGA 615
Qy 180 AlAGlyAspValHisSerValSerIleGlySerArgThrGlyTYRProMetSer 199

Db 616 GCACGAGATGATACATTGATCATCATCAAGGTTCAAGACTGGATGGCAGCATGTCA 675
Qy 200 ArgAsnTyRGlYAsnGlnSerAsnAsnTyRleuAsnGlyGlnGlyLeuSerPhe 219
Db 676 AGGACTGGGGCCAAATGGCAGACAACTTCTTAAAGCCCAAGCTTTCTTTC 735
Qy 220 GlnValThrLeuSerAspGlyArgThrLeuThrAlaTyRAsnLeuValPro 236
Db 736 CAAGTGAACGACGATGACGCGACGACTGTACTAGCAACAATCTTGCTCT 786

RESULT 10
BI932999
LOCUS
DEFINITION
B1932999.1 GI:16247471
KEYWORDS
SOURCE
ORGANISM
Lycopersicon esculentum (tomato)
Lycopersicon esculentum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids; lamiales; Solanales; Solanaceae; Solanum; Lycopersicon.

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
Contact: CUGI
Clemson University Genomics Institute
100 Jordan Hall, Clemson, SC 29634, USA
Email: <http://www.genome.clemson.edu/orders/index.html>
This clone is available through the Clemson University Genomics Institute
Seq primer: T3.

FEATURES
source
Location/Qualifiers
1..767
/organism="Lycopersicon esculentum"
/mol_type="mRNA"
/cultivar="TA946"
/db_xref="taxon:4081"
/clone="CTOC24J22"
/tissue_type="flower"
/dev_stage="buds 8mm to preanthesis"
/note="Vector: pBluescript SK(-); Site 1: EcoRI; Site 2: XhoI; supplier: Cornell University; sequencing: The Institute for Genomic Research; flower buds and flowers were taken from greenhouse plants (4-8 wks old, TA946). They were immediately frozen in liquid nitrogen and then size-separated while remaining frozen."

BASE COUNT 215 a 144 c 168 g 240 t
ORIGIN

Alignment Scores:
Pred. No.: 4.43e-91 Length: 767
Score: 1081.00 Matches: 188
Percent Similarity: 88.94% Conservative: 21
Best Local Similarity: 80.00% Mismatches: 26
Query Match: 77.55% Indels: 0
DB: 12 Gaps: 0

US-09-383-579C-10 (1-250) x B1932999 (1-767)

Qy 16 PhePhePheValPheThrPheAlaAspTyRGlYglYTPGlnSerGlyHisAlaThrPhe 35
Db 5 TTTGCTTCTTATTTCTTCTTCTGATTAAGAGATGGCAACTCTCTCATGCACTTTC 64
Qy 36 TYRGlYglYglYAspAlaSerGlyThrMetGlyGlyAlaCyeglyTyRGlYAsnLeuTYR 55

```

Db      65 TATGAGAGGGGGTGCATCCCTCTGCGACAAATGGGGGGTCTTGGAATGAAATTTGTA 124
Qy      56 SerGinglyTYrGlyThraSerThraValAlaLeuSerThraAlaLeuPheAsnAnglyLeu 75
Db      125 ACCCAAGGGGTATGGAACCTAACGACGACGACTAAGTACGACTATTCAACATGGTTTA 184
Qy      76 SerCyGlyAlaCyPheGluMetThrCySerThraAspProLysTrpCySerProGly 95
Db      185 ACTTGCGGTGGCTGTATATAGCTCACTTCCAAACAAAGCAGCTCAATGGTGTCTCCAAAGG 244
Qy      96 ThrIleArgValThraIleThraPheCysProProAsnPheAlaLeuProAsnAsn 115
Db      245 ACTATTACTGCTACGTCGCACTAATTTTGTCTCCGAAACCGCTCTACTTAAACATAAT 304
Qy      116 GtGlyTYrCyAsnProProLeuGlnHisPheAspMetAlaGluProAlaPheLeuGln 135
Db      305 GGTGGTGGTGGCAATCTCTCTCCCAACATTTGATTGACAACTCTCTTCTTGCA 364
Qy      136 IleAlaGlnTrpArgAlaGlyIleValProValSerPheArgValProCysMetLys 155
Db      365 ATTGCTAAATACAAACCCGGTATCGTCTGTATCTTTGCAAGGGTGGCTGTATGACA 424
Qy      156 LysGlyGlyValArgPheThrIleAsnGlyHisSerTrpPheAsnLeuValLeuIleThr 175
Db      425 AAGAAGAGATTAAGGTTTACAGTAATGACACTCTTTTCACTTGCTTTTATGACACA 484
Qy      176 AsnValGlyIleAlaGlyAspValHisSerValSerIleLysGlySerArgThrGlyTrp 195
Db      485 AATGTTGAGGTGCTGCTGATATTCATCATGATTCAATTAAAGGGCTAATCTGATGAG 544
Qy      196 GlnSerMetSerArgAsnTrpGlyGlnAsnTrpGlnSerAsnAsnTrpLeuAsnGlyGln 215
Db      545 CAAGCATATGTCAAGATATTTGGGGCCAAATTTGGCAAAAGCAATTCATATATATGCTCAA 604
Qy      216 GlyLeuSerPheGlnValThrLeuSerAspGlyArgThrLeuThraIleValAsnLeuVal 235
Db      605 AGCTCTTCACTTCATGATCACCACAACTGATGAGAGACACTCATTTGCAACAAATGCTGCA 664
Qy      236 ProSerAsnTrpGlnPheGlyGlnTrpGlyGlyProGlnPhe 250
Db      665 CCAATATATTTGGCAATTTTGACAACTTTTGAAGGGGCTCAATTT 709

RESULT 11
CB822230      864 bp      mRNA      linear      EST 16-MAY-2003
LOCUS      CB822230
DEFINITION      EST 3081 Half-Ripe Apricot Fruit Lambda Zap II Library Prunus
ACCESSION      CB822230
VERSION      CB822230.1 GI:29956247
KEYWORDS      EST.
SOURCE      Prunus armeniaca (apricot)
ORGANISM      Prunus armeniaca
Eukaryote; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids
1. euroids I; Rosales; Rosaceae; Amygdaloideae; Prunus.
1. (bases 1 to 864)
Boucher, J.P. and Textier, N.
High Throughput Detection of Isoenes among 5724 3' EST from
Apricot Fruit (Prunus armeniaca)
Unpublished
Contact: Audergon JM
Unité de génétique et amélioration des fruits et légumes
Institut National de la Recherche Agronomique
Domaine Saint-Maurice BP 94 84143 Montfavet cedex
Tel: 00-33-(0)4-32-72-26-68
Fax: 00-33-(0)4-32-72-26-62
Email: audergon@avignon.inra.fr
Seq primer: T7.
Location/Qualifiers
1. 864
/organism="Prunus armeniaca"
/mol_type="mRNA"

```

```

/cultivar="Bergeron"
/db_xref="taxon:36596"
/clone="be005X06"
/dev_stage="Half-Ripe stage"
/clone_lib="Half-Ripe Apricot Fruit Lambda Zap II Library"
/note="Organ: Fruit; Vector: Lambda Zap II; Site 1: Eco RI
; Site 2: XhoI; Oriented library, construction described
in Molecular cloning and expression of a cDNA encoding
1-aminocyclopropane-1-carboxylate (ACC) oxidase from
apricot fruit (Prunus armeniaca cv. Bergeron) by
Mbeguile-Mbeguile D, Chahine H, Gomez RM, Gouble B, Audergon
JM, Souty M, Albagnac G, Fils-Lycaon B in Physiol Plant
105:294-303 1999"
BASE COUNT      215 a      209 c      200 g      238 t      2 others
ORIGIN
Alignment Scores:
Pred. No.:      9,58e-91      Length:      864
Score:      1078.00      Matches:      200
Percent Similarity:      88.14%      Conservative:      23
Best Local Similarity:      79.05%      Mismatches:      26
Query Match:      77.33%      Indels:      5
DB:      14      Gaps:      4
US-09-383-579c-10 (1-250) x CB822230 (1-864)
Qy      1 MetAlaPhe--SerTrpSerProPheSerSerLeuPhe--LeuLeuProPhePhe 18
Db      77 ATGGCTTTTACCTCACTACACTTACCCATTCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 136
Qy      19 ValPheThrPheAlaAspTrp--GtGlyTYrGlyGlnSerGlyHisAlaIleThrPheTrpGly 37
Db      137 CAAGCACTTATGATGACATGAGAGATGGAAGGTGATGACATGATTTATGAT 196
Qy      38 GtGlyAspAlaSerGlyThrMetGlyIleAlaCysGlyTYrGlyAsnLeuTrpSerGln 57
Db      197 GGGGGTGAAGCTCTGGGACCATGGAGAGGTGCTTGATGATGAAATTTATAGCCAA 256
Qy      58 GtTYrGlyTYrAsnThrValAlaLeuSerThrAlaLeuPheAsnAnglyLeuSerCys 77
Db      257 GGGTATGGAACCAACACTGACCTCTCAAGCAGCTGTGTTCAACGATGGCTTGAGCTGT 316
Qy      78 GlyAlaCyPheGluMetThrCysThrAsnAspProLysTrpCysLeuProGlyThrIle 97
Db      317 GGGCTCTGTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 376
Qy      98 ArgValThraIleThraPheCysProProAsnPheAlaLeuProAsnAnglyGly 117
Db      377 ATGTCACCTGCCAACAATCTTGCCCTCTTAAGTCACTGATGATGATGATGATGATGATGAT 436
Qy      118 TrpCyAsnProProLeuGlnHisPheAspMetAlaGluProAlaPheLeuGlnIleAla 137
Db      437 TGGTCAACCTCTCTCTCCAGCACTTGAATTTGGCTGACCTGCTCTTCAAAATTTGCT 496
Qy      138 GtTYrArgAlaGlyIleValProValSerPheArgValProCysMetLysGlyGly 157
Db      497 CAATCCAGGCTGGAAATTTCCCATCTCTTCAAGAGGTTTCTTGTTGAAAAAGGA 556
Qy      158 GlyValArgPheThrIleAsnGlyHisSerTrpPheAsnLeuValLeuIleThrAsnVal 177
Db      557 GGGATTAAGTTCAACATCAACGCTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCA 616
Qy      178 GtGlyAlaGlyAspValHisSerValSerIleLysGlySerArgThrGlyTrpGlnSer 197
Db      617 GGAGGTGCGAGGGATGTGCACTCTGTTCAATCAAGGGGTCCAAACAGGGTGGCAAGCC 676
Qy      198 MetSerArgAsnTrpGlyGlnAsnTrpGlnSerAsnAsnTrpLeuAsnGlyGlnGlyLeu 217
Db      677 ATGTCAAGGAACCTGGGGCCAGAACTGGGACAGTAACTTCTTACTCTCAATGCGCAGCTCTTA 736
Qy      218 SerPheGlnValThrLeuSerAspGlyArgThrLeuThraIleValAsnLeuValProSer 237
Db      737 TC-TTTCAAGTCAACCAACGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 792

```

```

Oy      238 Aaattgpcglnphaglyglnthrtgctglnu1gproginpne 250
LOCUS   CD484188
DEFINITION
ACCESSION   CD484188
VERSION     CD484188.1
KEYWORDS    5', mRNA sequence.
SOURCE      EST.
ORGANISM    Amborella trichopoda
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; stem Magnoliophyta; Amborellaceae;
            Amborella.
REFERENCE   1 (bases 1 to 681)
            depamphilis,C., Solits,D., Solits,P., Farmerie,W., Ma,H., Tankeley
            ,S., Leebens-Mack,J., Field,D., Buzgo,M., Kim,S., Ilut,D., Landherr
            ,L., Hu,Y., Mall,K., Albert V., Carlson,J., Doyle,J., Frohlich,M.,
            Miller,W., Openheimer,D. and Theissen,G.,
            Generation of ESTs from early flower buds of Amborella trichopoda
            Unpublished
TITLE       JOURNAL
COMMENT     Contact: Claude depamphilis or James Leebens-Mack
            Mueller Laboratory
            Penn State University
            208 Mueller Laboratory, Department of Biology, ATTN Rm212, Penn
            State University, University Park, PA 16802, USA
            Tel: 814 863 6133
            Fax: 814 865 9131
            Email: cwd3@psu.edu or jh110@psu.edu
            The sequence provided is trimmed of vector and low quality regions.
            Full sequence and original trace file are available from the Plant
            Genome Network website (http://pgn.cornell.edu)
            Name: atr01-4ms1 row: d column: 02
            Seq primer: M13P.

FEATURES             Location/Qualifiers
     source            1..681
                     /organism="Amborella trichopoda"
                     /mol_type="mRNA"
                     /db_xref="taxon:13333"
                     /clone="atr01-4ms1-d02"
                     /tissue_type="flower buds"
                     /dev_stage="c=2.5mm buds"
                     /lab_host="SOLR"
                     /clone_id="Atr01"
                     /note="Vector: pBluescript SK (+/-); Site 1: EcoRI;
                     Site 2: XhoI; Amborella trichopoda Ball1. This library was
                     made from male flowers only. Only floral buds with
                     diameter of 2.5 mm or less were used for RNA isolation.
                     This is a directionally cloned, non-normalized library.
                     Avg. insert length: 1611; Primers: M13F and M13R;
                     Antibiotic: 50 ug/ml Ampicillin; Primary Titer: 2.24E6 pfu
                     total; Amplified Titer: 1.37E10 pfu/ml; Mass Excised
                     Titer: 3.53E9 total; This library has been generated by
                     the Floral Genome Project (FGP). We would like to thank
                     David Lorence at the National Tropical Botanical Garden
                     for providing plant material for library building. The
                     Floral Genome Project is funded by NSF's Plant Genome
                     Research Program (DBI-0115694). More information about the
                     project can be obtained at http://fgp.bio.psu.edu"

BASE COUNT      158 a      176 c      184 g      163 t
ORIGIN
Alignment Scores:
Pred. No.:      3.75e-90      Length:      681
Score:          1070.50      Matches:      188
Percent Similarity: 92.86%      Conservative: 20
Best Local Similarity: 83.93%      Mismatches:  15
Query Match:    76.79%      Indels:      2
DB:             14      Gaps:      1

```

	US-09-383-579C-10 (1.-250) x CD484188 (1.-681)
Oy	22 PheIlaAsprYrGylgYlTTPGIInSeGlyVhAlaThrPheTYrGylgYlVaSPAla 41
Db	9 TTTGGAGACATAT---GGATGGCACAGC-GGCCATGGCCATTATTAATGTGTGGTAGAAGCT 64
Oy	42 SerGlyThrMetGcYglYAlaCySGLYTYrGlyVAshNuTYrSerGlnGLTYrGlyYthr 61
Db	65 ACGGGGACTATGGGGGAGCATGTGGATATGGGAATCTGTRATGCCAAAGCTATGGCAGC 124
Oy	62 AsnThValAlaLeuSerThrAlaLeuPheaAsnAngLYleuSerCYsglyAlaCySphe 81
Db	125 AACACACAGAGCCCTGCAGCACTGCTCTCTTCACAAGATGGCTTGAGTTGTGGTCTGCTAT 184
Oy	82 GluMetThrcYsrThraAnaApproLYrTPCyLeuProGlyYthrILeaYValThThAla 101
Db	185 GAAATYGAGGTCAGCAATGAGCCCAAAGGTGGCTTCAGAGCTCATTTGTTGTACTGCA 244
Oy	102 ThrAsnPhcYSPrOPrOAnPhPeAlLeuProAsnaAnaNgLYglYTrPCyAsnPro 121
Db	245 ACCAATTTCTGCCCCCAAATTTGGGTTGTTCATAATGACAATGCTGTGGTGCACACC 304
Oy	122 ProLeuGlnHisPheaPmeValagLuprOAlaPheLeuGlnIleaIgINTyrArgAla 141
Db	305 CCTCTGCACAATTTTGACCTTGCTGGAACCTGCTTCCTGCAAAATGCTCAGTACAGGACT 364
Oy	142 GlyIleValProValSerPheaArgArgValProCYsmetLYsbGylgYlValArgPhe 161
Db	365 GGAATYTGTGCTTGAGGCTTTAGAAGATACCTGTGTGAAGAAAGGTGGAATAGGTTTC 424
Oy	162 ThrILeaNglYHISerTYrPheaAsnLeuValLeuILEThraenValIGLYAlaGLY 181
Db	425 ACCATCAATGGCCACTCTCTCACTTCACTTGTGTCTCACTAATGTAAGTGGGCGCGT 484
Oy	182 AspValHisserValSerILEgLYSerArgThrgLYTrPGInserMetSerArgasn 201
Db	485 GACATCCACGCGCGTGCATCAAGGATCCAAACGGTGGATGGCAGCCATGTCCAGAGAAC 544
Oy	202 TrPGLYglInentTPGINserAsnaAntYtleuanGLYglnGLYleuSerPheGlnVal 221
Db	545 TGGGGCCAAAATCGGCAGACCAATCTCTACTCTCATATGCGCAGACCTCTCTTCCAAGTA 604
Oy	222 ThreUsSerAPGlyArGTnrLeuThralATyrAsnLeuValProSerAentRPGInPhe 241
Db	605 ACCACCAAGTACGGCCCGCACCGTCAACAAGTTACACACTTGGCCTTCCAATGGCAGTTT 664
Oy	242 GLYglnThrTYr 245
Db	665 GGCCAAACTTTC 676
RESULT_13	
LOCUS	BE131139
DEFINITION	148-1090703 Ice plant lambda Uni-Zap XR expression library, 48 hours
SOURCE	NCl treatment Mesembryanthemum crystallinum cDNA clone 148-1090
ACCESSION	BE131139
VERSION	BE131139.1 GI:8578502
KEYWORDS	EST.
ORGANISM	Mesembryanthemum crystallinum (common iceplant)
AUTHORS	Mesembryanthemum crystallinum
TITLE	Eukaryote; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
JOURNAL	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
COMMENT	Caryophyllales; Astrocaceae; Mesembryanthemum.
	1 (bases 1 to 815)
	Cushman, J.C.
	An expressed sequence tag database for the common ice plant,
	Mesembryanthemum crystallinum
	Unpublished
	Contact: Cushman JC
	Department of Biochemistry
	University of Nevada

Best Local Similarity: 87.32% Mismatches: 13.
 Query Match: 76.04% Indels: 0
 DB: 13 Gaps: 0

US-09-383-579C-10 (1-250) x BQ990398 (1-747)

QY 38 G|Y|G|Y|A|P|A|S|E|S|E|G|Y|T|H|T|H|E|G|Y|G|Y|A|A|C|Y|S|G|Y|T|Y|G|Y|A|N|L|E|U|T|Y|S|E|G|I|N| 57
 DB 32 GGGGGGAGTGCCTCAGACAACTAGGAGTGGTGGTCTTCCGATATGAGAAATTTGATATAGCA 91
 QY 58 G|Y|T|Y|G|Y|T|H|A|N|T|H|A|L|A|L|E|U|S|E|T|H|T|A|L|E|U|P|H|E|A|N|G|Y|L|E|U|S|E|C|Y|S| 77
 DB 92 GGATATGATCAACAACTGCGGCACTTACCTCTCTATTCATTAATGTTGAGTTGT 151
 QY 78 G|Y|A|A|C|Y|S|P|H|E|G|I|U|E|T|H|T|Y|S|H|A|N|A|P|P|O|L|Y|T|P|C|Y|S|L|E|U|P|O|G|Y|T|H|T|I|E| 97
 DB 152 GGGCTGTATATGAGATGAGATGAGATGAGACCAACCAATATGATCTTCCCTGTTCCATA 211
 QY 98 A|Y|G|A|T|H|A|T|H|A|N|P|H|E|C|Y|S|P|P|O|L|A|N|P|H|E|A|L|E|U|P|O|A|N|A|N|G|Y|G|Y| 117
 DB 212 ATGTATCTCAACCAATTTCTGTCTCACTTACCTGCTTGTCTTAAGATATGATGGG 271
 QY 118 T|Y|C|Y|A|N|P|P|O|L|E|U|G|I|N|H|S|P|H|E|A|P|M|E|T|A|G|I|U|P|O|A|P|H|E|U|G|I|N|I|A|L|A| 137
 DB 272 TGGTCAACCTCCCTCTCAACATTTGACCTGCTGAGCCTGCTTCTTCAATATGCA 331
 QY 138 G|I|T|Y|A|G|A|G|Y|I|E|V|A|P|R|O|V|A|S|E|P|H|E|A|G|Y|A|P|P|O|C|Y|S|M|E|T|Y|S|G|Y| 157
 DB 332 CAAATATGAGCTGAAATTTGATCTGCTGCTATTTCAAGAGTCCCTTGTATGAGAAAGGA 391
 QY 158 G|Y|V|A|A|G|P|H|E|T|H|I|E|A|N|G|Y|H|S|E|T|Y|P|H|E|A|N|L|E|U|L|E|T|H|A|N|V|A| 177
 DB 392 GGGTAAAGTTACTATAATGAGCATTTGATTTCAACTTGGTTTGGATCACAAGCTT 451
 QY 178 G|Y|G|Y|A|A|G|Y|A|P|V|H|S|E|S|E|V|A|S|E|T|I|E|Y|S|G|Y|S|E|A|G|T|H|T|Y|T|P|G|I|N|S|E|R| 197
 DB 452 GGGAGTCCAGGGAGTGCACCTCGTATCAATCAAGGTCGAAAGCGGGTGGCAACC 511
 QY 198 M|E|S|E|A|R|A|N|T|P|G|Y|G|I|N|A|N|T|P|G|I|N|S|E|A|N|T|Y|L|E|U|A|N|G|Y|G|I|N|Y|L|E|U| 217
 DB 512 ATGTCAAGAACTGGGGGCAAACTGGCAAGCACTATCTTAACGGAAGTCTT 571
 QY 218 S|E|P|H|E|G|I|N|A|T|H|L|E|U|S|E|A|S|P|G|Y|A|G|T|H|L|E|U|T|H|A|T|Y|A|N|L|E|U|A|P|P|O|S|E|R| 237
 DB 572 TCTTTCAAGTCAACAAGTACGGAAGCATCAAGCTTATATGGCGCACCTCA 631
 QY 238 A|N|T|P|G|I|N|P|H|E|G|Y|G|I|N|T|Y|G|I|N|Y|P|G|I|N|P|H|E| 250
 DB 632 AACTGGCAATTTGGTCAACATTTCAAGGGGCTCAATTT 670

RESULT 15
 BU815493 685 bp mRNA linear EST 15-OCT-2002

LOCUS
 NO42011 Populus bark cDNA library Populus tremula x Populus
 tremuloides cDNA 5 prime, mRNA sequence.

ACCESSION
 BU815493

VERSION
 BU815493.1 GI:23974490

KEYWORDS
 EST.

SOURCE
 Populus tremula x Populus tremuloides

ORGANISM
 Populus tremula x Populus tremuloides
 Eukaryotes; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids
 1 (bases 1 to 685)

REFERENCE
 Umeberg, P., Bhalerao, R.R., Jansson, S. and Sterky, F.
 The Poplar tree transcriptome: Analysis of expressed sequence tags
 from multiple libraries

JOURNAL
 Unpublished

COMMENT
 Contact: BHALLERAO RUPALI R.
 Umea Plant Science Center
 Department of Plant Physiology
 University of Umea, 901 87 Umea, Sweden
 Tel: +46 90 786 5279

Fax: +46 90 786 6676
 Email: rupali.bhalerao@plantphys.uu.se.
 Location/Qualifiers

FEATURES

source

1..685

/organism="Populus tremula x Populus tremuloides"

/mol_type="mRNA"

/db_xref="taxon:47664"

/tissue_type="bark"

/clone_lib="Populus bark cDNA library"

BASE COUNT 155 a 172 c 180 g 178 t

ALIGNMENT SCORES:

Score: 4,49e-89 Length: 685
 Percent Similarity: 1059.00 Matches: 181
 Best Local Similarity: 81.17% Conserved: 20
 Query Match: 75.97% Mismatches: 22
 DB: 13 Indels: 0
 Gaps: 0

US-09-383-579C-10 (1-250) x BU815493 (1-685)

QY 28 T|Y|C|Y|A|N|P|P|O|L|E|U|G|I|N|H|S|A|T|H|P|H|E|T|Y|G|Y|G|Y|A|P|A|S|E|G|Y|T|H|T|H|E|G|Y| 47
 DB 3 TGGATTAATGCTCATGCAACATTTCTACGAGGTGATGATCTTGGCACAATGGTGT 62
 QY 48 A|L|C|Y|G|Y|T|Y|C|Y|A|N|L|E|U|T|Y|S|E|G|I|N|Y|T|Y|G|Y|T|H|A|N|T|H|A|L|A|L|E|U|S|E| 67
 DB 63 GCTTGGGTATGAGAACTGTGACAGCCAGGGGTAGCGTAATATCTGAGCTTTAAGC 122
 QY 68 T|H|A|L|E|U|P|H|E|A|N|G|Y|L|E|U|S|E|S|E|V|A|S|E|T|Y|A|A|C|Y|S|P|H|E|G|I|U|E|T|H|T|Y|S|H|A|N| 87
 DB 123 ACAAGCTCTGTTCAACACGGGTTAACTGATCTTCTTGAATCAGATGCGTGAAT 182
 QY 88 A|S|P|P|O|L|Y|T|P|C|Y|S|L|E|U|P|O|G|Y|T|H|I|E|A|N|G|Y|A|T|H|A|N|P|H|E|C|Y|S|P|P|O| 107
 DB 183 GACCCCAATATGAGGCTGCTGCTCATGATGATCAACCCCAATTTCTGCCCTCG 242
 QY 108 A|N|P|H|E|A|L|E|U|P|H|E|A|N|G|Y|G|Y|T|Y|T|P|C|Y|A|N|P|P|O|L|E|U|G|I|N|H|S|P|H|E|A|P| 127
 DB 243 AACAAATGCCCTGCTTCAACATGCGAGGGGTGTGTAATCTCTCAACACATTTGAT 302
 QY 128 M|E|A|G|I|U|P|R|O|A|L|H|E|U|G|I|N|I|E|A|G|I|T|Y|A|G|A|G|Y|I|E|V|A|P|R|O|V|A|S|E|R| 147
 DB 303 CTCTCCAGCTGTCTTCCACACATTTGCCATATAGACAGAAATTTGCTGTCT 362
 QY 148 P|H|E|A|G|Y|A|P|P|O|C|Y|S|M|E|T|Y|S|G|Y|G|Y|A|A|G|P|H|E|T|H|I|E|A|N|G|Y|H|S|E|S|E| 167
 DB 363 TACAGAAAGGTACCTGAGAGGAGGAGGATTAAGTTCAAGTCAACGGTCACTCC 422
 QY 168 T|Y|P|H|E|A|N|L|E|U|L|E|T|H|A|N|V|A|G|Y|G|Y|A|A|G|Y|A|P|V|H|S|E|S|E|V|A|S|E|R| 187
 DB 423 TACTTCAATCTAGTCTGATCACTTAACGTTGGGGTGTGTATGATCTTGTGTCTG 482
 QY 188 I|L|E|Y|G|I|S|E|A|R|T|H|G|Y|T|P|G|I|N|S|E|T|S|E|A|N|T|P|G|Y|G|I|N|A|N|T|P|G|I|N| 207
 DB 483 ATCAAGGGGTCCAGACTGCTTGGACCAATCTCAAGAACTGGGGCAAAATTTGGCAG 542
 QY 208 S|E|A|N|A|N|T|Y|L|E|U|A|N|G|Y|G|I|N|Y|L|E|U|S|E|P|H|E|G|I|N|A|T|H|L|E|U|S|E|A|S|P|G|Y|A|G| 227
 DB 543 AGCAACACATATCTCAATGAGCAAAATCTTTTAAAGTCAACCAAGTATGGTGA 602
 QY 228 T|H|L|E|U|T|H|A|T|Y|A|N|L|E|U|A|P|P|O|S|E|A|N|T|P|G|I|N|P|H|E|G|Y|G|I|N|T|Y|G|Y|G|Y| 247
 DB 603 ACCGTGTCTTCAATATGTTCTCTTGAAGTGTCTTGGCGAGACCTTCTCGCG 662
 QY 248 P|R|O|G|I|N|P|H|E| 250
 DB 663 GCCCAATTT 671

Search completed: December 19, 2003, 01:02:44
 Job time : 2053 secs

